

Haddad, M  
10/6/9323 Page 1  
Seq ID 1#4-6

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OM protein - protein search, using sw model

Run on: January 20, 2006, 17:33:55 ; Search time 116.923 Seconds  
(without alignments)  
300.628 Million cell updates/sec

Title: US-10-619-323-1\_COPY\_113\_192  
Perfect score: 80  
Sequence: 1 HKDEVIKEVQEFYKDTYNKL.....LETFTVKSCPAIKEVFNK 80

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

- Database : A\_Geneseq\_21.\*
- 1: Geneseq1980s.\*
  - 2: Geneseq1990s.\*
  - 3: Geneseq2000s.\*
  - 4: Geneseq2001s.\*
  - 5: Geneseq2002s.\*
  - 6: Geneseq2003as.\*
  - 7: Geneseq2003bs.\*
  - 8: Geneseq2004s.\*
  - 9: Geneseq2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query %	Length	ID	Description
1	80	100.0	227	2	AAR86834	Aar86834 Human CD9
2	80	100.0	227	5	ABR78366	Abbr78366 Human aci
3	80	100.0	227	5	AAE14636	Aae14636 Human CD9
4	80	100.0	227	6	ABU05057	Abu05057 Human exp
5	80	100.0	227	6	ABU05060	Abu05060 Human exp
6	80	100.0	227	7	ABW00436	Abw00436 Human CD9
7	80	100.0	227	7	ADK69862	Adk69862 Human CD9
8	80	100.0	227	8	ADL19366	Adl19366 Human CD9
9	80	100.0	227	9	AEA89005	Aea89005 Human CD9
10	80	100.0	228	2	AAK27525	Aak27525 Metabtaei
11	80	100.0	228	4	ABB44581	Abb44581 Human wou
12	80	100.0	228	6	ABU05059	Abu05059 Human exp
13	80	100.0	228	6	ABU05052	Abu05052 Human exp
14	80	100.0	228	6	ABU05048	Abu05048 Human exp
15	80	100.0	228	6	ABU05056	Abu05056 Human exp
16	80	100.0	228	6	ABU05049	Abu05049 Human exp
17	80	100.0	228	6	ABU05050	Abu05050 Human exp
18	80	100.0	228	6	ABU05053	Abu05053 Human exp
19	80	100.0	228	7	ABW01519	Abw01519 Protein #
20	80	100.0	228	7	ADD89037	Add89037 TAT278. 1
21	80	100.0	228	7	ADG32002	Adg32002 Human hom
22	80	100.0	228	8	ADJ57558	Adj57558 Human CD9
23	80	100.0	228	8	ADL26782	Adl26782 Human CD9
24	80	100.0	228	8	ADL82853	Adl82853 Human PRO

25	80	100.0	225	8	ADP23088	Adp23088 PRO polyp
26	80	100.0	228	8	ADR73450	Adr73450 Human CD9
27	80	100.0	228	8	ADV70263	Adv70263 Tumor-agg
28	80	100.0	228	9	ADY97163	Ady97163 Human CD9
29	80	100.0	228	9	ADY19604	Ady19604 PRO polyp
30	80	100.0	228	9	ADY14362	Ady14362 PRO polyp
31	80	100.0	228	9	AEb98450	Aeb98450 Human CD9
32	80	100.0	228	9	AEb84396	Aeb84396 Human can
33	80	100.0	275	3	AAg75156	Aag75156 Human col
34	80	100.0	275	6	ABU05055	Abu05055 Human exp
35	80	100.0	275	6	ABU05054	Abu05054 Human exp
36	47	58.8	79	2	AAW35851	Aaw35851 Human CD9
37	47	58.8	79	6	ABU05058	Abu05058 Human exp
38	43	53.8	454	4	ABG14067	Abg14067 Novel hum
39	40	50.0	209	4	AAg76051	Aag76051 Human col
40	38	47.5	38	8	ADJ57561	Adj57561 Human CD9
41	32	40.0	80	6	ABP76310	Abp76310 Human GEN
42	30	37.5	30	6	ABU05051	Abu05051 Human exp
43	25	31.2	25	8	ADJ57562	Adj57562 Human CD9
44	22	27.5	22	8	ADJ57564	Adj57564 Human CD9
45	22	27.5	24	8	ADJ57578	Adj57578 Human CD9
46	18	22.5	18	8	ADJ57563	Adj57563 Human CD9
47	15	18.8	226	7	ADB85281	Adb85281 Rat G9 su
48	13	16.2	226	4	ABB44580	Abb44580 Mouse wou
49	13	16.2	226	5	ABB57234	Abb57234 Mouse isc
50	13	16.2	226	9	ADV25799	Adv25799 Mouse CD9
51	13	16.2	226	9	AEA55045	Aea55045 Mouse CD9
52	10	12.5	10	6	ABU03385	Abu03385 Human exp
53	8	10.0	33	5	ABP43064	Abp43064 Human ova
54	8	10.0	303	5	ABP40370	Abp40370 Staphyloc
55	8	10.0	303	8	ADS04987	Ads04987 Staphyloc
56	7	8.8	58	5	ABU51670	Abu51670 Helicobac
57	7	8.8	100	2	AAW25679	Aaw25679 Soybean c
58	7	8.8	100	3	AAg40684	Aag40684 Zea maye
59	7	8.8	103	9	ADZ22202	Adz22202 Full leng
60	7	8.8	246	8	ADK67412	Adk67412 Plant ful
61	7	8.8	321	7	ABO77257	Abu77257 Pseudomon
62	7	8.8	516	4	AAU35716	Aau35716 Helicobac
63	7	8.8	516	6	ABU30739	Abu30739 Protein e
64	7	8.8	589	6	ADA35614	Ada35614 Acinetoba
65	7	8.8	608	6	ABR40692	Abbr40692 Zea maye
66	7	8.8	679	8	ADK66425	Adk66425 Plant ful
67	7	8.8	770	7	ABO78119	Abu78119 Pseudomon
68	7	8.8	781	7	ABO80180	Abu80180 Pseudomon
69	7	8.8	827	8	ADY07562	Ady07562 Plant ful
70	7	8.8	855	8	ADS21025	Ads21025 Bacterial
71	7	8.8	1020	6	ABU30092	Abu30092 Protein e
72	7	8.8	1104	7	ABR82748	Abrr82748 Cold- and
73	7	8.8	1104	7	ADG32553	Adg32553 Murine TR
74	7	8.8	1140	4	ABB64675	Abb64675 Drosophill
75	7	8.8	1196	4	ADC94317	Adc94317 E. faecili
76	7	8.8	2444	4	ABB71807	Abb71807 Drosophill
77	6	7.5	9	6	ABR67406	Abbr67406 Human pro
78	6	7.5	16	2	AAW31082	Aaw31082 Muguwort p
79	6	7.5	18	9	ADV67376	Adv67376 Amino aci
80	6	7.5	20	8	ADI95249	Adi95249 OSPF-rela
81	6	7.5	20	8	ADI95250	Adi95250 OSPF-rela
82	6	7.5	25	9	ADY28634	Ady28634 Novel mod
83	6	7.5	25	9	ADY28635	Ady28635 Novel mod
84	6	7.5	29	7	ADG14386	Adg14386 Cytochrom
85	6	7.5	31	7	ADD49210	Add49210 Human HMG
86	6	7.5	33	6	ABJ18835	Abj18835 Human Bcl
87	6	7.5	37	7	ADJ13922	Adj13922 Human end
88	6	7.5	42	3	AAg55485	Aag55485 Arabidops
89	6	7.5	43	5	AAO15500	Aao15500 Porphyra
90	6	7.5	62	5	ABP26527	Abp26527 Streptoco
91	6	7.5	62	8	ABO58008	Abu58008 Human gen
92	6	7.5	66	5	AAO15501	Aao15501 Porphyra
93	6	7.5	68	2	AAW98521	Aaw98521 H. pylori
94	6	7.5	69	2	AAJ39395	Aaj39395 Mutant Sh
95	6	7.5	69	2	AAJ43002	Aaj43002 Mutant Sh
96	6	7.5	71	7	ADF14031	Adf14031 Human end
97	6	7.5	72	4	AAW83932	Aaw83932 Human imm

98	6	7.5	72	4	ABG07225	Abg07225 Novel hum	171	6	7.5	123	4	AAO12084	Aao12084 Human pol
99	6	7.5	73	6	ABM73013	Abm73013 Staphyloc	172	6	7.5	125	4	AAU30896	Aau30896 Novel hum
100	6	7.5	74	5	ABM66173	Abm66173 Human imm	173	6	7.5	125	8	ADJ49997	Adj49997 Oil-assoc
101	6	7.5	74	5	ABP00618	Abp00618 Human ORF	174	6	7.5	125	8	ADJ49693	Adj49693 Oil-assoc
102	6	7.5	75	7	ABO66297	AbO66297 Klebsiell	175	6	7.5	126	8	ADJ49738	Adj49738 Oil-assoc
103	6	7.5	76	7	ADC94793	Adc94793 E. faeciu	176	6	7.5	127	8	ADP30103	Adp30103 Human sec
104	6	7.5	78	8	ADX74566	Adx74566 Plant ful	177	6	7.5	129	7	ADC00424	Adc00424 Enterohae
105	6	7.5	78	8	ADX74707	Adx74707 Plant ful	178	6	7.5	130	3	AG221210	Ag221210 Arabidops
106	6	7.5	81	7	ADD49202	Add49202 Human HMG	179	6	7.5	137	3	AB38546	Ab38546 Human sec
107	6	7.5	85	5	AAO15498	Aao15498 Porphyra	180	6	7.5	141	9	ADY17158	Ady17158 PRO polyph
108	6	7.5	85	7	ADG14378	Adg14378 Cytochrom	181	6	7.5	143	4	RAB50141	Rab50141 Human bra
109	6	7.5	88	3	AG211211	Ag211211 Arabidops	182	6	7.5	143	4	AAO10767	Aao10767 Human pol
110	6	7.5	88	7	ADD49206	Add49206 Human HMG	183	6	7.5	143	5	ABP00599	Abp00599 Human ORF
111	6	7.5	90	3	AB281899	Ab281899 Human HMG	184	6	7.5	144	6	ABP99886	Abp99886 Breast sp
112	6	7.5	90	4	ABG26793	Abg26793 Novel hum	185	6	7.5	144	7	ADC00619	Adc00619 Enterohae
113	6	7.5	90	5	AAO18887	Aao18887 Human ova	186	6	7.5	144	8	ADF85949	Adf85949 Human bre
114	6	7.5	90	7	ABU54863	Abu54863 Human ova	187	6	7.5	144	8	ADR94685	Adr94685 Novel S.
115	6	7.5	90	7	ADD49207	Add49207 Human HMG	188	6	7.5	144	9	AEA58555	Aea58555 Streptoco
116	6	7.5	90	8	ADO31118	Ado31118 N-end rul	189	6	7.5	146	4	AAU03698	Aau03698 Group B S
117	6	7.5	90	8	ADO31119	Ado31119 N-end rul	190	6	7.5	147	9	AEA28577	Aea28577 Strees co
118	6	7.5	90	8	ADP30101	Adp30101 Human sec	191	6	7.5	149	8	ADP99119	Adp99119 C. albica
119	6	7.5	90	8	ABM80042	Abm80042 Tumour-as	192	6	7.5	151	6	ABG74905	Abg74905 Human epi
120	6	7.5	90	8	ABM81597	Abm81597 Tumour-as	193	6	7.5	152	7	ADC00817	Adc00817 Enterohae
121	6	7.5	90	8	ABM80446	Abm80446 Tumour-as	194	6	7.5	153	4	AAU52790	Aau52790 Propionib
122	6	7.5	90	8	ADV70076	Adv70076 HLP-3P21	195	6	7.5	153	6	ABM49309	Abm49309 Propionib
123	6	7.5	91	6	ABU21061	Abu21061 Protein e	196	6	7.5	156	9	ABM90952	Abm90952 M. xanthu
124	6	7.5	92	2	AAW25678	Aaw25678 Soybean c	197	6	7.5	159	9	ADX38816	Adx38816 Human can
125	6	7.5	92	4	AAU46197	Aau46197 Propionib	198	6	7.5	161	5	ABG93444	Abg93444 Ehrlichia
126	6	7.5	92	6	ABM42716	Abm42716 Propionib	199	6	7.5	161	5	AAU73241	Aau73241 Human gra
127	6	7.5	92	8	ABM80011	Abm80011 Tumour-as	200	6	7.5	164	8	ADK16925	Adk16925 Nancarcha
128	6	7.5	93	5	ABG61520	Abg61520 Iron upta	201	6	7.5	165	4	RAO04331	Rao04331 Human pol
129	6	7.5	93	6	ABU01464	Abu01464 S. pneumo	202	6	7.5	165	8	ADO00803	Ado00803 Human dom
130	6	7.5	96	8	ADK75074	Adk75074 Plant ful	203	6	7.5	166	5	ABP32211	Abp32211 Human ORF
131	6	7.5	97	9	ADZ22210	Adz22210 Full leng	204	6	7.5	167	4	AAU69483	Aau69483 Human pur
132	6	7.5	97	9	ADZ22200	Adz22200 Full leng	205	6	7.5	169	7	ADH85764	Adh85764 Enterococ
133	6	7.5	98	8	ADY24162	Ady24162 Plant ful	206	6	7.5	170	8	ADN99424	Adn99424 Novel hum
134	6	7.5	98	8	ADX73597	Adx73597 Plant ful	207	6	7.5	171	3	AG211209	Ag211209 Arabidops
135	6	7.5	98	8	ADX90899	Adx90899 Plant ful	208	6	7.5	173	3	AB16715	Ab16715 Bacteriop
136	6	7.5	98	9	ADM85981	Adm85981 Coffea ca	209	6	7.5	175	4	ABG23712	Abg23712 Novel hum
137	6	7.5	99	8	ADM75277	Adm75277 Plant ful	210	6	7.5	175	9	ADU40601	Adu40601 Novel hum
138	6	7.5	100	8	ADK47228	Adk47228 Streptoco	211	6	7.5	175	9	AEA20954	Aea20954 Novel hum
139	6	7.5	100	8	ABM81534	Abm81534 Tumour-as	212	6	7.5	180	3	AAV99663	Aav99663 Human GTP
140	6	7.5	101	7	ADC00724	Adc00724 Enterohae	213	6	7.5	180	7	AD140624	Ad140624 Human pur
141	6	7.5	101	8	ADX74479	Adx74479 Plant ful	214	6	7.5	181	4	AAE03650	Aae03650 Human ext
142	6	7.5	102	4	AAU42900	Aau42900 Propionib	215	6	7.5	183	6	ABU01866	Abu01866 S. pneumo
143	6	7.5	102	4	ABG26794	Abg26794 Novel hum	216	6	7.5	183	8	ADS43039	Ads43039 Bacterial
144	6	7.5	102	6	ABM39419	Abm39419 Propionib	217	6	7.5	186	7	ADB64005	Adb64005 Human pro
145	6	7.5	102	7	ADC00521	Adc00521 Enterohae	218	6	7.5	188	5	ABB50051	Abb50051 Listeria
146	6	7.5	103	4	ABG11216	Abg11216 Novel hum	219	6	7.5	188	6	ABM67739	Abm67739 Photorhab
147	6	7.5	103	8	ADX73610	Adx73610 Plant ful	220	6	7.5	192	8	ADM87685	Adm87685 Human EST
148	6	7.5	103	8	ADX77283	Adx77283 Plant ful	221	6	7.5	194	7	ABO63259	AbO63259 Klebsiell
149	6	7.5	104	4	ABG11523	Abg11523 Novel hum	222	6	7.5	195	6	ADB12771	Adb12771 Vigna ung
150	6	7.5	104	7	ADD01190	Add01190 Human nuc	223	6	7.5	196	7	ADF05019	Adf05019 Bacterial
151	6	7.5	104	8	ADK74802	Adk74802 Plant ful	224	6	7.5	201	7	ABM85631	Abm85631 Human pro
152	6	7.5	105	8	ADX92298	Adx92298 Plant ful	225	6	7.5	207	5	ABP39643	Abp39643 Staphyloc
153	6	7.5	105	9	ADM76459	Adm76459 Chestnut	226	6	7.5	207	8	ADS05706	Ads05706 Staphyloc
154	6	7.5	105	9	ADY52137	Ady52137 Phormiditu	227	6	7.5	207	9	ADX38835	Adx38835 Human can
155	6	7.5	106	4	AG237111	Ag237111 Novel hum	228	6	7.5	210	4	AAE04375	Aae04375 Mouse can
156	6	7.5	109	5	ABP41531	Abp41531 Human ova	229	6	7.5	211	8	ADX75631	Adx75631 Plant ful
157	6	7.5	109	7	ADC95978	Adc95978 E. faeciu	230	6	7.5	213	9	AEA43741	Aea43741 Perhydrol
158	6	7.5	110	3	AY65677	Ay65677 C. elega	231	6	7.5	213	9	AEA43753	Aea43753 Perhydrol
159	6	7.5	110	5	AAO15499	Aao15499 Porphyra	232	6	7.5	213	9	AEA43723	Aea43723 Perhydrol
160	6	7.5	111	9	ADX38815	Adx38815 Human can	233	6	7.5	213	9	AEA43168	Aea43168 Perhydrol
161	6	7.5	112	8	ADX92395	Adx92395 Plant ful	234	6	7.5	217	9	ADK40957	Adk40957 Novel hum
162	6	7.5	112	8	ADK76263	Adk76263 Plant ful	235	6	7.5	217	8	ADR15676	Adr15676 Kinase 63
163	6	7.5	113	4	ABG11212	Abg11212 Novel hum	236	6	7.5	221	4	AAE00187	Aae00187 Bacillus
164	6	7.5	113	6	ABM73551	Abm73551 Staphyloc	237	6	7.5	221	5	ABP27511	Abp27511 Streptoco
165	6	7.5	116	8	ABM81735	Abm81735 Tumour-as	238	6	7.5	221	8	ADV88430	Adv88430 Streptoco
166	6	7.5	118	6	ABU43101	Abu43101 Protein e	239	6	7.5	221	8	ADV79683	Adv79683 Streptoco
167	6	7.5	120	4	ABG07228	Abg07228 Novel hum	240	6	7.5	221	8	ADV81843	Adv81843 Streptoco
168	6	7.5	122	5	ABP39688	Abp39688 Staphyloc	241	6	7.5	222	2	AA14159	Aar14159 Serine pr
169	6	7.5	122	6	ABP77038	Abp77038 N. gonorr	242	6	7.5	222	2	AA26467	Aar26467 Sequence
170	6	7.5	122	8	ADS05804	AdS05804 Staphyloc	243	6	7.5	222	3	AA43799	Aab43799 Human can



244	6	7.5	222	4	Aae00039	Bacillus	317	6	7.5	222	4	Aae00037	Bacillus
245	6	7.5	222	4	Aae00076	Bacillus	318	6	7.5	222	4	Aae00088	Bacillus
246	6	7.5	222	4	Aae00107	Bacillus	319	6	7.5	222	4	Aae00092	Bacillus
247	6	7.5	222	4	Aae00181	Bacillus	320	6	7.5	222	4	Aae00128	Bacillus
248	6	7.5	222	4	Aae00067	Bacillus	321	6	7.5	222	4	Aae00136	Bacillus
249	6	7.5	222	4	Aae00072	Bacillus	322	6	7.5	222	4	Aae00154	Bacillus
250	6	7.5	222	4	Aae00074	Bacillus	323	6	7.5	222	4	Aae00158	Bacillus
251	6	7.5	222	4	Aae00079	Bacillus	324	6	7.5	222	4	Aae00165	Bacillus
252	6	7.5	222	4	Aae00156	Bacillus	325	6	7.5	222	4	Aae00175	Bacillus
253	6	7.5	222	4	Aae00160	Bacillus	326	6	7.5	222	4	Aae00205	Bacillus
254	6	7.5	222	4	Aae00161	Bacillus	327	6	7.5	222	4	Aae00095	Bacillus
255	6	7.5	222	4	Aae00179	Bacillus	328	6	7.5	222	4	Aae00106	Bacillus
256	6	7.5	222	4	Aae00048	Bacillus	329	6	7.5	222	4	Aae00123	Bacillus
257	6	7.5	222	4	Aae00065	Bacillus	330	6	7.5	222	4	Aae00127	Bacillus
258	6	7.5	222	4	Aae00068	Bacillus	331	6	7.5	222	4	Aae00140	Bacillus
259	6	7.5	222	4	Aae00082	Bacillus	332	6	7.5	222	4	Aae00169	Bacillus
260	6	7.5	222	4	Aae00084	Bacillus	333	6	7.5	222	4	Aae00180	Bacillus
261	6	7.5	222	4	Aae00090	Bacillus	334	6	7.5	222	4	Aae00183	Bacillus
262	6	7.5	222	4	Aae00094	Bacillus	335	6	7.5	222	4	Aae00184	Bacillus
263	6	7.5	222	4	Aae00098	B. lichen	336	6	7.5	222	4	Aae00043	Bacillus
264	6	7.5	222	4	Aae00118	Bacillus	337	6	7.5	222	4	Aae00120	Bacillus
265	6	7.5	222	4	Aae00124	Bacillus	338	6	7.5	222	4	Aae00163	Bacillus
266	6	7.5	222	4	Aae00125	Bacillus	339	6	7.5	222	4	Aae00185	Bacillus
267	6	7.5	222	4	Aae00126	Bacillus	340	6	7.5	222	4	Aae00041	Bacillus
268	6	7.5	222	4	Aae00177	Bacillus	341	6	7.5	222	4	Aae00089	Bacillus
269	6	7.5	222	4	Aae00031	Bacillus	342	6	7.5	222	4	Aae00099	B. lichen
270	6	7.5	222	4	Aae00036	Bacillus	343	6	7.5	222	4	Aae00111	Bacillus
271	6	7.5	222	4	Aae00042	Bacillus	344	6	7.5	222	4	Aae00142	Bacillus
272	6	7.5	222	4	Aae00062	Bacillus	345	6	7.5	222	4	Aae00162	Bacillus
273	6	7.5	222	4	Aae00066	Bacillus	346	6	7.5	222	4	Aae00206	Bacillus
274	6	7.5	222	4	Aae00077	Bacillus	347	6	7.5	222	4	Aae00035	Bacillus
275	6	7.5	222	4	Aae00080	Bacillus	348	6	7.5	222	4	Aae00056	Bacillus
276	6	7.5	222	4	Aae00081	Bacillus	349	6	7.5	222	4	Aae00061	Bacillus
277	6	7.5	222	4	Aae00086	Bacillus	350	6	7.5	222	4	Aae00071	Bacillus
278	6	7.5	222	4	Aae00097	B. lichen	351	6	7.5	222	4	Aae00087	Bacillus
279	6	7.5	222	4	Aae00102	Bacillus	352	6	7.5	222	4	Aae00101	Bacillus
280	6	7.5	222	4	Aae00166	Bacillus	353	6	7.5	222	4	Aae00134	Bacillus
281	6	7.5	222	4	Aae00168	Bacillus	354	6	7.5	222	4	Aae00052	Bacillus
282	6	7.5	222	4	Aae00176	Bacillus	355	6	7.5	222	4	Aae00057	Bacillus
283	6	7.5	222	4	Aae00058	Bacillus	356	6	7.5	222	4	Aae00063	Bacillus
284	6	7.5	222	4	Aae00060	Bacillus	357	6	7.5	222	4	Aae00069	Bacillus
285	6	7.5	222	4	Aae00093	Bacillus	358	6	7.5	222	4	Aae00070	Bacillus
286	6	7.5	222	4	Aae00103	Bacillus	359	6	7.5	222	4	Aae00109	Bacillus
287	6	7.5	222	4	Aae00164	Bacillus	360	6	7.5	222	4	Aae00188	Bacillus
288	6	7.5	222	4	Aae00167	Bacillus	361	6	7.5	222	4	Aae00040	Bacillus
289	6	7.5	222	4	Aae00173	Bacillus	362	6	7.5	222	4	Aae00047	Bacillus
290	6	7.5	222	4	Aae00174	Bacillus	363	6	7.5	222	4	Aae00050	Bacillus
291	6	7.5	222	4	Aae00038	Bacillus	364	6	7.5	222	4	Aae00114	Bacillus
292	6	7.5	222	4	Aae00055	Bacillus	365	6	7.5	222	4	Aae00122	Bacillus
293	6	7.5	222	4	Aae00083	Bacillus	366	6	7.5	222	4	Aae00132	Bacillus
294	6	7.5	222	4	Aae00108	Bacillus	367	6	7.5	222	4	Aae00135	Bacillus
295	6	7.5	222	4	Aae00115	Bacillus	368	6	7.5	222	4	Aae00149	Bacillus
296	6	7.5	222	4	Aae000148	Bacillus	369	6	7.5	222	4	Aae00155	Bacillus
297	6	7.5	222	4	Aae000138	Bacillus	370	6	7.5	222	4	Aae00170	Bacillus
298	6	7.5	222	4	Aae000159	Bacillus	371	6	7.5	222	4	Aae00178	Bacillus
299	6	7.5	222	4	Aae000172	Bacillus	372	6	7.5	222	4	Aae00033	Bacillus
300	6	7.5	222	4	Aae00045	Bacillus	373	6	7.5	222	4	Aae00075	Bacillus
301	6	7.5	222	4	Aae00054	Bacillus	374	6	7.5	222	4	Aae00096	B. lichen
302	6	7.5	222	4	Aae00085	Bacillus	375	6	7.5	222	4	Aae00110	Bacillus
303	6	7.5	222	4	Aae000113	Bacillus	376	6	7.5	222	4	Aae00116	Bacillus
304	6	7.5	222	4	Aae000138	Bacillus	377	6	7.5	222	4	Aae00137	Bacillus
305	6	7.5	222	4	Aae000147	Bacillus	378	6	7.5	222	4	Aae00141	Bacillus
306	6	7.5	222	4	Aae000189	Bacillus	379	6	7.5	222	4	Aae00144	Bacillus
307	6	7.5	222	4	Aae000203	Bacillus	380	6	7.5	222	4	Aae00145	Bacillus
308	6	7.5	222	4	Aae00032	Bacillus	381	6	7.5	222	4	Aae00157	Bacillus
309	6	7.5	222	4	Aae00046	Bacillus	382	6	7.5	222	4	Aae00182	Bacillus
310	6	7.5	222	4	Aae00049	Bacillus	383	6	7.5	222	4	Aae00201	Bacillus
311	6	7.5	222	4	Aae00051	Bacillus	384	6	7.5	222	7	Aae00087	Human KPP
312	6	7.5	222	4	Aae00059	Bacillus	385	6	7.5	230	6	ABU33187	Protein e
313	6	7.5	222	4	Aae000119	Bacillus	386	6	7.5	230	9	ABE39502	L. pneumo
314	6	7.5	222	4	Aae000143	Bacillus	387	6	7.5	230	9	ABE36077	L. pneumo
315	6	7.5	222	4	Aae00146	Bacillus	388	6	7.5	235	6	ABU29765	Protein e
316	6	7.5	222	4	Aae00150	Bacillus	389	6	7.5	240	2	Aae22597	Foetal on

390	6	7.5	240	7	ADG73666	Adg73666	C. perfr	463	6	7.5	314	4	AAE00013	Aae00013	Bacillus
391	6	7.5	241	4	ABE71853	Abb71853	Drosophil	464	6	7.5	314	8	ADY08037	Ady08037	Plant ful
392	6	7.5	245	7	ABO77558	Abb77558	Pseudomon	465	6	7.5	316	2	AAE23730	Aar23730	Protease
393	6	7.5	247	6	ADB11458	Adb11458	Alloiooc	466	6	7.5	316	4	AAE00011	Aae00011	Bacillus
394	6	7.5	248	7	ABO76042	Abb76042	Pseudomon	467	6	7.5	316	8	ADG32274	Adg32274	Mutant B
395	6	7.5	248	9	ABE42645	Aeb42645	L. pneumo	468	6	7.5	318	4	AAE00015	Aae00015	Bacillus-
396	6	7.5	251	7	ADJ69728	Adj69728	Human hea	469	6	7.5	319	3	AAE16397	Aab16397	Pinus rad
397	6	7.5	251	8	ADK16903	Adk16903	Nanoarcha	470	6	7.5	319	3	AAE16397	Aab16397	Pinus rad
398	6	7.5	252	7	ADK16903	Adk16903	Pseudomon	471	6	7.5	319	7	ADY41573	Ady41573	Isoflavon
399	6	7.5	255	7	ADY70037	Adj70037	Human hea	472	6	7.5	319	8	ADP90917	Adp90917	Norway ra
400	6	7.5	255	9	ADY70494	Adj70494	Human bet	473	6	7.5	321	5	ABP29864	Abp29864	Streptoco
401	6	7.5	258	4	ABP75597	Aag75597	Human col	474	6	7.5	322	6	AAE37822	Aae37822	Rat 3 alp
402	6	7.5	259	6	ABP78102	Aag78102	N. gonorr	475	6	7.5	322	7	ADE55971	Ades55971	Rat Prote
403	6	7.5	259	6	ADP80694	Adp80694	Alloiooc	476	6	7.5	324	5	ABG76658	Abg76658	Zebrafish
404	6	7.5	261	2	AAW82855	Aaw82855	Ehrlichia	477	6	7.5	325	8	ADS28687	Ads28687	Bacterial
405	6	7.5	261	3	AAW78533	Aay78533	Ehrlichia	478	6	7.5	327	7	ADF05934	Adf05934	Bacterial
406	6	7.5	261	5	ABG93430	Abg93430	Ehrlichia	479	6	7.5	332	3	AAE53447	Aab53447	Human col
407	6	7.5	261	5	AU73327	Aau73327	Human gra	480	6	7.5	332	4	ABG18841	Abg18841	Novel hum
408	6	7.5	265	3	AAV94451	Aay94451	Human inf	481	6	7.5	334	3	AAE51994	Aab51994	Human sec
409	6	7.5	265	6	ABE74468	Abg74468	Human ras	482	6	7.5	334	3	AAE51993	Aab51993	Gene 38 h
410	6	7.5	265	7	ADC39998	Adc39998	Human rat	483	6	7.5	334	7	ABO78623	AbO78623	Pseudomon
411	6	7.5	265	7	ADC39998	Adc39998	Human ras	484	6	7.5	334	7	ABO78623	AbO78623	Pseudomon
412	6	7.5	265	7	ADP86497	Adp86497	Protein e	485	6	7.5	336	8	ADY22408	Ady22408	Plant ful
413	6	7.5	265	7	ABW01909	Abw01909	Human inf	486	6	7.5	339	4	AAE79432	Aab79432	Corynebac
414	6	7.5	265	8	ADP00801	Adp00801	Human rap	487	6	7.5	343	8	ADJ64325	Adj64325	Cartilage
415	6	7.5	265	8	ADP00807	Adp00807	Mouset RAP	488	6	7.5	344	7	ABO67971	AbO67971	Pseudomon
416	6	7.5	265	9	AEA26103	Aea26103	Human ren	489	6	7.5	345	6	ABR39092	AbR39092	Cercopith
417	6	7.5	273	8	AU11546	Aau11546	Human mdd	490	6	7.5	345	6	ABR39093	AbR39093	Cercopith
418	6	7.5	273	8	ADP56325	Adp56325	Human pro	491	6	7.5	345	7	ADP08054	Adp08054	Novel pro
419	6	7.5	274	8	ADP22698	Adp22698	Rice stre	492	6	7.5	345	9	ADU40424	Adu40424	Novel hum
420	6	7.5	275	8	ADS30082	Ads30082	Bacterial	493	6	7.5	346	8	ADP28819	Adp28819	Human tru
421	6	7.5	279	4	ABE86253	AbE86253	C. glutam	494	6	7.5	348	3	AAE24671	Aag24671	Arabidops
422	6	7.5	279	6	ABU44422	Abu44422	Protein e	495	6	7.5	348	4	ABG05182	AbG05182	Novel hum
423	6	7.5	280	6	ABU43599	Abu43599	Protein e	496	6	7.5	352	7	AAE38993	Aae38993	Human ant
424	6	7.5	281	8	ADP69516	Adp69516	Rice plan	497	6	7.5	353	6	ADP07962	Adp07962	Alloiooc
425	6	7.5	282	4	AAU34080	Aau34080	Staphyloc	498	6	7.5	356	4	ABE61320	AbE61320	Drosophil
426	6	7.5	288	2	AAW98949	Aaw98949	Streptoco	499	6	7.5	356	7	ADJ70253	Adj70253	Human hea
427	6	7.5	288	6	ADP80662	Adp80662	Alloiooc	500	6	7.5	360	3	AAE24670	Aag24670	Arabidops
428	6	7.5	289	6	ABU25294	Abu25294	Protein e	501	6	7.5	362	7	ADL14197	Adl14197	Human src
429	6	7.5	290	3	AAE58884	Aae58884	Breast an	502	6	7.5	362	7	ADK65829	Adk65829	Angiogene
430	6	7.5	292	4	AAU36847	Aau36847	Staphyloc	503	6	7.5	368	9	ADX38833	Adx38833	Human can
431	6	7.5	292	6	ABU16190	Abu16190	Protein e	504	6	7.5	369	3	ADX24669	Adx24669	Arabidops
432	6	7.5	292	6	ABW72449	Abw72449	Staphyloc	505	6	7.5	370	4	AAE93450	Aab93450	Human pro
433	6	7.5	293	5	ABE50136	AbE50136	Listeria	506	6	7.5	370	4	AAE47993	Aab47993	Priscatoy
434	6	7.5	293	6	ABU32844	Abu32844	Protein e	507	6	7.5	372	6	ADK43434	Adk43434	Acinetoba
435	6	7.5	296	3	AAE30066	Aae30066	Lactobaci	508	6	7.5	372	7	ADM05595	Adm05595	Human pro
436	6	7.5	297	8	ADP30102	Adp30102	Human sec	509	6	7.5	375	7	ADE76397	Ade76397	Baker's y
437	6	7.5	299	8	ADP30102	Adp30102	Human hea	510	6	7.5	375	9	AEA25916	Aea25916	Caenorhab
438	6	7.5	300	6	ABW72865	Abw72865	Staphyloc	511	6	7.5	376	9	ABE10653	Aeb10653	SIVBK28 a
439	6	7.5	300	7	ADH87377	Adh87377	Enterococ	512	6	7.5	377	5	ABP28195	Abp28195	Streptoco
440	6	7.5	303	2	AAI59676	Aai59676	Secreted	513	6	7.5	378	6	ADP07964	Adp07964	Alloiooc
441	6	7.5	303	7	ADJ69038	Adj69038	Human hea	514	6	7.5	379	8	ADN20362	Adn20362	Bacterial
442	6	7.5	303	7	ADJ69039	Adj69039	Human hea	515	6	7.5	381	4	AAE09695	Aae09695	Human gen
443	6	7.5	303	7	ADW77826	Adw77826	Human pro	516	6	7.5	381	7	ADC22073	Adc22073	Human pro
444	6	7.5	303	8	ADL82985	Adl82985	Human pro	517	6	7.5	382	6	ABU28948	Abu28948	Protein e
445	6	7.5	303	8	ADP19507	Adp19507	Human sec	518	6	7.5	384	4	AAU35149	Aau35149	Enterococ
446	6	7.5	303	8	ADP56144	Adp56144	Human pro	519	6	7.5	384	4	ABE58862	AbE58862	Drosophil
447	6	7.5	303	8	ADR89538	Adr89538	Apoptosis	520	6	7.5	384	8	ADX93638	Adx93638	Plant ful
448	6	7.5	303	8	ADR89540	Adr89540	Secreted	521	6	7.5	386	2	AAW92507	Aaw92507	Yeast del
449	6	7.5	303	9	ADZ89286	Adz89286	Secreted	522	6	7.5	387	5	ADE52958	Ade52958	FEN-1 rel
450	6	7.5	304	7	ADL22730	Adl22730	Human dis	523	6	7.5	387	9	ABE87185	Aeb87185	Yeast RAD
451	6	7.5	305	8	ADP63053	Adp63053	Transcrip	524	6	7.5	389	6	ABO00684	AbO00684	Novel hum
452	6	7.5	305	8	ADX73352	Adx73352	Plant ful	525	6	7.5	389	6	ADM77489	Adm77489	Human fib
453	6	7.5	305	9	AEA27129	Aea27129	Stress to	526	6	7.5	390	6	ABR43661	AbR43661	Human Max
454	6	7.5	306	8	ADU34158	Adu34158	Protein e	527	6	7.5	390	7	ADE54585	Ade54585	Human Pro
455	6	7.5	306	8	ADJ67144	Adj67144	Lactobaci	528	6	7.5	390	8	ADM87238	Adm87238	Human pro
456	6	7.5	306	8	ADX71183	Adx71183	Plant ful	529	6	7.5	390	8	ADP12987	Adp12987	Protein e
457	6	7.5	307	7	ADH87945	Adh87945	Enterococ	530	6	7.5	390	9	AEA26101	Aea26101	Human ren
458	6	7.5	308	5	ABB97523	Abb97523	Novel hum	531	6	7.5	392	7	ADA66100	Ada66100	DNAP-rela
459	6	7.5	308	6	ABU41449	Abu41449	Protein e	532	6	7.5	394	7	ADM26772	Adm26772	Hyperther
460	6	7.5	311	4	AAE95509	Aae95509	Human pro	533	6	7.5	395	9	ADX38832	Adx38832	Human can
461	6	7.5	312	2	AAV07109	Aav07109	Colon can	534	6	7.5	397	8	ADN17608	Adn17608	Bacterial
462	6	7.5	312	7	ADC96592	Adc96592	E. faeciu	535	6	7.5	398	6	ABU19092	AbU19092	Protein e

536	6	7.5	399	6	AD54651	Ada54651 Human pro	609	6	7.5	440	9	ADZ59839	Adz59839 SIV CP-MA
537	6	7.5	399	8	ADN18018	Adn18018 Bacterial	610	6	7.5	440	9	ADZ59820	Adz59820 SIV NC-MA
538	6	7.5	400	2	AAW01114	Aaw01114 Brain-spe	611	6	7.5	440	9	ADZ59842	Adz59842 SIV CP-MA
539	6	7.5	400	2	AAW83429	Aaw83429 Human Doc	612	6	7.5	440	9	ADZ59819	Adz59819 SIV BK-28
540	6	7.5	400	7	ADZ598281	Adz598281 Human Pro	613	6	7.5	440	9	ADZ59827	Adz59827 SIV NC-MA
541	6	7.5	400	7	ADZ5982919	Adz5982919 Human Pro	614	6	7.5	440	9	ADZ59830	Adz59830 SIV CP-MA
542	6	7.5	400	9	AE840157	Aeb40157 L. pneumo	615	6	7.5	440	9	ADZ59833	Adz59833 SIV CP-MA
543	6	7.5	402	5	AAE26853	Aae26853 Anabaena	616	6	7.5	440	9	ADZ59834	Adz59834 SIV CP-MA
544	6	7.5	403	7	ADZ59835	Adz59835 Mycobacte	617	6	7.5	440	9	ADZ59840	Adz59840 SIV CP-MA
545	6	7.5	403	7	ADZ5982917	Adz5982917 Rat Prote	618	6	7.5	440	9	ADZ59845	Adz59845 SIV CP-MA
546	6	7.5	403	8	ADN17541	Adn17541 Bacterial	619	6	7.5	440	9	ADZ59848	Adz59848 SIV CP-MA
547	6	7.5	403	8	ADZ59821794	Adz59821794 Bacterial	620	6	7.5	440	9	ADZ59831	Adz59831 SIV CP-MA
548	6	7.5	403	8	ADZ5983593	Adz5983593 Plant ful	621	6	7.5	440	9	ADZ59836	Adz59836 SIV CP-MA
549	6	7.5	403	9	AEA19980	Aea19980 Novel hum	622	6	7.5	440	9	ADZ59841	Adz59841 SIV CP-MA
550	6	7.5	405	2	AAZ27275	Aay27275 Mouse Doc	623	6	7.5	440	9	ADZ59844	Adz59844 SIV CP-MA
551	6	7.5	405	6	ABU02242	Abu02242 S. pneumo	624	6	7.5	440	9	ADZ59849	Adz59849 SIV CP-MA
552	6	7.5	405	7	ADZ598279	Adz598279 Rat Prote	625	6	7.5	442	8	ADZ59845	Adz59845 SIV CP-MA
553	6	7.5	406	3	AAZ81562	Aay81562 Streptoco	626	6	7.5	442	8	ADZ59848	Adz59848 SIV CP-MA
554	6	7.5	406	6	ADA35277	Ada35277 Acinetoba	627	6	7.5	449	8	ADN19753	Adn19753 Bacterial
555	6	7.5	408	6	ABP80737	Abp80737 N. gonorr	628	6	7.5	451	8	ADZ59836	Adz59836 SIV CP-MA
556	6	7.5	409	7	ADZ598166	Adz598166 Novel hum	629	6	7.5	452	7	ABO66041	Abo66041 Klebsiell
557	6	7.5	409	8	ADZ5983516	Adz5983516 Human hex	630	6	7.5	452	8	ADY10721	Ady10721 Plant ful
558	6	7.5	410	8	ADN17713	Adn17713 Bacterial	631	6	7.5	453	4	AAZ88601	Aaz88601 Human hyd
559	6	7.5	411	6	ABU47023	Abu47023 Protein e	632	6	7.5	453	5	ABJ10916	Abj10916 Human sec
560	6	7.5	411	6	ABU47648	Abu47648 Protein e	633	6	7.5	453	5	ABZ49460	Abz49460 Listeria
561	6	7.5	411	6	ABU31631	Abu31631 Protein e	634	6	7.5	453	8	ADS22125	Ads22125 Bacterial
562	6	7.5	411	6	ADZ5980696	Adz5980696 Alloloco	635	6	7.5	453	8	ADU06332	Adu06332 Novel bro
563	6	7.5	411	6	ADZ59805	Adz59805 Oil-assoc	636	6	7.5	454	4	AEA01133	Aea01133 Heat-resi
564	6	7.5	411	7	ADZ5987359	Adz5987359 B. lichen	637	6	7.5	455	5	ABP69701	Abp69701 Human pol
565	6	7.5	412	9	ABZ36782	Aeb36782 L. pneumo	638	6	7.5	455	5	ABO84784	Abo84784 Human can
566	6	7.5	413	2	AAW46822	Aaw46822 Amino aci	639	6	7.5	456	5	ABO09697	Abo09697 Amino aci
567	6	7.5	413	2	AAW05724	Aay05724 Ras bindi	640	6	7.5	459	8	ADZ22711	Adz22711 Bacterial
568	6	7.5	413	6	ABU49722	Abu49722 Protein e	641	6	7.5	460	2	AAZ29294	Aay29294 Protein e
569	6	7.5	413	6	ABZ62565	Abz62565 Mouse NOR	642	6	7.5	466	3	AAZ30538	Aaz30538 Arabidops
570	6	7.5	413	7	ADC40011	Adc40011 Mouse Nor	643	6	7.5	468	5	ABP41886	Abp41886 Human ova
571	6	7.5	413	7	ADC40010	Adc40010 Rat Maxp1	644	6	7.5	469	8	ABM83929	Abm83929 Human dia
572	6	7.5	413	7	ADZ54583	Adz54583 Rat Prote	645	6	7.5	472	3	AAZ30937	Aaz30937 Arabidops
573	6	7.5	413	8	ADZ54583	Adz54583 NOR-1 pr	646	6	7.5	474	6	ABU38287	Abu38287 Protein e
574	6	7.5	413	9	AEA26109	Aea26109 Human ren	647	6	7.5	475	3	ABJ10288	Abj10288 Murine fe
575	6	7.5	414	2	AAZ15484	Aaz15484 Protein e	648	6	7.5	475	4	ABG15897	Abg15897 Novel hum
576	6	7.5	416	2	AAZ37263	Aay37263 Chlamydia	649	6	7.5	475	7	ABO80748	Abo80748 Pseudomon
577	6	7.5	416	7	ABO79650	Abo79650 Pseudomon	650	6	7.5	475	7	ABO83632	Abo83632 Pseudomon
578	6	7.5	416	8	ADZ50949	Adz50949 Human nov	651	6	7.5	478	8	ADZ26074	Adz26074 Bacterial
579	6	7.5	417	4	ABZ64872	Abz64872 Drosophil	652	6	7.5	480	8	ADZ74151	Adz74151 Plant ful
580	6	7.5	418	6	ABU15361	Abu15361 Protein e	653	6	7.5	481	3	AAZ30936	Aaz30936 Arabidops
581	6	7.5	419	8	ADZ22929	Adz22929 Plant ful	654	6	7.5	481	4	AAZ07510	Aaz07510 Arabidops
582	6	7.5	420	4	ABG00313	Abg00313 Novel hum	655	6	7.5	481	5	ABZ93601	Abz93601 Herbicida
583	6	7.5	420	6	ABU21007	Abu21007 Protein e	656	6	7.5	481	7	ADZ75805	Adz75805 Thale cre
584	6	7.5	422	5	ABZ47734	Abb47734 Listeria	657	6	7.5	481	9	ADZ75805	Adz75805 Thale cre
585	6	7.5	424	8	ADZ21026	Adz21026 Bacterial	658	6	7.5	482	3	AAZ30065	Aaz30065 Arabidops
586	6	7.5	429	8	ADN19997	Adn19997 Bacterial	659	6	7.5	482	6	ADZ55398	Adz55398 Human pro
587	6	7.5	430	4	AAZ96652	Aaz96652 Putative	660	6	7.5	482	7	ABO70384	Abo70384 Pseudomon
588	6	7.5	433	3	AAZ19094	Aab19094 Protein e	661	6	7.5	487	4	ABZ59931	Abz59931 Drosophil
589	6	7.5	433	8	ADZ87472	Adz87472 S. cerevis	662	6	7.5	487	8	ADZ54443	Adz54443 Bacterial
590	6	7.5	433	8	ADZ43798	Adz43798 Bacterial	663	6	7.5	491	7	ABO73648	Abo73648 Pseudomon
591	6	7.5	437	5	AAW47762	Aaw47762 RNA bindi	664	6	7.5	494	5	ABZ53680	Abz53680 Lactococc
592	6	7.5	437	7	ABO68045	Abo68045 Pseudomon	665	6	7.5	494	8	ADY08905	Ady08905 Plant ful
593	6	7.5	438	7	ABO68045	Abo68045 Pseudomon	666	6	7.5	495	2	AAZ16126	Aaz16126 Mycoplaem
594	6	7.5	439	9	ADZ24223	Adz24223 Human NOV	667	6	7.5	495	6	ABU42299	Abu42299 Protein e
595	6	7.5	439	9	ADZ59823	Adz59823 SIV NC-MA	668	6	7.5	495	6	ABM72088	Abm72088 Staphyloc
596	6	7.5	439	9	ADZ59837	Adz59837 SIV CP-MA	669	6	7.5	495	7	ADZ5304	Adz5304 Bacterial
597	6	7.5	440	9	ADZ59846	Adz59846 SIV CP-MA	670	6	7.5	495	8	ADZ5020	Adz5020 Bacterial
598	6	7.5	440	9	ADZ59821	Adz59821 SIV NC-MA	671	6	7.5	495	9	ABM96319	Abm96319 M. xanthu
599	6	7.5	440	9	ADZ59829	Adz59829 SIV NC-MA	672	6	7.5	496	2	AAW76589	Aaw76589 Simtan im
600	6	7.5	440	9	ADZ59832	Adz59832 SIV CP-MA	673	6	7.5	496	2	AAW76591	Aaw76591 Simtan im
601	6	7.5	440	9	ADZ59847	Adz59847 SIV CP-MA	674	6	7.5	496	2	AAW76590	Aaw76590 Simtan im
602	6	7.5	440	9	ADZ59824	Adz59824 SIV NC-MA	675	6	7.5	496	2	AAW76592	Aaw76592 Simtan im
603	6	7.5	440	9	ADZ59825	Adz59825 SIV NC-MA	676	6	7.5	496	8	ADT60157	Adt60157 Plant pol
604	6	7.5	440	9	ADZ59828	Adz59828 SIV NC-MA	677	6	7.5	497	6	ABU43883	Abu43883 Protein e
605	6	7.5	440	9	ADZ59835	Adz59835 SIV CP-MA	678	6	7.5	497	6	ABU46520	Abu46520 Pseudomon
606	6	7.5	440	9	ADZ59843	Adz59843 SIV CP-MA	679	6	7.5	499	7	ABO79264	Abo79264 Pseudomon
607	6	7.5	440	9	ADZ59826	Adz59826 SIV NC-MA	680	6	7.5	500	6	ABU29861	Abu29861 Protein e
608	6	7.5	440	9	ADZ59838	Adz59838 SIV CP-MA	681	6	7.5	501	5	ABP25949	Abp25949 Streptoco

682	6	7.5	501	6	ABR53864	Abv53864	Protein s	755	6	7.5	538	8	ADE51817	Human sec
683	6	7.5	501	7	ADK64896	Adk64896	Disease t	756	6	7.5	538	8	ADE37675	Human sec
684	6	7.5	501	8	ADS21678	AdS21678	Bacterial	757	6	7.5	538	8	ADE37559	Human sec
685	6	7.5	502	3	AG30064	Aag30064	Arabidops	758	6	7.5	538	8	ADD95330	Human sec
686	6	7.5	503	7	AR82837	Arr82837	SiVnmac239	759	6	7.5	538	8	ADE38030	Human PRO
687	6	7.5	505	2	AA97731	Aar97731	Barley be	760	6	7.5	538	8	ADE76119	Human PRO
688	6	7.5	506	6	ADA54661	Ada54661	Human PRO	761	6	7.5	538	8	ADE39442	Human PRO
689	6	7.5	507	4	ABB65913	Abb65913	Drosophil	762	6	7.5	538	8	ADE04246	Human PRO
690	6	7.5	507	5	AAW48909	Aam48909	Zoysia te	763	6	7.5	538	8	ADE39843	Human PRO
691	6	7.5	508	2	AAW89793	Aaw89793	Staphyloc	764	6	7.5	538	8	ADE19708	Human PRO
692	6	7.5	509	7	ADH86922	Adh86922	Enterococ	765	6	7.5	538	8	ADE77286	Human sec
693	6	7.5	511	2	AAW57436	Aar57436	Human cal	766	6	7.5	538	8	ADE65394	Human PRO
694	6	7.5	511	8	ADf43328	Adf43328	Rat ppp3C	767	6	7.5	538	8	ADE76003	Human PRO
695	6	7.5	511	9	ADY18944	Ady18944	PRO polyp	768	6	7.5	538	8	ADE37914	Human PRO
696	6	7.5	512	4	AAW40648	Aam40648	Human pol	769	6	7.5	538	8	ADE64524	Human PRO
697	6	7.5	520	7	ABO75051	Abo75051	Pseudomon	770	6	7.5	538	8	ADE38859	Human PRO
698	6	7.5	521	4	AAW67636	Aag67636	Amino aci	771	6	7.5	538	8	ADE51933	Human sec
699	6	7.5	521	4	AAW67457	Aag67457	Amino aci	772	6	7.5	538	8	ADD90964	Human sec
700	6	7.5	521	5	ABB09696	Abb09696	Amino aci	773	6	7.5	538	8	ADD90964	Human sec
701	6	7.5	521	8	ADP43226	Adp43226	Mouss ppp	774	6	7.5	538	8	ADE38743	Human PRO
702	6	7.5	521	8	ADf43224	Adf43224	Human ppp	775	6	7.5	538	8	ADE37443	Human sec
703	6	7.5	521	8	ADN11631	Adn11631	Calcineur	776	6	7.5	538	8	ADE06260	Human PRO
704	6	7.5	521	9	ADY14781	Ady14781	PRO polyp	777	6	7.5	538	8	ADD90119	Human sec
705	6	7.5	521	9	ADY14794	Ady14794	PRO polyp	778	6	7.5	538	8	ADE38627	Human PRO
706	6	7.5	522	2	AAW69726	Aaw69726	Saccharom	779	6	7.5	538	8	ADE39558	Human PRO
707	6	7.5	522	9	ABE13006	Aeb13006	Yeast pro	780	6	7.5	538	8	ADD89163	Human PRO
708	6	7.5	522	9	ABE50108	Aeb50108	Yeast dis	781	6	7.5	538	8	ADD88930	Human PRO
709	6	7.5	526	2	AAW26174	Aar26174	Protein d	782	6	7.5	538	8	ADE19824	Human PRO
710	6	7.5	528	8	ADf53521	Adf53521	Mouse hex	783	6	7.5	538	8	ADE77402	Human sec
711	6	7.5	529	1	AAW70376	Aap70376	Sequence	784	6	7.5	538	8	ADE39326	Human PRO
712	6	7.5	529	8	ADf53524	Adf53524	Human hex	785	6	7.5	538	8	ADE38511	Human sec
713	6	7.5	529	8	ADf53528	Adf53528	Human hex	786	6	7.5	538	8	ADG11064	Human sec
714	6	7.5	529	8	ADU97368	Adu97368	Human pro	787	6	7.5	538	8	ADG10948	Human sec
715	6	7.5	529	9	ADU288299	Adu288299	Human hex	788	6	7.5	538	8	ADH31476	Human PRO
716	6	7.5	530	9	ABE13007	Aeb13007	Yeast alt	789	6	7.5	538	8	ADH38724	Human sec
717	6	7.5	530	9	ABE50109	Aeb50109	Yeast dis	790	6	7.5	538	8	ADH29359	Human sec
718	6	7.5	533	8	ADS28449	Ads28449	Bacterial	791	6	7.5	538	8	ADH23662	Human sec
719	6	7.5	534	2	AAW46823	Aaw46823	Amino aci	792	6	7.5	538	8	ADH26992	Human sec
720	6	7.5	534	2	AAW98948	Aaw98948	Streptoco	793	6	7.5	538	8	ADH28260	Novel hum
721	6	7.5	536	7	ADB64626	Adb64626	Human pro	794	6	7.5	538	8	ADH26876	Human sec
722	6	7.5	538	5	AAU08162	Aau08162	Human PRO	795	6	7.5	538	8	ADH38144	Novel hum
723	6	7.5	538	5	ABG34054	Abg34054	Human PRO	796	6	7.5	538	8	ADG68275	Human PRO
724	6	7.5	538	6	ADA01318	Ada01318	Human PRO	797	6	7.5	538	8	ADH38840	Human sec
725	6	7.5	538	6	AAO233973	Aao233973	Human KIA	798	6	7.5	538	8	ADH23778	Human sec
726	6	7.5	538	6	ADA43747	Ada43747	Human sec	799	6	7.5	538	8	ADH40154	Human PRO
727	6	7.5	538	6	ADA43515	Ada43515	Human sec	800	6	7.5	538	8	ADH40038	Human PRO
728	6	7.5	538	6	ADA01190	Ada01190	Human PRO	801	6	7.5	538	8	ADH31360	Human PRO
729	6	7.5	538	7	ADA01074	Ada01074	Human sec	802	6	7.5	538	8	ADH29238	Human sec
730	6	7.5	538	7	ADA43631	Ada43631	Human sec	803	6	7.5	538	8	ADH49453	Novel hum
731	6	7.5	538	7	ADA06893	Ada06893	Human PRO	804	6	7.5	538	8	ADH51917	Novel hum
732	6	7.5	538	7	ADA08381	Ada08381	Novel hum	805	6	7.5	538	8	ADH49772	Novel hum
733	6	7.5	538	7	ADU99674	Adu99674	Human PRO	806	6	7.5	538	8	ADH52373	Novel hum
734	6	7.5	538	7	ADB86957	Adb86957	Human PRO	807	6	7.5	538	8	ADH52489	Novel hum
735	6	7.5	538	7	ADB66112	Adb66112	Human sec	808	6	7.5	538	8	ADH58486	Novel hum
736	6	7.5	538	7	ADB99790	Adb99790	Human PRO	809	6	7.5	538	8	ADH51801	Novel hum
737	6	7.5	538	7	ADB99445	Adb99445	Novel hum	810	6	7.5	538	8	ADH58362	Novel hum
738	6	7.5	538	7	ADB65996	Adb65996	Human sec	811	6	7.5	538	8	ADH13559	Novel hum
739	6	7.5	538	7	ADC23394	Adc23394	Human tra	812	6	7.5	538	8	ADK00815	Human PRO
740	6	7.5	538	7	ADC26087	Adc26087	Human PRO	813	6	7.5	538	8	ADL08556	Human sec
741	6	7.5	538	7	ADE04914	Ade04914	Human PRO	814	6	7.5	541	7	ADC96021	E. faeciu
742	6	7.5	538	7	ADL11220	Adl11220	Human PRO	815	6	7.5	549	2	AAW63672	Polypepti
743	6	7.5	538	7	ADD88151	Add88151	Human PRO	816	6	7.5	549	4	AAU35613	Haemophil
744	6	7.5	538	7	ADD95446	Add95446	Human PRO	817	6	7.5	549	4	AAU35613	Haemophil
745	6	7.5	538	7	ADU06376	Adu06376	Human sec	818	6	7.5	549	6	ABU30527	Protein e
746	6	7.5	538	7	ADU38151	Adu38151	Human PRO	819	6	7.5	549	8	ADQ39810	Human myo
747	6	7.5	538	7	ADH88267	Adh88267	Human PRO	820	6	7.5	549	9	ADY30809	Human sec
748	6	7.5	538	7	ADU90848	Adu90848	Human sec	821	6	7.5	549	9	ADY30807	Human sec
749	6	7.5	538	7	ADU99403	Adu99403	Human sec	822	6	7.5	550	2	AAW63674	Polypepti
750	6	7.5	538	7	ADG06496	Adg06496	Human PRO	823	6	7.5	550	4	AAU35613	Mouse Kio
751	6	7.5	538	7	ADG05447	Adg05447	Human PRO	824	6	7.5	557	6	ABU50079	Protein e
752	6	7.5	538	7	ADG82448	Adg82448	Human PRO	825	6	7.5	558	6	ABR83611	Human at1
753	6	7.5	538	7	ADJ37351	Adj37351	Human tum	826	6	7.5	558	6	ABR82443	Human ARP
754	6	7.5	538	8	ADU51701	Adu51701	Human sec	827	6	7.5	558	8	ADQ74857	Human and

828	6	7.5	558	8	ADR70103	Human atl	901	6	7.5	4	AU69897	Human pro
829	6	7.5	558	8	ADY70455	Human bet	902	6	7.5	4	ABU71788	Prostate
830	6	7.5	560	2	ADW28505	Mugwort g	903	6	7.5	5	ABU95357	Human p78
831	6	7.5	562	4	ABB60336	Drosophil	904	6	7.5	6	ABR54469	Prostate
832	6	7.5	565	9	ADW28506	Human kio	905	6	7.5	6	ADB14268	Human pro
833	6	7.5	567	8	ADR66342	Human pro	906	6	7.5	6	ABR39130	Human tra
834	6	7.5	567	8	ADR66684	Human pro	907	6	7.5	6	ABR39128	Human tra
835	6	7.5	567	9	ADW28508	Mouse kio	908	6	7.5	6	ADG26684	Human pro
836	6	7.5	569	4	ABM69913	Drosophil	909	6	7.5	6	ADG26684	Human pro
837	6	7.5	569	7	ABM66636	Rice abio	910	6	7.5	6	ABO83196	Pseudomon
838	6	7.5	570	3	AAO3813	Human ves	911	6	7.5	6	ADG31780	Human nov
839	6	7.5	570	3	AAO3813	Human ves	912	6	7.5	6	ADG31780	Human nov
840	6	7.5	570	4	ABR94478	Human pro	913	6	7.5	6	ABU19464	UL15 DNA
841	6	7.5	570	5	ABR57217	Mouse isc	914	6	7.5	6	ABU19464	UL15 DNA
842	6	7.5	570	7	ADG61222	Mouse isc	915	6	7.5	6	ADL70765	Rat trans
843	6	7.5	570	7	ADG61224	Human pro	916	6	7.5	6	ADL24459	Rat trans
844	6	7.5	570	8	ADP12603	Protein e	917	6	7.5	6	ADY54162	Amino aci
845	6	7.5	570	8	ADP12603	Protein e	918	6	7.5	6	ADY54162	Amino aci
846	6	7.5	571	5	ABP25425	Streptoco	919	6	7.5	6	ADT60464	Plant pol
847	6	7.5	571	8	ADJ48639	Streptoco	920	6	7.5	6	ADW25719	Human alp
848	6	7.5	571	8	ADV88216	Streptoco	921	6	7.5	6	ADO09744	Human gen
849	6	7.5	571	8	ADV79469	Streptoco	922	6	7.5	6	ABO70760	Pseudomon
850	6	7.5	571	8	ADV81641	Streptoco	923	6	7.5	6	ADF30710	Rat angio
851	6	7.5	572	7	ABO75250	Pseudomon	924	6	7.5	6	ABU42822	Protein e
852	6	7.5	572	9	ABO76340	Pseudomon	925	6	7.5	6	ADG01138	Enterobae
853	6	7.5	572	9	AE931419	Microbial	926	6	7.5	6	ABG11428	Novel hum
854	6	7.5	574	8	ADJ48650	Streptoco	927	6	7.5	6	ABP38787	Staphyloc
855	6	7.5	578	4	ABG04478	Novel hum	928	6	7.5	6	ABO79598	Pseudomon
856	6	7.5	581	4	ABB58513	Drosophil	929	6	7.5	6	ADY31754	Candida t
857	6	7.5	581	7	ADJ37921	D melanog	930	6	7.5	6	ADG42261	Patty alc
858	6	7.5	582	8	ADN47488	Thermococ	931	6	7.5	6	ADG42265	Patty alc
859	6	7.5	586	2	AAK07274	Reverse t	932	6	7.5	6	ADG42267	Patty alc
860	6	7.5	586	2	AAK11520	Reverse t	933	6	7.5	6	AAU34857	E. coli c
861	6	7.5	586	2	AAK11520	Reverse t	934	6	7.5	6	ABU47919	Protein e
862	6	7.5	586	3	AAK11520	Reverse t	935	6	7.5	6	ABU15299	Protein e
863	6	7.5	586	3	AAK11520	Reverse t	936	6	7.5	6	ABU15299	Protein e
864	6	7.5	588	8	ADS42756	Bacterial	937	6	7.5	6	ADG42267	Patty alc
865	6	7.5	589	4	ABG21171	Novel hum	938	6	7.5	6	ABU73214	Human gra
866	6	7.5	594	4	ABG19168	Novel hum	939	6	7.5	6	ABG59070	Drosophil
867	6	7.5	598	8	ADX74760	Plant ful	940	6	7.5	6	ADJ67542	Human ova
868	6	7.5	599	5	ABB53321	Lactococ	941	6	7.5	6	ADP81154	Protein o
869	6	7.5	599	8	ADS15133	Pseudomon	942	6	7.5	6	ABG60766	Drosophil
870	6	7.5	600	7	ABO72357	Pseudomon	943	6	7.5	6	ADG44105	Bacterial
871	6	7.5	610	5	AAU2039	Clostridi	944	6	7.5	6	ABM86046	Rice abio
872	6	7.5	610	6	ABU25105	Protein e	945	6	7.5	6	ADG42265	Patty alc
873	6	7.5	610	7	ADP15932	Aspergill	946	6	7.5	6	ADG42267	Patty alc
874	6	7.5	610	7	ADD15931	Aspergill	947	6	7.5	6	ABU41695	Human PRO
875	6	7.5	610	7	ADD15930	Wild-type	948	6	7.5	6	ABU41695	Human PRO
876	6	7.5	612	9	ADY30892	Campyloba	949	6	7.5	6	ABU41695	Human PRO
877	6	7.5	618	7	ABO73672	Pseudomon	950	6	7.5	6	ABU41695	Human PRO
878	6	7.5	624	8	ADY23706	Plant ful	951	6	7.5	6	ABU84306	Human sec
879	6	7.5	625	9	ADY30893	Campyloba	952	6	7.5	6	ABR66180	Human sec
880	6	7.5	630	9	ABM91886	M. xanthu	953	6	7.5	6	ABR66180	Human sec
881	6	7.5	631	9	ABO71672	Pseudomon	954	6	7.5	6	ABR65570	Human sec
882	6	7.5	631	9	ADX26407	Novel cei	955	6	7.5	6	ABU99510	Human sec
883	6	7.5	632	3	AAB42782	Human ORF	956	6	7.5	6	ABU82749	Human PRO
884	6	7.5	632	3	AAB26916	Nitric ox	957	6	7.5	6	ABU89870	Novel hum
885	6	7.5	632	7	ABU62617	Pseudomon	958	6	7.5	6	ABR68119	Human sec
886	6	7.5	632	9	ADX26263	Novel cel	959	6	7.5	6	ABU96172	Novel hum
887	6	7.5	633	8	ADX74359	Plant ful	960	6	7.5	6	ABU92603	Human sec
888	6	7.5	634	5	AAE20287	Human trp	961	6	7.5	6	ABO08680	Human sec
889	6	7.5	640	5	ABG92655	Herbicida	962	6	7.5	6	ABO02732	Human sec
890	6	7.5	642	7	ADG73672	Human aCB	963	6	7.5	6	ABR74886	Human sec
891	6	7.5	643	4	ABB61390	Drosophil	964	6	7.5	6	ABR94648	Human sec
892	6	7.5	645	4	AAG66531	Human pro	965	6	7.5	6	ABO25197	Novel hum
893	6	7.5	645	8	ADO19794	Human int	966	6	7.5	6	ABU85621	Human PRO
894	6	7.5	645	8	ABM80947	Tumour-as	967	6	7.5	6	ABU98781	Novel hum
895	6	7.5	645	8	ADP56088	Human PRO	968	6	7.5	6	ABU97996	Novel hum
896	6	7.5	645	9	AEA18850	Amino aci	969	6	7.5	6	ABU91702	Novel hum
897	6	7.5	646	4	AAU30243	Novel hum	970	6	7.5	6	ABU72203	Novel hum
898	6	7.5	650	6	ABU20817	Protein e	971	6	7.5	6	ABU89395	Human PRO
899	6	7.5	650	7	ABO83588	Pseudomon	972	6	7.5	6	ABU86236	Human sec
900	6	7.5	652	4	AAAM01252	P78BP N-t	973	6	7.5	6	ABU80477	Human PRO

974 6 7.5 735 6 ABR99395  
 975 6 7.5 735 6 ABR98785  
 976 6 7.5 735 6 ABO16308  
 977 6 7.5 735 6 ABR92208  
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 994 6 7.5 735 6 ABU84883  
 995 6 7.5 735 6 ABU65612  
 996 6 7.5 735 6 ABO07460  
 997 6 7.5 735 6 ABO03647  
 998 6 7.5 735 6 ABR67095  
 999 6 7.5 735 6 ABO15698  
 1000 6 7.5 735 6 ABU55979

Abt-99395 Human sec  
 Abt-98785 Human sec  
 Abo16308 Human sec  
 ABR92208 Human sec  
 Abo18849 Human sec  
 ABR78270 Human sec  
 Abt-85006 Novel hum  
 Abo00145 Novel hum  
 Abo11477 Human sec  
 Abo02122 Human sec  
 Abt-88696 Novel hum  
 Abo83391 Human sec  
 Abo06192 Novel hum  
 ABR59228 Human sec  
 Abo09290 Human sec  
 Abo19154 Novel hum  
 Abo11172 Human sec  
 ABR66790 Human sec  
 Abo16003 Human sec  
 Abo13709 Human sec  
 Abt-84883 Human sec  
 Abt-65612 Human sec  
 Abo07460 Human PRO  
 Abo03647 Human sec  
 ABR67095 Human sec  
 Abo15698 Human sec  
 Abt-55979 Human sec

## ALIGNMENTS

RESULT 1  
 AAR86834  
 ID AAR86834 standard; protein; 227 AA.

XX AC AAR86834;  
 XX DT 12-JUL-1996 (first entry)  
 XX DE Human CD9 sequence.

XX KW CD9 antigen; stimulated T cell; antibody; ligand; proliferation;  
 KW monoclonal antibody; ES5.2D8; 27 kD accessory protein; epitope;  
 XX KW immune response; cancer; infectious disease; growth factor.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Modified-site 51 /note= "Potential N-linked glycosylation site"  
 FT Modified-site 52 /note= "Potential N-linked glycosylation site"  
 FT Domain 111..194 /note= "Extracellular domain"  
 FT Domain 195..220 /note= "Transmembrane domain"  
 FT Domain 221..227 /note= "Cytoplasmic domain"

XX PN WO9533823-A1.

XX PD 14-DEC-1995.

XX PF 01-DEC-1994; 94WO-US013782.

XX PR 03-JUN-1994; 94US-00253751.

XX PR 03-JUN-1994; 94US-00253964.

XX PA (USNA ) US SEC OF NAVY.

XX PA (UNMI ) UNIV MICHIGAN.

XX PA (REPK ) REPLIGEN CORP.

XX PA (DAND ) DANA FARBER CANCER INST INC.

XX June CH, Thompson CB, Nabel G, Gray GS, Rennert PD, Freeman GJ;  
 XX WPI; 1996-040230/04.  
 XX Selectively inducing CD8 positive T cell proliferation - by activating  
 XX the T cells and stimulating CD9 cell surface ligand, useful for  
 XX immunotherapy of, e.g. cancer.  
 XX Example 10; Page 38-39; 79pp; English.

XX This sequence represents CD9 from the surface of stimulated T cells. The  
 XX antigen at residues 31-37 of human CD9 (see AAR86832) is bound by an  
 XX antibody or other ligand to stimulate the T cell population to  
 XX proliferate and expand leading to a 100- to 10000-fold increase in cell  
 XX number compared to the original population. The antigenic sequence fits  
 XX the generic sequence given in AAR86827. This epitope is recognised by the  
 XX monoclonal antibody (Mab) ES5.2D8. CD9 is a 27 kD accessory protein found  
 XX on activated T cells. The epitope was recognised by screening a phage  
 XX display library. Selective proliferation of an antigen-specific T cell  
 XX population is useful in cases where the immune response is to be up  
 XX regulated, e.g. in the treatment of cancer or infectious diseases. By  
 XX causing proliferation of the T cell population by stimulating T cell  
 XX epitope removes the need for exogenous growth factors or accessory cells

SQ Sequence 227 AA;

Query Match 100.0%; Score 80; DB 2; Length 227;

Best Local Similarity 100.0%; Pred. No. 1e-73;

Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVKEVQSFYKDTYNNKLTQDEPORETLLKAIHYALNCCGLAGGVQFISDIPCKDV 60

Db 112 HKDEVKEVQSFYKDTYNNKLTQDEPORETLLKAIHYALNCCGLAGGVQFISDIPCKDV 171

QY 61 LETFTVKSCPDAIKEVFDNK 80

Db 172 LETFTVKSCPDAIKEVFDNK 191

RESULT 2

ABB78366

ID ABB78366 standard; protein; 227 AA.

XX AC ABB78366;

XX DT 16-DEC-2002 (first entry)

XX DE Amino acid sequence of CD9.

XX KW T cell; T cell proliferation; infectious disease; cancer; immunotherapy;

XX immunotherapy; CD9.

XX OS Homo sapiens.

XX US2002115214-A1.

XX PD 22-AUG-2002.

XX PF 26-JAN-1996; 96US-00592711.

XX PR 23-NOV-1988; 88US-00275433.

XX PR 07-APR-1992; 92US-00864805.

XX PR 07-APR-1992; 92US-00864807.

XX PR 07-APR-1992; 92US-00864866.

XX PR 04-JUN-1993; 93US-00073223.

XX PR 03-JUN-1994; 94US-00253964.

XX PR 10-MAR-1995; 95US-00403253.

XX PR 04-MAY-1995; 95US-00435816.

XX (JUNE/) JUNE C H.

XX (THOM/) THOMPSON C B.

XX (NABE/) NABEL G J.

PA (GRAY/) GRAY G S.  
 XX (RENN/) RENNERT P D.  
 PI June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;  
 XX WPI; 2002-712476/77.  
 DR  
 XX Inducing a population of T cells to proliferate, by activating population  
 PT of T cells and stimulating an accessory molecule on the surface of the T  
 PT cells with a ligand which binds the accessory molecule.  
 XX  
 PS Example 10; Page 25; 88pp; English.  
 XX  
 CC The specification describes method for inducing a population of T cells  
 CC to proliferate. The method involves activating population of T cells,  
 CC stimulating an accessory molecule on T cell surface with a ligand  
 CC protein) which binds the molecule, to induce proliferation of T cells,  
 CC monitoring proliferation of T cells in response to continuing exposure to  
 CC the ligand, and reactivating and restimulating T cells when rate of  
 CC proliferation has decreased to induce further proliferation of the cells.  
 CC The method is useful for inducing proliferation of T cells, for use in  
 CC treatment of infectious disease, cancer and immunotherapy. The method  
 CC allows for the expansion of a population of T cells in numbers sufficient  
 CC to reconstitute an individual's total CD4+ or CD8+ T cell population.  
 CC The resulting T cell population can be genetically transduced and used  
 CC for immunotherapy or can be used in methods of in vitro analyses of  
 CC infectious agents. A population of tumour-infiltrating lymphocytes can be  
 CC obtained from an individual afflicted with cancer and the T cells  
 CC stimulated to proliferate to sufficient numbers. The resulting T cell  
 CC population can be genetically transduced to express tumour necrosis  
 CC factor (TNF) or other factor and restored to the individual. CD4+ T cells  
 CC expanded by this method are useful in the treatment of HIV infection in  
 CC an individual. The present sequence represents CD9, an antigen present on  
 CC the surface of activated T cells  
 XX  
 SQ Sequence 227 AA;  
 Query Match 100.0%; Score 80; DB 5; Length 227;  
 Best Local Similarity 100.0%; Pred. No. 1e-73;  
 Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HKDEVKEVQBFYKDTYNKLTQDEPQRETLKAIHYALNCCGLAGGVEQFISDIPKDV 60  
 DB 112 HKDEVKEVQBFYKDTYNKLTQDEPQRETLKAIHYALNCCGLAGGVEQFISDIPKDV 171  
 QY 61 LETFTVKSCPDAIKEVFDNK 80  
 DB 172 LETFTVKSCPDAIKEVFDNK 191  
 RESULT 3  
 AAEL14636  
 ID AAEL14636 standard; protein; 227 AA.  
 XX AAEL14636;  
 AC  
 DT 16-JUL-2002 (first entry)  
 XX  
 DE Human CD9 antigen.  
 XX  
 KW T cell; CD3; accessory molecule; CD28; cancer; infectious disease;  
 KW immunotherapy; human immunodeficiency virus; HIV infection; cytokine;  
 KW human; CD9 antigen.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6352694-B1.  
 XX  
 PD 05-MAR-2002.  
 XX  
 PF 10-MAR-1995; 95US-00403253.  
 XX  
 PR 03-JUN-1994; 94US-00253964.

XX (GEMY ) GENETICS INST INC.  
 PA (UNMI ) UNIV MICHIGAN.  
 XX  
 PI June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;  
 XX WPI; 2002-314696/35.  
 DR  
 XX Inducing T cell population to proliferate, useful in cancer therapy,  
 PT comprises activating T cells by contacting T cells in vitro with  
 PT immobilized anti-CD3 antibody and stimulating accessory molecule on T  
 PT cell surface.  
 XX  
 PS Example 10; Col 42; 71pp; English.  
 XX  
 CC The invention relates to a method of inducing T cell population to  
 CC proliferate for use in therapy comprising activating T cells by  
 CC contacting T cells in vitro with anti-CD3 antibody which is immobilised  
 CC on solid phase surface, and stimulating accessory molecule on T cell  
 CC surface in vitro with anti-CD28 antibody, or stimulatory form of natural  
 CC ligand for CD28 such as B7-1 or B7-2. The method is useful for inducing a  
 CC population of T cells to proliferate in sufficient numbers for use in  
 CC therapy e.g., for treating cancer or an infectious disease. The method  
 CC can be used to selectively expand the population of CD28+, CD4+, CD8+,  
 CC CD28RA+ or CD28RO+ T cells for immunotherapy. The T cell population  
 CC resulting by the method can be genetically transduced and used for  
 CC immunotherapy or can be used for in vitro analysis of infectious agents  
 CC such as human immunodeficiency virus (HIV). Proliferation of a population  
 CC of CD4+ T cells obtained from an individual infected with HIV can be  
 CC achieved and the cells rendered resistant to HIV infection. Following the  
 CC expansion of the T cells to sufficient numbers, the expanded T cells are  
 CC restored to the individual. Also CD4+ T cells expanded by the above  
 CC mentioned is useful for treating HIV infection in an individual. A  
 CC population of tumour-infiltrating lymphocytes can be obtained from an  
 CC individual afflicted with cancer and the T cells stimulated to  
 CC proliferate to sufficient numbers and restored to the individual. The  
 CC supernatants from cultures of T cells expanded from above mentioned  
 CC method are useful as a rich source of cytokines and can be used to  
 CC sustain T cells in vivo or ex vivo. Stimulating and expanding a  
 CC population of antigen specific T cells are useful in therapeutic  
 CC conditions where it is desirable to upregulate an immune response. The T  
 CC cell proliferation occurs in the absence of exogenous growth factors or  
 CC accessory cells. The present sequence is human CD9 antigen which is  
 CC expressed on surface of activated T cells  
 XX  
 SQ Sequence 227 AA;  
 Query Match 100.0%; Score 80; DB 5; Length 227;  
 Best Local Similarity 100.0%; Pred. No. 1e-73;  
 Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HKDEVKEVQBFYKDTYNKLTQDEPQRETLKAIHYALNCCGLAGGVEQFISDIPKDV 60  
 DB 112 HKDEVKEVQBFYKDTYNKLTQDEPQRETLKAIHYALNCCGLAGGVEQFISDIPKDV 171  
 QY 61 LETFTVKSCPDAIKEVFDNK 80  
 DB 172 LETFTVKSCPDAIKEVFDNK 191  
 RESULT 4  
 ABU05057  
 ID ABU05057 standard; protein; 227 AA.  
 XX ABU05057;  
 AC  
 XX  
 DT 29-JAN-2003 (first entry)  
 XX  
 DE Human expressed protein tag (EPT) #1723.  
 XX  
 KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
 KW protease; protease inhibitor; transporter; cytoskeletal protein;  
 KW receptor; transcription factor; cancer; MHC;



```
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chiciz RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1723; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 227 AA;
Query Match 100.0%; Score 80; DB 6; Length 227;
Best Local Similarity 100.0%; Pred. No. 1e-73;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HKDEVKEVQVFYKDTYNNKLTQDPQRETILKAHYALNCCGLAGGVQFISDICKKDV 60
DB 112 HKDEVKEVQVFYKDTYNNKLTQDPQRETILKAHYALNCCGLAGGVQFISDICKKDV 171
QY 61 LETFTVKSCPDAIKEVFNK 80
DB 172 LETFTVKSCPDAIKEVFNK 191
RESULT 5
ABU05060
ID ABU05060 standard; protein; 227 AA.
XX
AC ABU05060;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1726.
```

```
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chiciz RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1726; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor.
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 227 AA;
Query Match 100.0%; Score 80; DB 6; Length 227;
Best Local Similarity 100.0%; Pred. No. 1e-73;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HKDEVKEVQVFYKDTYNNKLTQDPQRETILKAHYALNCCGLAGGVQFISDICKKDV 60
DB 112 HKDEVKEVQVFYKDTYNNKLTQDPQRETILKAHYALNCCGLAGGVQFISDICKKDV 171
QY 61 LETFTVKSCPDAIKEVFNK 80
DB 172 LETFTVKSCPDAIKEVFNK 191
RESULT 6
ABW00436
ID ABW00436 standard; protein; 227 AA.
XX
AC ABW00436;
```

```
XX 15-JAN-2004 (first entry)
XX Human CD9 antigenic protein.
XX HIV infection; human immunodeficiency virus; therapy; antigen; human.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Domain 111..194
XX /note= "Extracellular domain"
XX Domain 195..220
XX /note= "Transmembrane domain"
XX Domain 221..227
XX /note= "Cytoplasmic domain"
XX US2003099643-A1.
XX 29-MAY-2003.
XX 08-JUL-1999; 99US-00350202.
XX 23-NOV-1988; 88US-00275433.
XX 22-NOV-1989; 89WO-US005304.
XX 07-APR-1992; 92US-00864807.
XX 07-APR-1992; 92US-00864807.
XX 07-APR-1992; 92US-00864807.
XX 04-JUN-1993; 93US-00073223.
XX 04-JUN-1993; 93US-00073223.
XX 03-JUN-1994; 94US-00253694.
XX 10-MAR-1995; 95US-00403253.
XX (JUNE/) JUNE C H.
XX (THOM/) THOMPSON C B.
XX (NABEL/) NABEL G J.
XX (GRAY/) GRAY G S.
XX (RENN/) RENNERT P D.
XX June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;
XX WPI; 2003-801206/75.
XX Treating HIV infection in individual by isolating T cells from
XX leukocytes, contacting T cells with anti-CD3 antibody for T cell
XX proliferation, separating antibody from T cells, monitoring proliferation
XX of T cells.
XX Example 10; Page 23; Opp; English.
XX The present invention relates to a novel method of treating human
XX immunodeficiency virus (HIV) infection in an individual. The method
XX involves isolating population of CD4 T cells from leukocytes, contacting
XX population of CD4+ T cells with an anti-CD3 antibody for stimulating T
XX cell proliferation, separating antibody from T cells, monitoring
XX proliferation of T cells, restimulating T cells with antibody and
XX restoring T cells to individual. The present sequence is human CD9
XX antigenic protein. This sequence is used to illustrate the method of the
XX invention
XX Sequence 227 AA;
Query Match 100.0%; Score 80; DB 7; Length 227;
Best Local Similarity 100.0%; Pred. No. 1e-73;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HKDEVIKEVQEFYKDTYNKLTQBPQRETLKAIHYALNCCGLAGGVQFISDIPCKDV 60
Db 112 HKDEVIKEVQEFYKDTYNKLTQBPQRETLKAIHYALNCCGLAGGVQFISDIPCKDV 171
QY 61 LETFTVKSCPDAIKEVFDNK 80
Db 172 LETFTVKSCPDAIKEVFDNK 191
```

```
RESULT 7
ADK69862
ID ADK69862 standard; protein; 227 AA.
XX AC ADK69862;
XX DT 06-MAY-2004 (first entry)
XX DE Human CD9 protein.
XX KW CD28-associated signal; immunotherapy; infectious disease; cancer;
XX leukopenia; human.
XX OS Homo sapiens.
XX PN US6534055-B1.
XX PD 18-MAR-2003.
XX PP 04-MAY-1995; 95US-00435816.
XX PR 07-APR-1992; 92US-00864805.
XX PR 07-APR-1992; 92US-00864807.
XX PR 07-APR-1992; 92US-00864807.
XX PR 04-JUN-1993; 93US-00073223.
XX PR 03-JUN-1994; 94US-00253694.
XX PR 10-MAR-1995; 95US-00403253.
XX (GENY ) GENETICS INST INC.
XX June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;
XX WPI; 2003-531074/50.
XX Expanding T cell populations, useful for preparing renewable sources of T
XX cells (e.g. CD4+) for immunotherapy or diagnostics, by stimulating a CD28
XX -associated signal on the surface of the cells with an anti-CD28
XX antibody, B7-1 or B7-2.
XX Example 10; SEQ ID NO 6; 82pp; English.
XX The invention relates to a method for expanding a population of T cells
XX to about 100-10000-fold over the original T cell population, or to about
XX 10 log 1 0 to 12 log 1 2. The method comprises stimulating a CD28-
XX associated signal on the surface of the T cells with agent comprising an
XX anti-CD28 antibody, B7-1 or B7-2. The method is useful for inducing a
XX population of T cells (e.g. CD4+, CD28+, CD8+, CD28RA+ or CD28RO+ T
XX cells) to proliferate. The method is particularly useful for preparing a
XX renewable source of CD4+ T cells. The expanded T cell population can be
XX genetically transduced, and used for immunotherapy to treat a variety of
XX human diseases (e.g. infectious diseases or cancer), or used in
XX diagnostic protocols. T cells were obtained from leukopenia of a
XX normal donor, and purified with FICOLL density gradient centrifugation,
XX followed by magnetic immunobead sorting. The present sequence is CD9 used
XX in the exemplification of the invention.
XX Sequence 227 AA;
Query Match 100.0%; Score 80; DB 7; Length 227;
Best Local Similarity 100.0%; Pred. No. 1e-73;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HKDEVIKEVQEFYKDTYNKLTQBPQRETLKAIHYALNCCGLAGGVQFISDIPCKDV 60
Db 112 HKDEVIKEVQEFYKDTYNKLTQBPQRETLKAIHYALNCCGLAGGVQFISDIPCKDV 171
QY 61 LETFTVKSCPDAIKEVFDNK 80
Db 172 LETFTVKSCPDAIKEVFDNK 191
RESULT 8
```



KW lung, glioblastoma.  
XX Homo sapiens.  
XX  
PN EP508417-A2.  
XX  
XX 14-OCT-1992.  
XX  
XX 09-APR-1992; 92EP-00106093.  
XX  
XX 12-APR-1991; 91JP-00079996.  
PR 17-APR-1991; 91JP-00085396.  
PR 07-FEB-1992; 92JP-00022321.  
XX  
XX (TAKE ) TAKEDA CHEM IND LTD.  
PA (MIYA/) MIYAKE M.  
XX  
XX Ikeyama S, Koyama M, Senoo M, Miyake M;  
XX  
XX WPI; 1992-341723/42.  
DR N-PSDB; AAQ29182.  
XX  
XX New monoclonal antibody M31-15 specific for metastasis-controlling  
PT peptide - useful for treating and preventing cancer and metastasis.  
XX  
XX Claim 7; Fig 4; 34pp; English.  
XX  
XX The sequence is that of a cancer cell surface protein which is capable of  
CC suppressing the motility of cancer cells. It is specifically recognised  
CC by the monoclonal (Mab) antibody M31-15, which is useful for suppressing  
CC cancer metastasis. The polypeptide and Mab M31-15 are therefore useful in  
CC the prophylaxis and treatment of cancer, e.g. lung, glioblastoma and  
CC other metastatic cancers. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
XX Sequence 228 AA;  
SQ  
Query Match 100.0%; Score 80; DB 2; Length 228;  
Best Local Similarity 100.0%; Pred. NO. 1e-73;  
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HKDEVKEQVEFYKDTYKLTQKDEPQRETLKAIHYALNCCGLAGGVEQFISDIPCCKDV 60  
Db 113 HKDEVKEQVEFYKDTYKLTQKDEPQRETLKAIHYALNCCGLAGGVEQFISDIPCCKDV 172  
QY 61 LETFTVKSCPDAIKEVFDNK 80  
Db 173 LETFTVKSCPDAIKEVFDNK 192  
RESULT 11  
ID ABB44581  
XX ABB44581 standard; protein; 228 AA.  
XX  
AC ABB44581;  
XX  
XX 25-JAN-2002 (first entry)  
XX  
XX Human wound healing related polypeptide SEQ ID NO 38.  
DE  
XX  
XX Human; mouse; vulnery; dermatological; skin disorder; wound healing;  
KW Gene therapy.  
KW  
XX Homo sapiens.  
XX  
XX CA2325226-A1.  
XX  
XX 17-MAY-2001.  
XX  
XX 16-NOV-2000; 2000CA-02325226.  
XX  
XX 17-NOV-1999; 99DE-01055349.  
PR 17-DEC-1999; 99US-0172511P.  
PR 20-JUN-2000; 2000DE-01030149.

XX  
PA (SWIT-) SWITCH BIOTECH AG.  
XX  
PI Regenbogen J, Wolf E, Coppelt A, Werner S, Halle J;  
XX  
XX WPI; 2001-433142/47.  
XX  
XX Use of novel polypeptide or its variant or nucleic acid encoding the  
PT polypeptide for diagnosing and/or preventing and/or treating skin  
PT disorders and/or treatment in wound healing or for identifying active  
PT substances.  
XX  
XX PS Disclosure; Page 193-194; 265pp; English.  
XX  
XX The invention relates to the use of a polypeptide (ABB44544-ABB44601,  
CC ABB44605-ABB44623) or its variant or encoding nucleic acid (ABA81990-  
CC ABA81995, ABA82016-ABA82032) with vulnery and/or dermatological  
CC activity for the diagnosis, prevention and treatment of skin disorders  
CC and treatment in wound healing or for the identification of  
CC pharmacologically active substances. The nucleic acids are useful in gene  
CC therapy. Note: The printed sequence listing for this specification was  
CC incomplete, terminating part way through SEQ ID NO 106. The remaining  
CC data was obtained from EPO data for an equivalent patent (SP1114862)  
XX  
XX Sequence 228 AA;  
SQ  
Query Match 100.0%; Score 80; DB 4; Length 228;  
Best Local Similarity 100.0%; Pred. NO. 1e-73;  
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HKDEVKEQVEFYKDTYKLTQKDEPQRETLKAIHYALNCCGLAGGVEQFISDIPCCKDV 60  
Db 113 HKDEVKEQVEFYKDTYKLTQKDEPQRETLKAIHYALNCCGLAGGVEQFISDIPCCKDV 172  
QY 61 LETFTVKSCPDAIKEVFDNK 80  
Db 173 LETFTVKSCPDAIKEVFDNK 192  
RESULT 12  
ID ABU05059 standard; protein; 228 AA.  
XX  
XX ABU05059;  
XX  
XX 29-JAN-2003 (first entry)  
XX  
XX Human expressed protein tag (EPT) #1725.  
XX  
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
XX  
XX Homo sapiens.  
XX  
XX WO200278524-A2.  
XX  
XX 10-OCT-2002.  
XX  
XX 28-MAR-2002; 2002WO-US009671.  
XX  
XX 28-MAR-2001; 2001US-0279495P.  
PR 21-MAY-2001; 2001US-0292544P.  
PR 08-AUG-2001; 2001US-0310801P.  
PR 01-OCT-2001; 2001US-0326370P.  
PR 04-DEC-2001; 2001US-0336780P.  
PR 20-FEB-2002; 2002US-0358985P.  
XX  
XX (ZYCO-) ZYCO INC.  
XX  
XX Chicx RM, Tomlinson AJ, Urban RG; PI

```
XX DR WPI; 2003-040607/03.
XX PT
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX PT cytoskeletal proteins, receptors or transcription factors), useful for
XX PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX PT leukemia.
XX PS Example 2; SEQ ID NO 1725; 134pp; English.
XX CC The invention describes a purified polypeptide, which comprises a
XX CC fragment of a kinase, phosphatase, protease, protease inhibitor,
XX CC transporter, cytoskeletal protein, receptor or transcription factor. The
XX CC polypeptide is useful as an immunogenic composition for eliciting in a
XX CC mammal an immunogenic response directed against any of the purified
XX CC polypeptide. The purified polypeptide, or the antibody that binds to this
XX CC polypeptide, is useful for treating cancer. The polypeptide is also
XX CC useful for identifying compounds that binds to a naturally processed
XX CC class I or class II MHC-binding polypeptide. The polypeptides and
XX CC polynucleotides are particularly useful for treating or preventing
XX CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX CC lymphoma or leukaemia. These are also useful for screening agents for
XX CC treating the above mentioned diseases. This sequence represents an
XX CC expressed protein tag (EPT) isolated from human tissue for translational
XX CC profiling. Note: This sequence does not appear in the printed
XX CC specification but was obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 228 AA;
XX
XX Query Match 100.0%; Score 80; DB 6; Length 228;
XX Best Local Similarity 100.0%; Pred. No. 1e-73;
XX Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 HKDEVIKEVQEFYKDTYNNKLTQDEPQRETLLKAIHYALNCCGLAGGVQFISDIPCKKDV 60
XX DB 113 HKDEVIKEVQEFYKDTYNNKLTQDEPQRETLLKAIHYALNCCGLAGGVQFISDIPCKKDV 172
XX
XX QY 61 LETFTVKSCPDAIKEVFNK 80
XX DB 173 LETFTVKSCPDAIKEVFNK 192
XX
XX RESULT 13
XX ABU05052
XX ID ABU05052 standard; protein; 228 AA.
XX AC ABU05052;
XX
XX DT 29-JAN-2003 (first entry)
XX DE Human expressed protein tag (EPT) #1718.
XX
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX KW protease; protease inhibitor; transporter; cytoskeletal protein;
XX KW receptor; transcription factor; cancer; MHC;
XX KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX OS Homo sapiens.
XX XX WO200278524-A2.
XX FN WO200278524-A2.
XX PD 10-OCT-2002.
XX
XX PF 28-MAR-2002; 2002WO-US009671.
XX PR 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX PR 01-OCT-2001; 2001US-0326370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002US-035985P.
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XX PA (ZYCO-) ZYCOs INC.
XX PI Chicx RM, Tomlinson AJ, Urban RG;
XX DR WPI; 2003-040607/03.
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX PT cytoskeletal proteins, receptors or transcription factors), useful for
XX PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX PT leukemia.
XX PS Example 2; SEQ ID NO 1718; 134pp; English.
XX CC The invention describes a purified polypeptide, which comprises a
XX CC fragment of a kinase, phosphatase, protease, protease inhibitor,
XX CC transporter, cytoskeletal protein, receptor or transcription factor. The
XX CC polypeptide is useful as an immunogenic composition for eliciting in a
XX CC mammal an immunogenic response directed against any of the purified
XX CC polypeptide. The purified polypeptide, or the antibody that binds to this
XX CC polypeptide, is useful for treating cancer. The polypeptide is also
XX CC useful for identifying compounds that binds to a naturally processed
XX CC class I or class II MHC-binding polypeptide. The polypeptides and
XX CC polynucleotides are particularly useful for treating or preventing
XX CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX CC lymphoma or leukaemia. These are also useful for screening agents for
XX CC treating the above mentioned diseases. This sequence represents an
XX CC expressed protein tag (EPT) isolated from human tissue for translational
XX CC profiling. Note: This sequence does not appear in the printed
XX CC specification but was obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 228 AA;
XX
XX Query Match 100.0%; Score 80; DB 6; Length 228;
XX Best Local Similarity 100.0%; Pred. No. 1e-73;
XX Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 HKDEVIKEVQEFYKDTYNNKLTQDEPQRETLLKAIHYALNCCGLAGGVQFISDIPCKKDV 60
XX DB 113 HKDEVIKEVQEFYKDTYNNKLTQDEPQRETLLKAIHYALNCCGLAGGVQFISDIPCKKDV 172
XX
XX QY 61 LETFTVKSCPDAIKEVFNK 80
XX DB 173 LETFTVKSCPDAIKEVFNK 192
XX
XX RESULT 14
XX ABU05048
XX ID ABU05048 standard; protein; 228 AA.
XX AC ABU05048;
XX
XX DT 29-JAN-2003 (first entry)
XX DE Human expressed protein tag (EPT) #1714.
XX
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX KW protease; protease inhibitor; transporter; cytoskeletal protein;
XX KW receptor; transcription factor; cancer; MHC;
XX KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX OS Homo sapiens.
XX XX WO200278524-A2.
XX FN WO200278524-A2.
XX PD 10-OCT-2002.
XX
XX PF 28-MAR-2002; 2002WO-US009671.
XX PR 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
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PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chiciz RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 1714; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 228 AA;
Query Match 100.0%; Score 80; DB 6; Length 228;
Best Local Similarity 100.0%; Pred. No. 1e-73;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HKDEVIKEVQEFYKDTYNKLTQDEPQRETLKAIHYALNCCGLAGGVEQFISDICKDV 60
Db 113 HKDEVIKEVQEFYKDTYNKLTQDEPQRETLKAIHYALNCCGLAGGVEQFISDICKDV 172
QY 61 LETFTVKSCPDAIKEVFDNK 80
Db 173 LETFTVKSCPDAIKEVFDNK 192
RESULT 15
ABU05056
ID ABU05056 standard; protein; 228 AA.
AC
ABU05056;
XX
XX 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1722.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
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PF 28-MAR-2002; 2002WO-US009671.
XX
XX 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
XX (ZYCO-) ZYCOS INC.
XX
XX Chiciz RM, Tomlinson AJ, Urban RG;
XX
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 1722; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 228 AA;
Query Match 100.0%; Score 80; DB 6; Length 228;
Best Local Similarity 100.0%; Pred. No. 1e-73;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HKDEVIKEVQEFYKDTYNKLTQDEPQRETLKAIHYALNCCGLAGGVEQFISDICKDV 60
Db 113 HKDEVIKEVQEFYKDTYNKLTQDEPQRETLKAIHYALNCCGLAGGVEQFISDICKDV 172
QY 61 LETFTVKSCPDAIKEVFDNK 80
Db 173 LETFTVKSCPDAIKEVFDNK 192
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Search completed: January 20, 2006, 17:42:25  
Job time : 141.923 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2006, 17:21:43 ; Search time 94.7654 Seconds  
(without alignments)  
176.187 Million cell updates/sec

Title: US-10-619-323-4

Perfect score: 207

Sequence: 1 KDEPQRETLKAIHYALNCCGLAGVQVFISDICKPKDV 38

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 1130394

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

A\_Geneseq\_21.\*

- 1: Geneseq1980s.\*
- 2: Geneseq1990s.\*
- 3: Geneseq2000s.\*
- 4: Geneseq2001s.\*
- 5: Geneseq2002s.\*
- 6: Geneseq2003as.\*
- 7: Geneseq2003bs.\*
- 8: Geneseq2004s.\*
- 9: Geneseq2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	207	100.0	38	ADJ57561	Human CD9
2	128	61.8	30	ABU05051	Human exp
3	60	29.0	22	ADJ57564	Human CD9
4	44	21.3	33	AAY45292	Human sec
5	44	21.3	44	ABG99705	Conus sp
6	43	20.8	23	AAR26006	Influenza
7	43	20.8	23	AAB70092	Cationic
8	43	20.8	23	AAB34271	Synthetic
9	43	20.8	26	AAR26004	Influenza
10	43	20.8	26	AAB70090	Cationic
11	43	20.8	26	AAB34269	Synthetic
12	43	20.8	44	ABM95674	M. xanthu
13	42.5	20.5	50	AAB20282	Human nov
14	41.5	20.0	32	ABG99385	Conus sp
15	41.5	20.0	49	AAV55679	E. coli y
16	41	19.8	32	AAR13376	Adult T-c
17	41	19.8	44	AAU16377	Peptide #
18	41	19.8	44	AAU74910	Human col
19	41	19.8	44	ABG35365	Peptide #
20	41	19.8	44	AAU28874	Peptide #
21	41	19.8	44	ABG30202	Peptide #
22	41	19.8	44	ABG20807	Protein #
23	41	19.8	44	AAU68569	Human bon
24	41	19.8	44	AAU56196	Human bra

25	41	19.8	44	4	ABG50232	Human liv
26	41	19.8	44	4	AAU04113	Peptide #
27	41	19.8	44	5	ABG38147	Human pep
28	41	19.8	46	2	AAU31910	Spider ve
29	41	19.8	49	3	AAY55680	H. influe
30	40.5	19.6	32	5	ABG99768	Conus sp
31	40.5	19.6	32	5	ABG99387	Conus sp
32	40	19.3	25	2	AAU47052	HIV-1 V3
33	40	19.3	44	4	AAU84731	Human imm
34	40	19.3	45	3	AAY55688	M. genita
35	40	19.3	47	4	ABU41557	Peptide #
36	40	19.3	47	4	AAU35348	Peptide #
37	40	19.3	47	4	AAU75236	Human bon
38	40	19.3	47	4	AAU62428	Human bra
39	40	19.3	47	4	ABG56998	Human liv
40	40	19.3	47	5	ABU44889	Human pep
41	39.5	19.1	32	5	ABG99769	Conus sp
42	39.5	19.1	40	3	AAU21587	Cone snai
43	39	18.8	17	9	ADU66592	Integrin
44	39	18.8	20	3	AAY66841	T cell an
45	39	18.8	28	5	AAU18036	Human ion
46	39	18.8	29	4	AAU85963	Human imm
47	39	18.8	41	4	ABU16717	Human ner
48	39	18.8	45	3	AAY66046	Transcrip
49	39	18.8	45	4	AAU19061	Peptide #
50	39	18.8	45	4	ABU38268	Peptide #

ALIGNMENTS

RESULT 1

ADJ57561

ID ADJ57561 standard; protein; 38 AA.

XX AC ADJ57561;

XX DT 06-MAY-2004 (first entry)

XX DE Human CD9 fibronectin-binding domain polypeptide fragment.

XX KW Human; CD9; antithrombotic; antiarteriosclerotic; vasotropic;

XX KW haemostatic; angiogenic; cytostatic.

XX OS Homo sapiens.

XX PN WO2004007695-A2.

XX PD 22-JAN-2004.

XX PF 14-JUL-2003; 2003WO-US022050.

XX PR 12-JUL-2002; 2002US-0395864P.

XX PA (UYTE-) UNIV TENNESSEE RES FOUND.

XX PI Jennings LK, Longhurst CM, Cook GA, Zhang C, White MW;

XX PI Crossno JT, Lu Y;

XX WPI; 2004-122924/12.

XX PT Interfering with CD9 binding to fibronectin by binding a fibronectin-binding domain of the CD9 protein or polypeptide, useful in treating thrombosis, atherosclerosis, restenosis, bleeding disorders, angiogenesis and cancers.

XX PT Claim 7; SEQ ID NO 4; 126pp; English.

XX CC The present sequence is that of a polypeptide fragment from the fibronectin-binding domain of human CD9 ADJ57558. The peptide, or an antibody that binds to it, is used in claimed methods for: interfering with CD9 binding to fibronectin; modifying adhesion, motility or spreading of a CD9-expressing cell on fibronectin; inhibiting

CC proliferation or survival of CD9-expressing cells; modifying pericellular  
 CC fibronectin matrix assembly; modifying invasiveness of a cell through a  
 CC collagen and/or laminin matrix; and modifying cell-to-cell interaction.  
 CC The methods are based on the finding that increased CD9 expression is  
 CC implicated in (i) decreased adhesiveness of cells to extracellular matrix  
 CC (via alpha5-beta1 integrin) and/or decreased cell invasiveness and/or  
 CC decreased pericellular fibronectin matrix assembly, and/or (ii) increased  
 CC cell motility, spreading, proliferation, cell survival against apoptosis,  
 CC and/or cell-to-cell contacts. Conditions or disease states involving  
 CC proliferation or survival of CD9-expressing cells can be treated, e.g.  
 CC thrombosis, atherosclerosis, vein graft failure, restenosis, transplant  
 CC arteriopathy, bleeding disorders, angiogenesis, and primary and  
 CC metastatic cancers including breast cancer, prostate cancer, colon  
 CC cancer, melanoma, ovarian cancer, neuroblastoma, glioma and glioblastoma.  
 XX  
 SQ Sequence 38 AA;

Query Match 100.0%; Score 207; DB 8; Length 38;  
 Best Local Similarity 100.0%; Pred. No. 5,1e-22;  
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAIHYALNCCGLAGGVQFTSDICPKKDV 38  
 |||||  
 Db 1 KDEPQRETLKAIHYALNCCGLAGGVQFTSDICPKKDV 38

RESULT 2  
 ABU05051  
 ID ABU05051 standard; protein; 30 AA.  
 XX  
 AC ABU05051;  
 XX  
 DT 29-JAN-2003 (first entry)  
 XX  
 DE Human expressed protein tag (EPT) #1717.  
 XX  
 KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
 KW protease; protease inhibitor; transporter; cytoskeletal protein;  
 KW receptor; transcription factor; cancer; MHC;  
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200278524-A2.  
 XX  
 PD 10-OCT-2002.  
 XX  
 PF 28-MAR-2002; 2002WO-US0095671.  
 XX  
 PR 28-MAR-2001; 2001US-0279495P.  
 PR 21-MAY-2001; 2001US-0292544P.  
 PR 08-AUG-2001; 2001US-0310801P.  
 PR 01-OCT-2001; 2001US-0326370P.  
 PR 04-DEC-2001; 2001US-0336780P.  
 PR 20-FEB-2002; 2002US-0358985P.  
 XX  
 PA (ZYCO-) ZYCO INC.  
 XX  
 XX Chiciz RM, Tomlinson AJ, Urban RG;  
 XX WPI; 2003-040607/03.  
 XX  
 XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
 PT cytoskeletal proteins, receptors or transcription factors), useful for  
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
 PT leukemia.  
 XX  
 XX Example 2; SEQ ID NO 1717; 134pp; English.  
 PS  
 XX The invention describes a purified polypeptide, which comprises a  
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
 CC transporter, cytoskeletal protein, receptor or transcription factor. The

CC polypeptide is useful as an immunogenic composition for eliciting in a  
 CC mammal an immunogenic response directed against any of the purified  
 CC polypeptide. The purified polypeptide, or the antibody that binds to this  
 CC polypeptide, is useful for treating cancer. The polypeptide is also  
 CC useful for identifying compounds that binds to a naturally processed  
 CC class I or class II MHC-binding polypeptide. The polypeptides and  
 CC polynucleotides are particularly useful for treating or preventing  
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
 CC lymphoma or leukaemia. These are also useful for screening agents for  
 CC treating the above mentioned diseases. This sequence represents an  
 CC expressed protein tag (EPT) isolated from human tissue for translational  
 CC profiling. Note: This sequence does not appear in the printed  
 CC specification but was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 30 AA;

Query Match 61.8%; Score 128; DB 6; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 8.7e-11;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 LNCCGLAGGVQFTSDICPKKDV 38  
 |||||  
 Db 1 LNCCGLAGGVQFTSDICPKKDV 23

RESULT 3  
 ADJ57564  
 ID ADJ57564 standard; peptide; 22 AA.  
 XX  
 AC ADJ57564;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Human CD9 fibronectin-binding domain peptide fragment.  
 XX  
 KW Human; CD9; antithrombotic; antiarteriosclerotic; vasotropic;  
 KW haemostatic; antiangiogenic; cytostatic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004007685-A2.  
 XX  
 PD 22-JAN-2004.  
 XX  
 PF 14-JUL-2003; 2003WO-US022050.  
 XX  
 PR 12-JUL-2002; 2002US-0395864P.  
 XX  
 PA (UYTE-) UNIV TENNESSEE RES FOUND.  
 XX  
 XX Jennings IK, Longhurst CM, Cook GA, Bao J, Zhang C, White MM;  
 PI Crossno JT, Lu Y;  
 XX WPI; 2004-122924/12.  
 XX  
 PT Interfering with CD9 binding to fibronectin by binding a fibronectin-  
 PT binding domain of the CD9 protein or polypeptide, useful in treating  
 PT thrombosis, atherosclerosis, restenosis, bleeding disorders, angiogenesis  
 PT and cancers.  
 XX  
 XX Example 1; SEQ ID NO 7; 126pp; English.  
 PS  
 XX The present sequence is that of a peptide fragment from the extracellular  
 CC domain (amino acids 125-146) of human CD9 ADJ57558. The peptide was used  
 CC in an example from the invention to investigate the interaction between  
 CC CD9 and fibronectin. Peptide fragments ADJ57560-ADJ57563 of human CD9 are  
 CC used in claimed methods for: interfering with CD9 binding to fibronectin;  
 CC modifying adhesion, motility or spreading of a CD9-expressing cell on  
 CC fibronectin; inhibiting proliferation or survival of CD9-expressing cells  
 CC ; modifying pericellular fibronectin matrix assembly; modifying  
 CC invasiveness of a cell through a collagen and/or laminin matrix; and  
 CC modifying cell-to-cell interaction. The methods are based on the finding

CC that increased CD9 expression is implicated in (i) decreased adhesiveness  
 CC of cells to extracellular matrix (via alpha5-beta1 integrin) and/or  
 CC decreased cell invasiveness and/or decreased pericellular fibronectin  
 CC matrix assembly, and/or (ii) increased cell motility, spreading,  
 CC proliferation, cell survival against apoptosis, and/or cell-to-cell  
 CC contacts. Conditions or disease states involving proliferation or  
 CC survival of CD9-expressing cells can be treated, e.g. thrombosis,  
 CC atherosclerosis, vein graft failure, restenosis, transplant arteriopathy,  
 CC bleeding disorders, angiogenesis, and primary and metastatic cancers  
 CC including breast cancer, prostate cancer, colon cancer, melanoma, ovarian  
 CC cancer, neuroblastoma, glioma and glioblastoma.  
 XX  
 SQ Sequence 22 AA;

Query Match 29.0%; Score 60; DB 8; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 0.36;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAI 12  
 |||||  
 Db 11 KDEPQRETLKAI 22

RESULT 4  
 AAY45292  
 ID AAY45292 standard; protein; 33 AA.

XX AC AAY45292;

XX DT 23-NOV-1999 (first entry)

XX DE Human secreted protein fragment encoded from gene 4.

XX KW Secreted protein; human; gene therapy; diagnosis; treatment; cancer;  
 KW protein therapy; tumor; neurodegenerative disorder; blood disorder; AIDS;  
 KW developmental abnormality; leukemia; immune system; autoimmune disease;  
 KW hepatic disease; renal disease; inflammation; allergy; schizophrenia;  
 KW Alzheimer's disease; cognitive disorder; arthritis; infection; psoriasis;  
 KW transplant rejection; diabetes; asthma; sepsis; acne; metabolic disorder;  
 KW cardiovascular disorder; food additive; preservative.

XX OS Homo sapiens.

XX PN WO9946289-A1.

XX PD 16-SEP-1999.

XX PF 11-MAR-1999; 99WO-US005721.

XX PR 12-MAR-1998; 98US-0077686P.

XX PR 12-MAR-1998; 98US-0077687P.

XX PR 12-MAR-1998; 98US-0077696P.

XX PR 12-MAR-1998; 98US-0077714P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ruben SM, Ferrie AM, Rosen CA, Florence C, Young PE, Yu G, Ni J;

XX DR WPI; 1999-551363/46.

XX DR N-PSDB; AA227236.

XX PT New isolated human genes, useful for diagnosis and treatment of, e.g.

XX PT cancers.

XX PS Disclosure; 195; 306pp; English.

XX CC This invention describes novel human genes and the secreted proteins they  
 CC encode. The polynucleotides and their corresponding secreted polypeptides  
 CC are useful for preventing, treating or ameliorating medical conditions  
 CC e.g. by protein or gene therapy. Also pathological conditions can be  
 CC diagnosed by determining the amount of the new polypeptides in a sample  
 CC or by determining the presence of mutations in the new polynucleotides.  
 CC Specific uses are described for each of the polynucleotides of the

CC invention, based on which tissues they are most highly expressed in, and  
 CC include developing products for the diagnosis or treatment of cancer,  
 CC tumors, neurodegenerative disorders, developmental abnormalities, blood  
 CC disorders, leukemias, diseases of the immune system, autoimmune diseases,  
 CC hepatic and renal disease, inflammation, allergies, Alzheimer's and  
 CC cognitive disorders, schizophrenia, arthritis, infections, AIDS,  
 CC transplant rejection, diabetes, asthma, sepsis, acne, psoriasis,  
 CC cardiovascular disorders, and metabolic disorders. The polypeptides or  
 CC polynucleotides can also be used as food additives or preservatives. The  
 CC polypeptides are also useful for identifying their binding partners.  
 CC AAY45290-Y45389 represent human secreted protein fragments described in  
 XX the method of the invention  
 XX

SQ Sequence 33 AA;

Query Match 21.3%; Score 44; DB 2; Length 33;  
 Best Local Similarity 42.9%; Pred. No. 1.1e+02;  
 Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 10 KAIHYVALNCCGLAG 23

Db 16 KVVXFGACCGVSG 29

RESULT 5

ABG99705

ID ABG99705 standard; peptide; 44 AA.

XX AC ABG99705;

XX DT 17-JAN-2003 (first entry)

XX DE Conus sp conotoxin-associated peptide SEQ ID 490.

XX KW Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;

KW ligand-gated ion channel modulator; pain-relief.

XX OS Conus radiatus.

XX PN WO200264740-A2.

XX PD 22-AUG-2002.

XX PF 11-FEB-2002; 2002WO-US003887.

XX PR 09-FEB-2001; 2001US-0267408P.

XX PA (COGN-) COGNETIX INC.

PA (UTAH ) UNIV UTAH RES FOUND.

XX PI Olivera BM, McIntosh JM, Watkins M, Garrett JE, Cruz LJ;

PI Grilley M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;

XX DR WPI; 2002-706921/76.

XX PT New cone snail conotoxin peptides, useful as a pain reliever for  
 PT alleviating pain in an individual suffering from pain or who is about to  
 PT be subjected to a pain-causing event, or for treating voltage-gated ion  
 PT channel disorders.

XX PS Claim 1; Page 281; 305pp; English.

XX CC This invention describes novel conotoxin peptides from the cone snail,  
 CC genus Conus which have analgesic activity and can act as a voltage-gated  
 CC ion channel modulator or a ligand-gated ion channel modulator. The  
 CC conotoxin peptide is useful as a pain-relieving agent for alleviating  
 CC pain in an individual who is either exhibiting pain or is about to be  
 CC subjected to a pain-causing event. The conotoxin peptide is also useful  
 CC for treating or preventing disorders associated with voltage-gated ion  
 CC channel disorders, ligand-gated ion channel disorders or receptor  
 CC disorders. The radiolabeled conotoxin peptide is also useful for  
 CC characterizing a new site on these receptors or channels, and for  
 CC screening and identifying novel small molecules that interact with the

CC above-mentioned channels or receptors, which are monoamine transporters.  
CC ABG99360-ABG99853 represent the conotoxin protein and peptides described  
CC in the disclosure of the invention  
XX  
SQ Sequence 44 AA;

Query Match 21.3%; Score 44; DB 5; Length 44;  
Best Local Similarity 37.5%; Pred. No. 1.6e+02;  
Matches 9; Conservative 1; Mismatches 12; Indels 2; Gaps 1;  
QY 14 YALNCCGLAGVGEQFISDI--CPK 35  
| | | | | : | | | |  
Db 1 YGLGAGTCGSSSNCVRDYDCPK 24

RESULT 6  
AAR26006  
ID AAR26006 standard; peptide; 23 AA.

XX AAR26006;

XX 25-MAR-2003 (revised)

DT 26-JAN-1993 (first entry)

XX Influenza fusion peptide #3.

XX Haemagglutinin; cysteine; liposome.

XX Synthetic.

XX EP497997-A1.

PD 12-AUG-1992.

XX 02-FEB-1991; 91EP-00101414.

XX 02-FEB-1991; 91EP-00101414.

XX (NIPP ) NIPPON INST BIOLOGICAL SCIENCE.

PI Glueck R, Herrmann P, Klein P;

XX WPI; 1992-270078/33.

XX Drug-contg. phospholipid bi:layer vesicle with cell-specific markers on  
PT membrane - where markers have at least 90 per cent biological activity,  
PT used as pharmaceuticals against e.g. cancer and AIDS.

XX Disclosure; Fig 2; 13pp; English.

XX The sequences given in AAR26004-19 are Influenza fusion peptides, derived  
CC from the Influenza virus haemagglutinin gene which were used for the  
CC preparation of synthetic membrane vesicles. The arrangement of at least  
CC one, pref. three cysteine residues at one end of these peptides has been  
CC found useful for the fusion activity, for the fusion of the liposome to  
CC the target cell membrane. The liposomes produced using these peptides can  
CC contain at least one active drug and can be used to target cells infected  
CC with cancer or AIDS. (Updated on 25-MAR-2003 to correct PN field.)  
CC (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to  
CC correct PI field.)

XX Sequence 23 AA;

Query Match 20.8%; Score 43; DB 2; Length 23;  
Best Local Similarity 50.0%; Pred. No. 1.1e+02;  
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 18 CCGLAGGVEQFISD 31

Db 2 CCGLFGAIGAGFIEN 15

RESULT 7

XX Virosome; vesicle; cationic lipid bilayer; viral fusion peptide;

AAB70092

ID AAB70092 standard; peptide; 23 AA.

XX AAB70092;

XX 14-MAY-2001 (first entry)

XX Cationic virosome crosslinker #3 for polypeptide binding.

XX Cationic virosome; cytostatic; gene therapy; lipid bilayer vesicle;  
KW viral haemagglutinin; drug delivery; cancer; leukaemia; viral infection;  
crosslinker.

XX Unidentified.

XX NZ504444-A.

PD 24-NOV-2000.

XX 10-MAY-2000; 200NZ-00504444.

PR 08-MAY-1996; 96EP-00107282.

PR 04-MAY-1997; 97NZ-00332666.

XX (NIKA-) NIKA HEALTH PROD LTD.

XX Walti ER, Gluck R, Klein P;

XX WPI; 1997-558673/51.

XX Vesicle with cationic lipid bilayer that includes viral fusion peptide -  
PT used for delivery of genetic material to cells, especially for gene  
PT therapy of cancer, leukaemia and viral infections.

XX Disclosure; Page 14; 41pp; English.

XX The present sequence is a crosslinker which is capable of linking to the  
CC surface of a novel cationic virosome and is capable of binding  
CC polypeptides. The cationic virosome is a lipid bilayer vesicle comprising  
CC a membrane with a net positive charge and contains 5-30 weight % based on  
CC total lipids, 1,3-dioleoyloxy-2-(6-carboxy-spermyl)-propyl-amide  
CC (DOSPER), together with other lipids and at least one active fusogenic  
CC peptide. The fusogenic peptide is a viral haemagglutinin that causes the  
CC vesicle to be internalised by target cells through phagocytosis or  
CC endocytosis. The virosome is useful for delivering a desired drug or  
CC substance, preferably a nucleic acid, to target cells (resting or  
CC proliferating mammalian cells) such as cancer cells, leukaemic cells or  
CC virally infected cells in vitro, in diagnostic or medical applications  
CC and for the manufacture of medicament for carrying out non-infectious  
CC gene therapy

XX Sequence 23 AA;

Query Match 20.8%; Score 43; DB 2; Length 23;  
Best Local Similarity 50.0%; Pred. No. 1.1e+02;  
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 18 CCGLAGGVEQFISD 31

Db 2 CCGLFGAIGAGFIEN 15

RESULT 8

AAW34271

ID AAW34271 standard; peptide; 23 AA.

XX AAW34271;

XX 14-MAY-1998 (first entry)

XX Synthetic lipid vesicle fusion peptide 3.

XX Virosome; vesicle; cationic lipid bilayer; viral fusion peptide;

KW drug delivery system; membrane; gene therapy; diagnosis; treatment;  
 KW cancer; leukaemia; viral infection.  
 OS Synthetic.  
 XX WO9741834-A1.  
 PN  
 PD 13-NOV-1997.  
 XX  
 XX 04-MAY-1997; 97WO-EP002268.  
 XX  
 XX 08-MAY-1996; 96EP-00107282.  
 PR  
 XX (NIKA-) NIKA HEALTH PROD LTD.  
 PA  
 XX Waelti ER, Glueck R, Klein P;  
 PI  
 XX WPI; 1997-558673/51.  
 DR  
 XX  
 XX Vesicle with cationic lipid bilayer that includes viral fusion peptide -  
 PT used for delivery of genetic material to cells, especially for gene  
 PT therapy of cancer, leukaemia and viral infections.  
 XX  
 XX Disclosure; Page 10; 52pp; English.  
 XX  
 CC Peptides AAW34269-W34284 represent novel lipid vesicles with positively  
 CC charged lipid bilayer membranes composed of a cationic and/or  
 CC polycationic lipid and at least one natural or synthetic viral fusion  
 CC peptide integrated in, or covalently linked to, the membrane. Such  
 CC peptides are used as drug delivery systems, preferably for (non-)specific  
 CC delivery of genetic material to target cells or tissues, particularly for  
 CC diagnosis, treatment (especially antisense treatment) of cancer,  
 CC leukaemia and viral infections in humans or animals. Genetic material is  
 CC delivered, without infection, to resting or proliferating cells, in vitro  
 CC or in vivo. When the genetic material is an antisense molecule, it is  
 CC targeted to mRNA encoding a (proto)oncogene. The continuous lipid layer  
 CC does not leak. The peptides do not need to fuse with, or destabilise,  
 CC plasma membranes in order to enter the cytoplasm, since the fusion  
 CC peptide ensures cell penetration by endocytosis (after which fusion of  
 CC the vesicle and endosomal membrane occurs). The genetic material thus has  
 CC a greater chance of reaching the nucleus before it is degraded or  
 CC expelled. Transfer of the material is 1000-20000 times more efficient  
 CC than when using liposomes or conventional virosomes, so smaller doses can  
 CC be used, avoiding possible toxicity associated with the genetic material  
 XX  
 SQ Sequence 23 AA;  
 Query Match 20.8%; Score 43; DB 2; Length 23;  
 Best Local Similarity 50.0%; Pred. No. 1.1e+02;  
 Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
 QY 18 CCGLAGGVEQFISD 31  
 Db ||||| : || :  
 2 CCGLFGAAGFIEN 15  
 RESULT 9  
 AAR26004  
 ID AAR26004 standard; peptide; 26 AA.  
 AC  
 XX  
 XX AAR26004;  
 DT 25-MAR-2003 (revised)  
 DT 26-JAN-1993 (first entry)  
 DE Influenza fusion peptide #1.  
 XX  
 XX Haemagglutinin; cysteine; liposome.  
 KW  
 XX  
 OS Synthetic.  
 XX  
 XX EP497997-A1.  
 PN  
 XX

PD 12-AUG-1992.  
 XX  
 XX 02-FEB-1991; 91EP-00101414.  
 XX  
 PR 02-FEB-1991; 91EP-00101414.  
 XX  
 PA (NIPP ) NIPPON INST BIOLOGICAL SCIENCE.  
 XX  
 XX Glueck R, Herrmann P, Klein P;  
 PI  
 XX WPI; 1992-270078/33.  
 DR  
 XX Drug-contg. phospholipid bi-layer vesicle with cell-specific markers on  
 PT membrane - where markers have at least 90 per cent biological activity,  
 PT used as pharmaceuticals against e.g. cancer and AIDS.  
 XX  
 XX Disclosure; Fig 2; 13pp; English.  
 XX  
 CC The sequences given in AAR26004-19 are influenza fusion peptides, derived  
 CC from the influenza virus haemagglutinin gene which were used for the  
 CC preparation of synthetic membrane vesicles. The arrangement of at least  
 CC one, pref. three cysteine residues at one end of these peptides has been  
 CC found useful for the fusion activity, for the fusion of the liposome to  
 CC the target cell membrane. The liposomes produced using these peptides can  
 CC contain at least one active drug and can be used to target cells infected  
 CC with cancer or AIDS. (Updated on 25-MAR-2003 to correct PN field.)  
 CC (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to  
 CC correct PI field.)  
 XX  
 SQ Sequence 26 AA;  
 Query Match 20.8%; Score 43; DB 2; Length 26;  
 Best Local Similarity 50.0%; Pred. No. 1.2e+02;  
 Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
 QY 18 CCGLAGGVEQFISD 31  
 Db ||||| : || :  
 2 CCGLFGAAGFIEN 15  
 RESULT 10  
 AAB70090  
 ID AAB70090 standard; peptide; 26 AA.  
 XX  
 XX AAB70090;  
 XX  
 XX 14-MAY-2001 (first entry)  
 DT  
 XX  
 XX Cationic virosome crosslinker #1 for polypeptide binding.  
 DE  
 XX  
 KW Cationic virosome; cytostatic; gene therapy; lipid bilayer vesicle;  
 KW viral haemagglutinin; drug delivery; cancer; leukaemia; viral infection;  
 KW crosslinker.  
 XX  
 XX Unidentified.  
 OS  
 XX NZ504444-A.  
 PN  
 XX 24-NOV-2000.  
 PD  
 XX  
 XX 10-MAY-2000; 2000NZ-00504444.  
 PF  
 XX 08-MAY-1996; 96EP-00107282.  
 PR  
 XX 04-MAY-1997; 97NZ-00332666.  
 XX  
 XX (NIKA-) NIKA HEALTH PROD LTD.  
 PA  
 XX Waelti ER, Glueck R, Klein P;  
 PI  
 XX WPI; 1997-558673/51.  
 DR  
 XX Vesicle with cationic lipid bilayer that includes viral fusion peptide -  
 PT used for delivery of genetic material to cells, especially for gene

PT therapy of cancer, leukaemia and viral infections.  
XX Disclosure; Page 14; 41pp; English.  
XX The present sequence is a crosslinker which is capable of linking to the  
CC surface of a novel cationic virosome and is capable of binding  
CC polypeptides. The cationic virosome is a lipid bilayer vesicle comprising  
CC a membrane with a net positive charge and contains 5-30 weight % based on  
CC total lipids, 1,3-dioleoyloxy-2-(6-carboxy-spermyl)-propyl-amide  
CC (DOSPER), together with other lipids and at least one active fusogenic  
CC peptide. The fusogenic peptide is a viral haemagglutinin that causes the  
CC vesicle to be internalised by target cells through phagocytosis or  
CC endocytosis. The virosome is useful for delivering a desired drug or  
CC substance, preferably a nucleic acid, to target cells (resting or  
CC proliferating mammalian cells) such as cancer cells, leukaemic cells or  
CC virally infected cells in vitro, in diagnostic or medical applications  
CC and for the manufacture of medicament for carrying out non-infectious  
CC gene therapy  
XX  
SQ Sequence 26 AA;  
Query Match 20.8%; Score 43; DB 2; Length 26;  
Best Local Similarity 50.0%; Pred. No. 1.2e+02;  
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
QY 18 CCGLAGGVQVFISD 31  
Db ||||| : ||| :  
2 CCGLFGAIGAFIEN 15  
RESULT 11  
AAW34269  
ID AAW34269 standard; peptide; 26 AA.  
XX  
AC AAW34269;  
XX  
XX 14-MAY-1998 (first entry)  
XX  
DE Synthetic lipid vesicle fusion peptide 1.  
XX  
XX Virosome; vesicle; cationic lipid bilayer; viral fusion peptide;  
KW drug delivery system; membrane; gene therapy; diagnosis; treatment;  
KW cancer; leukaemia; viral infection.  
XX  
OS Synthetic.  
XX  
XX WO9741834-A1.  
XX  
XX 13-NOV-1997.  
XX  
XX 04-MAY-1997; 97WO-EP002268.  
XX  
XX 08-MAY-1996; 96EP-00107282.  
XX  
XX (NIKA-) NIKA HEALTH PROD LTD.  
XX  
XX Waelti ER, Glueck R, Klein P;  
XX  
XX WPI; 1997-558673/51.  
XX  
XX Vesicle with cationic lipid bilayer that includes viral fusion peptide -  
PT used for delivery of genetic material to cells, especially for gene  
PT therapy of cancer, leukaemia and viral infections.  
XX  
XX Disclosure; Page 10; 52pp; English.  
XX  
XX Peptides AAW34269-W34284 represent novel lipid vesicles with positively  
CC charged lipid bilayer membranes composed of a cationic and/or  
CC polycationic lipid and at least one natural or synthetic viral fusion  
CC peptide integrated in, or covalently linked to, the membrane. Such  
CC peptides are used as drug delivery systems, preferably for (non-)specific  
CC delivery of genetic material to target cells or tissues, particularly for  
CC diagnosis, treatment (especially antisense treatment) of cancer,

CC leukaemia and viral infections in humans or animals. Genetic material is  
CC delivered, without infection, to resting or proliferating cells, in vitro  
CC or in vivo. When the genetic material is an antisense molecule, it is  
CC targeted to mRNA encoding a (proto)oncogene. The continuous lipid layer  
CC does not leak. The peptides do not need to fuse with, or destabilise,  
CC plasma membranes in order to enter the cytoplasm, since the fusion of  
CC peptide ensures cell penetration by endocytosis (after which fusion of  
CC the vesicle and endosomal membrane occurs). The genetic material thus has  
CC a greater chance of reaching the nucleus before it is degraded or  
CC expelled. Transfer of the material is 1000-20000 times more efficient  
CC than when using liposomes or conventional virosomes, so smaller doses can  
CC be used, avoiding possible toxicity associated with the genetic material  
XX  
SQ Sequence 26 AA;  
Query Match 20.8%; Score 43; DB 2; Length 26;  
Best Local Similarity 50.0%; Pred. No. 1.2e+02;  
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
QY 18 CCGLAGGVQVFISD 31  
Db ||||| : ||| :  
2 CCGLFGAIGAFIEN 15  
RESULT 12  
ABW95674  
ID ABW95674 standard; protein; 44 AA.  
XX  
AC ABW95674;  
XX  
XX 02-JUN-2005 (first entry)  
XX  
DE M. xanthus protein sequence, seq id 14873.  
XX  
XX Transgenic plant; DNA replication; gene regulation; gene expression.  
KW  
XX Myxococcus xanthus.  
OS  
XX US6833447-B1.  
XX  
XX 21-DEC-2004.  
XX  
XX 10-JUL-2001; 2001US-00902540.  
XX  
XX 10-JUL-2000; 2000US-0217883P.  
XX  
XX (MONS ) MONSANTO TECHNOLOGY LLC.  
XX  
XX Goldman BS, Hinkle GJ, Slater SC, Wiegand RC;  
XX  
XX WPI; 2005-028716/03.  
XX  
XX New substantially purified Myxococcus xanthus nucleic acid molecule  
PT encoding a nitrite reductase, useful for determining gene expression,  
PT identifying mutations in a gene of interest, and for constructing  
PT mutations in a gene of interest.  
XX  
XX Example 2; SEQ ID NO 14873; 25pp; English.  
XX  
XX The invention relates to a substantially purified nucleic acid molecule  
CC encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a  
CC recombinant DNA construct for expression of a nitrite reductase gene in a  
CC plant cell, and a plant cell comprising the recombinant DNA construct.  
CC The nucleic acid is useful for determining gene expression, identifying  
CC mutations in a gene of interest, and for constructing mutations in a gene  
CC of interest. Sequences given in records for SEQ IDs 9692-16825 represent  
CC a group of 7134 Myxococcus xanthus proteins and peptides. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from USPRO  
XX  
SQ Sequence 44 AA;  
Query Match 20.8%; Score 43; DB 9; Length 44;

[illegible]



PR 17-NOV-2000; 2000US-0249216P.  
PR 17-NOV-2000; 2000US-0249217P.  
PR 17-NOV-2000; 2000US-0249218P.  
PR 17-NOV-2000; 2000US-0249244P.  
PR 17-NOV-2000; 2000US-0249245P.  
PR 17-NOV-2000; 2000US-0249264P.  
PR 17-NOV-2000; 2000US-0249265P.  
PR 17-NOV-2000; 2000US-0249297P.  
PR 17-NOV-2000; 2000US-0249299P.  
PR 17-NOV-2000; 2000US-0249300P.  
PR 01-DEC-2000; 2000US-0250160P.  
PR 01-DEC-2000; 2000US-0250391P.  
PR 05-DEC-2000; 2000US-0251030P.  
PR 05-DEC-2000; 2000US-0251988P.  
PR 05-DEC-2000; 2000US-0256719P.  
PR 06-DEC-2000; 2000US-0251479P.  
PR 08-DEC-2000; 2000US-0251856P.  
PR 08-DEC-2000; 2000US-0251868P.  
PR 08-DEC-2000; 2000US-0251869P.  
PR 08-DEC-2000; 2000US-0251989P.  
PR 08-DEC-2000; 2000US-0251990P.  
PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-0259678P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX Rosen CA, Barash SC, Ruben SM;  
XX WPI; 2001-457726/49.  
DR N-PSDB; AAS32385.  
XX  
PT Isolated polypeptide for treating, preventing and prognosing disorders  
PT related to the endocrine system including endocrine disorders,  
PT reproductive disorders, and gastrointestinal disorders and also for  
PT testing and detection e.g. diagnosis.  
XX  
PS Claim 11; SEQ ID NO 339; 558pp; English.  
XX  
XX The invention relates to cDNAs encoding novel human endocrine antigens or  
CC a fragment having biological activity, a domain, an epitope, full length  
CC protein, variant, allelic variant or a species homologue of the  
CC cDNA/antigen. The DNAs and polypeptides are useful for preventing,  
CC treating or ameliorating a medical condition when administered (e.g. by  
CC gene therapy or antisense-therapy). Identifying mutations in the genes  
CC coding for the antigens is useful for diagnosing a pathological condition  
CC or a susceptibility to a pathological condition. The DNAs, antigens and  
CC antibodies raised against the antigens useful for treating, preventing  
CC and/or prognosing disorders related to the endocrine system or hormone  
CC imbalance or reproductive disorders, cancers of endocrine tissues,  
CC disorders of the pancreas (e.g. diabetes mellitus), the adrenal glands  
CC (e.g. hirsutism), ovaries, the thyroid (e.g. hyperthyroidism), the  
CC hypothalamus and testes (e.g. vanishing testes syndrome), many examples  
CC of diseases and disorders are given in the specification. The present  
CC sequence represents an endocrine antigen of the invention. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 50 AA;  
Query Match 20.5%; Score 42.5; DB 4; Length 50;  
Best Local Similarity 42.3%; Pred. NO. 3e+02; 8; Indels 5; Gaps 1;  
Matches 11; Conservative 2; Mismatches 8;  
QY 6 RETLKAIHYALNCCGLAGVEQFISD 31  
|:|:|  
Db 17 RKTIVA----QCCGLKGFENNAISD 37  
|:|:|  
RESULT 14  
AEG99385  
ID AEG99385 standard; peptide; 32 AA.  
XX

AC ABG99385;  
XX  
DT 17-JAN-2003 (first entry)  
XX  
DE Conus sp conotoxin-associated peptide SEQ ID 39.  
XX  
KW Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;  
KW ligand-gated ion channel modulator; pain-relief.  
XX  
OS Conus arenatus.  
XX WO200264740-A2.  
XX  
XX 22-AUG-2002.  
XX  
PF 11-FEB-2002; 2002WO-US003887.  
XX  
PR 09-FEB-2001; 2001US-0267408P.  
XX  
PA (COGN-) COGNETIX INC.  
PA (UTAH) UNIV UTAH RES FOUND.  
XX  
PI Olivera BM, McIntosh JM, Watkins M, Garrett JE, Cruz LJ;  
PI Grilley M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;  
XX WPI; 2002-706921/76.  
DR  
XX  
XX New cone snail conotoxin peptides, useful as a pain reliever for  
PT alleviating pain in an individual suffering from pain or who is about to  
PT be subjected to a pain-causing event, or for treating voltage-gated ion  
PT channel disorders.  
XX  
PS Claim 1; Page 122; 305pp; English.  
XX  
CC This invention describes novel conotoxin peptides from the cone snail,  
CC genus Conus which have analgesic activity and can act as a voltage-gated  
CC ion channel modulator or a ligand-gated ion channel modulator. The  
CC conotoxin peptide is useful as a pain-relieving agent for alleviating  
CC pain in an individual who is either exhibiting pain or is about to be  
CC subjected to a pain-causing event. The conotoxin peptide is also useful  
CC for treating or preventing disorders associated with voltage-gated ion  
CC channel disorders, ligand-gated ion channel disorders or receptor  
CC disorders. The radiolabeled conotoxin peptide is also useful for  
CC characterising a new site on these receptors or channels, and for  
CC screening and identifying novel small molecules that interact with the  
CC above-mentioned channels or receptors, which are monoamine transporters.  
CC ABG99360-ABG99853 represent the conotoxin protein and peptides described  
CC in the disclosure of the invention  
XX  
SQ Sequence 32 AA;  
Query Match 20.0%; Score 41.5; DB 5; Length 32;  
Best Local Similarity 43.8%; Pred. No. 2.5e+02;  
Matches 7; Conservative 3; Mismatches 5; Indels 1; Gaps 1;  
QY 18 CCGLAGVEQFISD 33  
|:|:|:|:|:|:|  
Db 17 CCGLXNG-QXFCAXVC 31  
|:|:|:|:|:|:|  
RESULT 15  
AA55679  
ID AA55679 standard; protein; 49 AA.  
XX  
XX AA55679;  
XX  
XX 07-FEB-2000 (first entry)  
XX  
XX E. coli ycfB peptide motif 3.  
XX  
KW ycfB polypeptide; gram negative bacteria; gram positive bacteria;  
KW antibacterial; bacterial infection; bacterial viability; antibiotic.  
XX



CC measuring human gene expression in a sample derived from human cervical  
CC epithelial cells. By measuring gene expression, the probes are therefore  
CC useful in grading and/or staging of diseases of the cervix, notably  
CC cervical cancer. Note: The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX  
SQ Sequence 44 AA;  
Query Match 19.8%; Score 41; DB 4; Length 44;  
Best Local Similarity 47.4%; Pred. No. 4.2e+02;  
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAHYALNCC 19  
||| :||| :|||  
DB 10 KDRASQSLQKIYCGNCC 28

RESULT 18  
AAG74910  
ID AAG74910 standard; protein; 44 AA.  
AC AAG74910;  
XX  
DT 03-SEP-2001 (first entry)  
XX  
DE Human colon cancer antigen protein SEQ ID NO:5674.  
XX  
KW Human; colon cancer; colon cancer antigen; diagnosis; detection;  
KW colorectal carcinoma; chromosome 19.  
XX  
OS Homo sapiens.  
XX  
PN WO200122920-A2.  
XX  
PD 05-APR-2001.  
XX  
PF 28-SEP-2000; 2000WO-US026524.  
XX  
PR 29-SEP-1999; 99US-0157137P.  
PR 03-NOV-1999; 99US-0163280P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Ruben SM, Barash SC, Birse CE, Rosen CA;  
XX  
DR WPI; 2001-235357/24.  
DR N-PSDB; AAH34315.  
XX  
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,  
PT useful for preventing, diagnosing and/or treating colorectal cancers.  
XX  
XX Claim 11; Page 7216; 9803pp; English.

CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon  
CC cancer-associated nucleic acid molecules (N) and proteins (P), where the  
CC proteins are collectively known as colon cancer antigens. The colon  
CC cancer antigens have cytostatic activity and can be used in gene therapy  
CC and vaccine production. N and P may be used in the prevention, diagnosis  
CC and treatment of diseases associated with inappropriate P expression. For  
CC example, N and P may be used to treat disorders associated with decreased  
CC expression by rectifying mutations or deletions in a patient's genome  
CC that affect the activity of P by expressing inactive proteins or to  
CC supplement the patients own production of P. Additionally, N may be used  
CC to produce the colon cancer-associated Ps, by inserting the nucleic acids  
CC into a host cell and culturing the cell to express the proteins. N and P  
CC can be used in the prevention, diagnosis and treatment of colorectal  
CC carcinomas and cancers. AAH37196 to AAH37204 and AAG77789 represent  
CC sequences used in the exemplification of the present invention. N.B.  
CC Pages 666 to 682 and page 7053 of the sequence listing were missing at  
CC time of publication, meaning no sequences are present for SEQ ID NO:1027  
CC to 1052, 7921 and 7922

SQ Sequence 44 AA;  
Query Match 19.8%; Score 41; DB 4; Length 44;  
Best Local Similarity 35.0%; Pred. No. 4.2e+02;  
Matches 7; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 17 NCCGLAGGVEQFISDICKK 36  
||| : : :|||  
DB 3 NCITVTNEILSLLSICKK 22

RESULT 19  
ABB35365  
ID ABB35365 standard; peptide; 44 AA.  
XX  
AC ABB35365;  
XX  
DT 04-FEB-2002 (first entry)  
XX  
DE Peptide #2871 encoded by human foetal liver single exon probe.  
XX  
KW Human; foetal liver; gene expression; single exon nucleic acid probe.  
XX  
OS Homo sapiens.  
XX  
PN WO200157277-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US000669.  
XX  
PR 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
DR WPI; 2001-483447/52.  
XX  
PT Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human fetal liver.  
XX  
PS Claim 27; SEQ ID NO 28000; 639pp + Sequence Listing; English.

CC The invention relates to a single exon nucleic acid probe for measuring  
CC human gene expression in a sample derived from human foetal liver. The  
CC single exon nucleic acid probes may be used for predicting, measuring and  
CC displaying gene expression in samples derived from human fetal liver. The  
CC present sequence is a peptide encoded by a single exon nucleic acid probe  
CC of the invention. Note: The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX  
SQ Sequence 44 AA;  
Query Match 19.8%; Score 41; DB 4; Length 44;  
Best Local Similarity 47.4%; Pred. No. 4.2e+02;  
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAHYALNCC 19  
||| :||| :|||  
DB 10 KDRASQSLQKIYCGNCC 28

RESULT 20  
AAM28874  
ID AAM28874 standard; protein; 44 AA.



PF 30-JAN-2001; 2001WO-US000666.  
XX 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
XX 04-OCT-2000; 2000GB-00024263.  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
PA Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2001-488899/53.  
XX Single exon nucleic acid probes for analyzing gene expression in human  
PT hearts.  
XX Claim 15; SEQ ID NO 22577; 530pp; English.  
XX The present invention relates to single exon nucleic acid probes for  
CC measuring human gene expression in a sample derived from human heart (see  
CC ABA21535-ABA41305). The present sequence is a protein encoded by one such  
CC probe. The probes may be used for predicting, measuring and displaying  
CC gene expression in samples derived from the human heart via microarrays.  
CC By measuring gene expression, the probes are useful for predicting, the  
CC diagnosing, grading, staging, monitoring and prognosing diseases of the  
CC human heart and vascular system e.g. cardiovascular disease,  
CC hypertension, cardiac arrhythmias and congenital heart disease. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 44 AA;  
Query Match 19.8%; Score 41; DB 4; Length 44;  
Best Local Similarity 47.4%; Pred. No. 4.2e+02;  
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;  
QY 1 KDEPQRETLKAIHYALNCC 19  
DB 10 KDRASQTLQKIYCGNGC 28  
|||:|:|:|:|  
RESULT 23  
AAM68569  
ID AAM68569 standard; protein; 44 AA.  
XX  
AC AAM68569;  
XX  
DT 06-NOV-2001 (first entry)  
XX  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 28875.  
XX  
DE Human bone marrow expressed exon; gene expression analysis; probe;  
KW microarray; cancer; leukaemia; lymphoma; myeloma.  
KW  
XX Homo sapiens.  
OS  
XX WO200157276-A2.  
FN  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US000666.  
XX  
XX 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
XX 04-OCT-2000; 2000GB-00024263.  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
PA Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2001-488899/52.  
XX Single exon nucleic acid probes for analyzing gene expression in human  
PT brains.  
XX Example 4; SEQ ID NO 28301; 650pp + Sequence Listing; English.  
XX The present invention provides a number of single exon nucleic acid  
CC probes which are derived from genomic sequences expressed in the human  
CC brain. They can be used to measure gene expression in brain cell samples,

XX (MOLE-) MOLECULAR DYNAMICS INC.  
PA Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2001-488900/53.  
XX Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human bone marrow.  
XX Example 4; SEQ ID NO 28875; 658pp + Sequence Listing; English.  
XX The present invention provides a number of single exon nucleic acid  
CC probes which are derived from genomic sequences expressed in the human  
CC bone marrow. They can be used to measure gene expression in bone marrow  
CC samples, which may enable the improved diagnosis and treatment of cancers  
CC such as lymphoma, leukaemia and myeloma. The present sequence is a  
CC protein encoded by one of the probes of the invention  
XX  
XX Sequence 44 AA;  
Query Match 19.8%; Score 41; DB 4; Length 44;  
Best Local Similarity 47.4%; Pred. No. 4.2e+02;  
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;  
QY 1 KDEPQRETLKAIHYALNCC 19  
DB 10 KDRASQTLQKIYCGNGC 28  
|||:|:|:|:|  
RESULT 24  
AAM56196  
ID AAM56196 standard; protein; 44 AA.  
XX  
AC AAM56196;  
XX  
DT 05-NOV-2001 (first entry)  
XX  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 28301.  
XX  
DE Human; brain expressed exon; gene expression analysis; probe; microarray;  
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.  
KW  
XX Homo sapiens.  
OS  
XX WO200157275-A2.  
FN  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US000667.  
XX  
XX 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
XX 04-OCT-2000; 2000GB-00024263.  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
PA Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2001-483446/52.  
XX Single exon nucleic acid probes for analyzing gene expression in human  
PT brains.  
XX Example 4; SEQ ID NO 28301; 650pp + Sequence Listing; English.  
XX The present invention provides a number of single exon nucleic acid  
CC probes which are derived from genomic sequences expressed in the human  
CC brain. They can be used to measure gene expression in brain cell samples,

CC which may enable the diagnosis and improved treatment of nervous system  
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,  
CC epilepsy and cancers. The present sequence is a protein encoded by one of  
CC the probes of the invention

XX SQ Sequence 44 AA;

Query Match 19.8%; Score 41; DB 4; Length 44;  
Best Local Similarity 47.4%; Pred. No. 4.2e+02;  
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 KDEPQRETAKIHYALNCC 19  
|||:|:|  
Db 10 KDRASQTLQKIYCGNGC 28

RESULT 25

ABG50232  
ID ABG50232 standard; peptide; 44 AA.

XX AC ABG50232;

DT 25-FEB-2003 (first entry)

XX Human liver peptide, SEQ ID No 28880.

XX Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;  
KW hypercholesterolaemia; coronary heart disease.

XX OS Homo sapiens.

XX PN WO200157273-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000664.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488898/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

PT gene expression in human adult liver.

XX Claim 27; SEQ ID NO 28880; 658pp; English.

XX The invention relates to a single exon nucleic acid probe (SENP) (I) for  
CC measuring human gene expression in a sample derived from human adult  
CC liver, comprising one of 13109 defined nucleotide sequences given in the  
CC specification (or complements/ fragments). The probe hybridises at high  
CC stringency to a nucleic acid molecule expressed in the human adult liver.  
CC (I) may be used for predicting, measuring and displaying gene expression  
CC in samples derived from human adult liver. The genes identified may be  
CC involved in genetic liver diseases such as cirrhosis,  
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is  
CC associated with coronary heart disease. ABG47348-ABG59930 represent human  
CC liver single exon encoded peptides of the invention. Note: The sequence  
CC information for this patent does not appear in the printed specification  
CC but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 44 AA;

Query Match 19.8%; Score 41; DB 4; Length 44;  
Best Local Similarity 47.4%; Pred. No. 4.2e+02;  
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 KDEPQRETAKIHYALNCC 19  
|||:|:|  
Db 10 KDRASQTLQKIYCGNGC 28

RESULT 26

AA04113  
ID AA04113 standard; protein; 44 AA.

XX AC AA04113;

XX DT 09-OCT-2001 (first entry)

XX DE Peptide #2795 encoded by probe for measuring breast gene expression.

XX KW Probe; human; breast disease; breast cancer; development disorder;  
KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.

XX OS Homo sapiens.

XX PN WO200157270-A2.

XX PD 09-AUG-2001.

XX PF 29-JAN-2001; 2001WO-US000661.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-476286/51.

XX Novel single exon nucleic acid probe used to measuring gene expression in

PT a human breast.

XX Claim 27; SEQ ID NO 12853; 322pp; English.

XX The present invention relates to novel single exon nucleic acid probes  
CC (see AAI00010-AA110067). The present sequence is a peptide encoded by one  
CC such probe. The probes are useful for measuring human gene expression in  
CC a human breast sample, where the probe hybridises at high stringency to a  
CC nucleic acid expressed in the human breast. The probes are useful for  
CC predicting, diagnosing, grading, staging, monitoring and prognosing  
CC diseases of the human breast, particularly those diseases with polygenic  
CC aetiology. The diseases include: breast cancer, disorders of development,  
CC inflammatory diseases of the breast, fibrocystic changes, proliferative  
CC breast disease and non-carcinoma tumours. Note: The sequence data for  
CC this patent did not form part of the printed specification, but was  
CC obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 44 AA;

Query Match 19.8%; Score 41; DB 4; Length 44;  
Best Local Similarity 47.4%; Pred. No. 4.2e+02;  
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 KDEPQRETAKIHYALNCC 19  
|||:|:|  
Db 10 KDRASQTLQKIYCGNGC 28

RESULT 27  
 ABG38147  
 ID ABG38147 standard; peptide; 44 AA.  
 XX  
 AC ABG38147;  
 XX  
 DT 19-AUG-2002 (first entry)  
 XX  
 DE Human peptide encoded by genome-derived single exon probe SEQ ID 27812.  
 XX  
 KW Human; single exon probe; asthma; lung cancer; COPD; ILD;  
 KW chronic obstructive pulmonary disease; interstitial lung disease;  
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;  
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;  
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;  
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;  
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;  
 KW primary ciliary dyskinesia; pulmonary hypertension;  
 KW hyaline membrane disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200186003-A2.  
 XX  
 PD 15-NOV-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US000665.  
 XX  
 PR 04-FEB-2000; 2000US-0180312P.  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX  
 XX WPI; 2002-114183/15.  
 XX  
 XX Spatially-addressable set of single exon nucleic acid probes, used to  
 PT measure gene expression in human lung samples.  
 XX  
 PS Claim 27; SEQ ID NO 27812; 634pp; English.  
 XX  
 CC The invention relates to a spatially-addressable set of single exon  
 CC nucleic acid probes for measuring gene expression in a sample derived  
 CC from human lung comprising single exon nucleic acid probes having one of  
 CC 12614 nucleic acid sequences mentioned in the specification, or their  
 CC complements or the 12387 open reading frames derived from the 12614  
 CC probes. Also included are a microarray comprising the novel set of probes  
 CC; the novel set of probes which hybridise at high stringency to a nucleic  
 CC acid expressed in the human lung; measuring gene expression in a sample  
 CC derived from human lung, comprising (a) contacting the array with a  
 CC collection of detectably labeled nucleic acids derived from human lung  
 CC mRNA, and (b) measuring the label detectably bound to each probe of the  
 CC array; identifying exons in a eukaryotic genome, comprising (a)  
 CC algorithmically predicting at least one exon from genomic sequences of  
 CC the eukaryote; and (b) detecting specific hybridisation of detectably  
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,  
 CC having a fragment identical to the predicted exon, the probe is included  
 CC in the above mentioned microarray; assigning exons to a single gene,  
 CC comprising (a) identifying exons from genomic sequence by the method  
 CC above and (b) measuring the expression of each of the exons in several  
 CC tissues and/or cell types using hybridisation to a single exon  
 CC microarrays having a probe with the exon, where a common pattern of  
 CC expression of the exons in the tissues and/or cell types indicates that  
 CC the exons should be assigned to a single gene; a peptide comprising one  
 CC of 12011 sequences, mentioned in the specification, or encoded by the  
 CC probes/open reading frames (ORF). The probes are used for gene expression

CC analysis, and for identifying exons in a gene, particularly using human  
 CC lung derived mRNA and for the study of lung diseases such as asthma, lung  
 CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung  
 CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,  
 CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-  
 CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary  
 CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,  
 CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary  
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The  
 CC present sequence is a peptide/protein encoded by a single exon probe of  
 CC the invention. Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 44 AA;

Query Match 19.8%; Score 41; DB 5; Length 44;  
 Best Local Similarity 47.4%; Pred. No. 4.2e+02;  
 Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 KDEPQRETLLKAIHYALNCC 19  
 |||:|:|:|:|:|:|:|:|:|  
 Db 10 KDRAGSQTLQKIIYCGNGC 28

RESULT 28  
 AAY31910  
 ID AAY31910 standard; protein; 46 AA.  
 XX  
 AC AAY31910;

DT 21-DEC-1999 (first entry)

DE Spider venom insecticidal toxin.

KW Spider venom; toxin; insecticide; peatocide; transgenic plant;  
 KW biological control; crop protection.

OS Segestria florentina.

PN WO9949035-A2.

PD 30-SEP-1999.

PF 23-MAR-1999; 99WO-GB000907.

PR 26-MAR-1998; 98RU-00105686.

PA (ZENEC) ZENECA LTD.

PI Windass JD, Blake AN, Grishin EV, Nosyreva ED, Koslov SA;  
 PI Lipkin AV;

XX WPI; 1999-591091/50.

DR N-PSDB; AAZ20006.

XX Segestria florentina derived insecticidal agents and related  
 XX polynucleotides.

PS Claim 8; Page 17; 40pp; English.

XX The present sequence comprises the sequence of a F5.5/F5.6/F5.7 family  
 CC toxin of Segestria florentina spider venom. The sequence was deduced from  
 CC cDNA (see AAZ20006) produced by PCR amplification of S. florentina venom  
 CC gland cDNA. Claimed insecticidal agents include the partial and extended  
 CC peptides given in AAY31905-17. These peptides can be isolated from S.  
 CC florentina spider venom and/or are encoded by S. florentina venom gland  
 CC mRNA. Nucleic acid sequences (see AAZ20001-11) encoding these toxins may  
 CC be incorporated into insect viruses such as baculoviruses for use in  
 CC biological control of insect pests, or into recombinant plants for crop  
 CC protection

XX Sequence 46 AA;



Query Match 19.8%; Score 41; DB 2; Length 46;  
Best Local Similarity 57.1%; Pred. No. 4.4e+02;  
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 7 ETLKAIHYALNCCG 20  
||: || ||||  
Db 7 ETVCIHNNHNCG 20

## RESULT 29

AAV55680  
ID AAY55680 standard; protein; 49 AA.

XX AC AAY55680;

XX DT 07-FEB-2000 (first entry)

XX DE H. influenza ycfB peptide motif 3.

XX KW ycfB polypeptide; gram negative bacteria; gram positive bacteria;  
XX KM antibacterial; bacterial infection; bacterial viability; antibiotic.

XX OS Haemophilus influenzae.

XX PN WO9954462-A2.

XX PD 28-OCT-1999.

XX PF 20-APR-1999; 99WO-EP002638.

XX PR 22-APR-1998; 98GB-00008350.

XX PA (GLAX ) GLAXO GROUP LTD.

XX PI Arigoni F, Edgerton MD, Loferer H, Peitsch MC;

XX DR WPI; 2000-013249/01.

XX PT Novel bacterial polypeptides used to identify broad spectrum antibiotics.

XX PS Claim 3; Fig 2C; 56pp; English.

XX This invention discloses a novel family of polypeptides, designated the ycfB family, required for the growth of both gram negative and gram positive bacteria. The novel polypeptide of ycfB family is defined by: (a) a HSP score of greater than or equal to 100 when compared with one of the amino acid sequences of the ycfB family members given in the specification, when the BLAST algorithm is used with a BLOSUM62 scoring matrix; (b) containing a set of amino acid sequences which are positively identified when position dependent scoring matrices according to tables 1-4 (given in the specification) are used to yield a p-value of less than 110-60; or (c) comprising any one of the sequences shown in AAY55710-711. The ycfB polypeptides and polynucleotides can be used in method to identify antagonists and antibacterial compounds. These antagonists and compounds can be used to treat bacterial infections. The polypeptides of the invention are essential proteins for bacterial viability, and represent new targets for antibiotics. Sequences AAY55447-709 represent different motifs of the ycfB family polypeptides of various bacterial species

XX SQ Sequence 49 AA;

Query Match 19.8%; Score 41; DB 3; Length 49;  
Best Local Similarity 50.0%; Pred. No. 4.8e+02;  
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 19 CGLAGGVQFIS 30  
||: ||||: ||

Db 14 CGMSGGVDSVS 25

## RESULT 30

## ABG99768

ID ABG99768 standard; peptide; 32 AA.

XX AC ABG99768;

XX DT 17-JAN-2003 (first entry)

XX DE Conus sp conotoxin-associated peptide SEQ ID 553.

XX KW Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;  
XX KM ligand-gated ion channel modulator; pain-relief.

XX OS Conus sp.

XX PN WO200264740-A2.

XX PD 22-AUG-2002.

XX PF 11-FEB-2002; 2002WO-US003887.

XX PR 09-FEB-2001; 2001US-0267408P.

XX PA (COGN-) COGNETIX INC.

XX PU (UTAH ) UNIV UTAH RES FOUND.

XX PI Olivera BM, McIntosh JM, Watkins M, Garrett JE, Cruz LJ;

XX PD Grille M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;

XX DR WPI; 2002-706921/76.

XX New cone snail conotoxin peptides, useful as a pain reliever for PT alleviating pain in an individual suffering from pain or who is about to be subjected to a pain-causing event, or for treating voltage-gated ion channel disorders.

XX PS Claim 1; Page 289; 305pp; English.

XX This invention describes novel conotoxin peptides from the cone snail, genus Conus which have analgesic activity and can act as a voltage-gated ion channel modulator or a ligand-gated ion channel modulator. The conotoxin peptide is useful as a pain-relieving agent for alleviating pain in an individual who is either exhibiting pain or is about to be subjected to a pain-causing event. The conotoxin peptide is also useful for treating or preventing disorders associated with voltage-gated ion channel disorders, ligand-gated ion channel disorders or receptor disorders. The radiolabeled conotoxin peptide is also useful for characterizing a new site on these receptors or channels, and for screening and identifying novel small molecules that interact with the above-mentioned channels or receptors, which are monoamine transporters. CC ABG99360-ABG99853 represent the conotoxin protein and peptides described in the disclosure of the invention

XX SQ Sequence 32 AA;

Query Match 19.6%; Score 40.5; DB 5; Length 32;  
Best Local Similarity 43.8%; Pred. No. 3.5e+02;  
Matches 7; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 18 CCGLAGGVQFISDIC 33  
||| | : | : |

Db 17 CCGLENG-QPFCAPVC 31

## RESULT 31

## ABG99387

ID ABG99387 standard; peptide; 32 AA.

XX AC ABG99387;

XX DT 17-JAN-2003 (first entry)

XX DE Conus sp conotoxin-associated peptide SEQ ID 42.

KW Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;  
 KW ligand-gated ion channel modulator; pain-relief.  
 XX  
 OS Conus arenatus.  
 XX  
 PN WO200264740-A2.  
 XX  
 PD 22-AUG-2002.  
 XX  
 XX 11-FEB-2002; 2002WO-US003887.  
 PF  
 XX 09-FEB-2001; 2001US-0267408P.  
 PR  
 XX (COGN-) COGNETIX INC.  
 PA (UTAH) UNIV UTAH RES FOUND.  
 XX  
 XX Olivera BM, McIntosh JM, Watkins M, Garrett JE, Cruz LJ;  
 PI Grilleley M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;  
 XX WPI; 2002-706921/76.  
 DR  
 XX New cone snail conotoxin peptides, useful as a pain reliever for  
 PT alleviating pain in an individual suffering from pain or who is about to  
 PT be subjected to a pain-causing event, or for treating voltage-gated ion  
 PT channel disorders.  
 XX  
 XX Claim 1; Page 123; 305pp; English.  
 PS  
 XX This invention describes novel conotoxin peptides from the cone snail,  
 CC genus Conus which have analgesic activity and can act as a voltage-gated  
 CC ion channel modulator or a ligand-gated ion channel modulator. The  
 CC conotoxin peptide is useful as a pain-relieving agent for alleviating  
 CC pain in an individual who is either exhibiting pain or is about to be  
 CC subjected to a pain-causing event. The conotoxin peptide is also useful  
 CC for treating or preventing disorders associated with voltage-gated ion  
 CC channel disorders. Ligand-gated ion channel disorders or receptor  
 CC disorders. The radiolabeled conotoxin peptide is also useful for  
 CC characterising a new site on these receptors or channels, and for  
 CC screening and identifying novel small molecules that interact with the  
 CC above-mentioned channels or receptors, which are monoamine transporters.  
 CC ABG9360-ABG99853 represent the conotoxin protein and peptides described  
 CC in the disclosure of the invention  
 XX  
 XX Sequence 32 AA;  
 SQ  
 Query Match 19.6%; Score 40.5; DB 5; Length 32;  
 Best Local Similarity 41.2%; Pred. No. 3.5e+02;  
 Matches 7; Conservative 4; Mismatches 5; Indels 1; Gaps 1;  
 QY 17 NCGLAGGVQPTSDIC 33  
 :||| | : : :  
 Db 16 HCCGLXNG-QXFCALC 31  
 RESULT 32  
 AAW47052  
 ID AAW47052 standard; peptide; 25 AA.  
 XX  
 AC AAW47052;  
 XX  
 XX 15-MAY-1998 (first entry)  
 DT  
 XX HIV-1 V3 loop peptide sequence 4 (strain SC.B).  
 DE  
 XX Human rhinovirus; HRV 14; influenza virus; HIV-1; V3 loop; chimeric;  
 KW immunogenic epitope; immunisation; immune response; vaccine; pathogen;  
 KW tumour; Human immunodeficiency virus type 1.  
 XX  
 OS Synthetic.  
 XX Human immunodeficiency virus 1.  
 OS  
 PN US5714374-A.  
 XX

PD 03-FEB-1998.  
 XX  
 PF 17-MAR-1995; 95US-00406347.  
 XX  
 PR 12-SEP-1990; 90US-00582335.  
 PR 01-APR-1993; 93US-00041790.  
 PR 12-SEP-1994; 94US-00304635.  
 XX  
 XX (RUTF) UNIV RUTGERS STATE NEW JERSEY.  
 PA  
 XX Arnold EV, Arnold GF;  
 PI WPI; 1998-129862/12.  
 DR  
 XX Chimeric human rhino-viruses expressing heterologous antigens for use in  
 PT vaccines, etc. - is constructed by inserting heterologous nucleotide  
 PT sequence encoding chimeric region into the nucleotide sequence of human  
 PT rhinovirus encoding part of a neutralising immunogenic site.  
 XX  
 XX Example 3; Col 23; 27pp; English.  
 PS  
 XX This peptide sequence is from the human immunodeficiency virus (HIV-1) V3  
 CC loop sequence library. A library of chimeric human rhinovirus 14 (HRV 14)  
 CC displaying many HIV-1 V3 loop sequences in a vast array of conformations  
 CC can be constructed. A recombinant chimeric HRV can be constructed by  
 CC inserting a heterologous nucleotide sequence encoding a chimeric region  
 CC into the nucleotide sequence of a HRV encoding part of a neutralising  
 CC immunogenic site. The chimeric region is expressed on the surface of the  
 CC chimeric virus and is capable of participating in an immune reaction. The  
 CC rhinovirus is an HRV serotype that binds to ICAM-1. The chimeric region  
 CC is presented in neutralising immunogenic site Nim-II of viral protein  
 CC VP2. The virus is a retrovirus, preferably HIV-1 or HIV-2. The virus can  
 CC also be an orthomyxovirus, preferably an influenza virus for other  
 CC chimeric constructs. The chimeric region is from the haemagglutinin  
 CC antigen of the influenza virus, the region comprising amino acids 128-136  
 CC of the haemagglutinin antigen. In other chimeric constructs, a HRV 14  
 CC chimeric region can also be presented in neutralising immunogenic site  
 CC Nim-IA of viral protein VP1. The virus can be a picorna virus, preferably  
 CC poliovirus, where the chimeric region is from the N-Agi site of the polio  
 CC virus and comprises amino acids 93-100 of the N-Agi site and the  
 CC poliovirus is of type 3. When the chimeric region is of nonviral origin,  
 CC it is derived from a neoplasm, parasite or bacterium. Multiple  
 CC neutralising sites of the chimeric rhinovirus contain a chimeric region  
 CC which at each neutralising site is different. The rhinoviruses are used  
 CC in vaccines against the pathogen or tumour from which the heterologous  
 CC sequence is derived. It can be used for generating antibodies for passive  
 CC immunisation and immunodiagnostic testing and for research into  
 CC antigenicity and immunogenicity. Chimeric human rhinoviruses are only  
 CC mildly pathogenic and have numerous potential serotypes and can elicit  
 CC significant mucosal and serum immunological responses  
 XX  
 XX Sequence 25 AA;  
 SQ  
 Query Match 19.3%; Score 40; DB 2; Length 25;  
 Best Local Similarity 58.3%; Pred. No. 3.1e+02;  
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 4 FQETLKAIHYA 15  
 | :|||  
 Db 10 PNNNTKSIHYA 21  
 RESULT 33  
 AAM84731  
 ID AAM84731 standard; protein; 44 AA.  
 XX  
 AC AAM84731;  
 XX  
 XX 07-NOV-2001 (first entry)  
 DT  
 XX Human immune/haematopoietic antigen SEQ ID NO:12324.  
 DE  
 XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;  
 KW

KW cytostatic; gene therapy; vaccine; metastasis.

OS Homo sapiens.

PN WO200157182-A2.

PP 09-AUG-2001.

XX 17-JAN-2001; 2001WO-US001354.

XX 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184564P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

PR 26-JUL-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-0225213P.

PR 14-AUG-2000; 2000US-0225214P.

PR 14-AUG-2000; 2000US-0225266P.

PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-0225268P.

PR 14-AUG-2000; 2000US-0225270P.

PR 14-AUG-2000; 2000US-0225447P.

PR 14-AUG-2000; 2000US-0225757P.

PR 14-AUG-2000; 2000US-0225758P.

PR 14-AUG-2000; 2000US-0225759P.

PR 18-AUG-2000; 2000US-0226279P.

PR 22-AUG-2000; 2000US-0226681P.

PR 22-AUG-2000; 2000US-0226868P.

PR 22-AUG-2000; 2000US-0227182P.

PR 23-AUG-2000; 2000US-0227009P.

PR 30-AUG-2000; 2000US-0228924P.

PR 01-SEP-2000; 2000US-0229287P.

PR 01-SEP-2000; 2000US-0229343P.

PR 01-SEP-2000; 2000US-0229344P.

PR 01-SEP-2000; 2000US-0229345P.

PR 05-SEP-2000; 2000US-0229509P.

PR 05-SEP-2000; 2000US-0229513P.

PR 06-SEP-2000; 2000US-0230437P.

PR 06-SEP-2000; 2000US-0230438P.

PR 08-SEP-2000; 2000US-0231242P.

PR 08-SEP-2000; 2000US-0231243P.

PR 08-SEP-2000; 2000US-0231244P.

PR 08-SEP-2000; 2000US-0231413P.

PR 08-SEP-2000; 2000US-0231414P.

PR 08-SEP-2000; 2000US-0232080P.

PR 08-SEP-2000; 2000US-0232081P.

PR 12-SEP-2000; 2000US-0231968P.

PR 14-SEP-2000; 2000US-0232397P.

PR 14-SEP-2000; 2000US-0232398P.

PR 14-SEP-2000; 2000US-0232399P.

PR 14-SEP-2000; 2000US-0232400P.

PR 14-SEP-2000; 2000US-0232401P.

PR 14-SEP-2000; 2000US-0233063P.

PR 14-SEP-2000; 2000US-0233064P.

PR 21-SEP-2000; 2000US-0233065P.

PR 21-SEP-2000; 2000US-0234223P.

PR 21-SEP-2000; 2000US-0234274P.

PR 25-SEP-2000; 2000US-0234397P.

PR 25-SEP-2000; 2000US-0234998P.

PR 26-SEP-2000; 2000US-0235484P.

PR 27-SEP-2000; 2000US-0235834P.

PR 27-SEP-2000; 2000US-0235836P.

PR 29-SEP-2000; 2000US-0236327P.

PR 29-SEP-2000; 2000US-0236367P.

PR 29-SEP-2000; 2000US-0236368P.

PR 29-SEP-2000; 2000US-0236369P.

PR 29-SEP-2000; 2000US-0236370P.

PR 02-OCT-2000; 2000US-0236802P.

PR 02-OCT-2000; 2000US-0237037P.

PR 02-OCT-2000; 2000US-0237038P.

PR 02-OCT-2000; 2000US-0237039P.

PR 02-OCT-2000; 2000US-0237040P.

PR 13-OCT-2000; 2000US-0239935P.

PR 13-OCT-2000; 2000US-0239937P.

PR 20-OCT-2000; 2000US-0240960P.

PR 20-OCT-2000; 2000US-0241221P.

PR 20-OCT-2000; 2000US-0241222P.

PR 20-OCT-2000; 2000US-0241785P.

PR 20-OCT-2000; 2000US-0241786P.

PR 20-OCT-2000; 2000US-0241787P.

PR 20-OCT-2000; 2000US-0241808P.

PR 20-OCT-2000; 2000US-0241809P.

PR 20-OCT-2000; 2000US-0241826P.

PR 01-NOV-2000; 2000US-0244617P.

PR 08-NOV-2000; 2000US-0246474P.

PR 08-NOV-2000; 2000US-0246475P.

PR 08-NOV-2000; 2000US-0246476P.

PR 08-NOV-2000; 2000US-0246477P.

PR 08-NOV-2000; 2000US-0246478P.

PR 08-NOV-2000; 2000US-0246523P.

PR 08-NOV-2000; 2000US-0246524P.

PR 08-NOV-2000; 2000US-0246525P.

PR 08-NOV-2000; 2000US-0246526P.

PR 08-NOV-2000; 2000US-0246527P.

PR 08-NOV-2000; 2000US-0246528P.

PR 08-NOV-2000; 2000US-0246532P.

PR 08-NOV-2000; 2000US-0246609P.

PR 08-NOV-2000; 2000US-0246610P.

PR 08-NOV-2000; 2000US-0246611P.

PR 08-NOV-2000; 2000US-0246613P.

PR 17-NOV-2000; 2000US-0249207P.

PR 17-NOV-2000; 2000US-0249208P.

PR 17-NOV-2000; 2000US-0249209P.

PR 17-NOV-2000; 2000US-0249210P.

PR 17-NOV-2000; 2000US-0249211P.

PR 17-NOV-2000; 2000US-0249212P.

PR 17-NOV-2000; 2000US-0249213P.

PR 17-NOV-2000; 2000US-0249214P.

PR 17-NOV-2000; 2000US-0249215P.

PR 17-NOV-2000; 2000US-0249245P.

PR 17-NOV-2000; 2000US-0249264P.

PR 17-NOV-2000; 2000US-0249265P.

PR 17-NOV-2000; 2000US-0249297P.

PR 17-NOV-2000; 2000US-0249299P.

PR 17-NOV-2000; 2000US-0249300P.

PR 01-DEC-2000; 2000US-0250160P.

PR 01-DEC-2000; 2000US-0250391P.

PR 05-DEC-2000; 2000US-0251030P.

PR 05-DEC-2000; 2000US-0251988P.

PR 05-DEC-2000; 2000US-0256719P.

PR 06-DEC-2000; 2000US-0251479P.

PR 08-DEC-2000; 2000US-0251856P.

PR 08-DEC-2000; 2000US-0251868P.

PR 08-DEC-2000; 2000US-0251869P.

PR 08-DEC-2000; 2000US-0251989P.

PR 08-DEC-2000; 2000US-0251990P.

PR 11-DEC-2000; 2000US-0254097P.

PR 05-JAN-2001; 2001US-02559678P.

```
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Rosen CA, Barash SC, Ruben SM;
XX DR WPI; 2001-483426/52.
XX DR N-PSDB; AAK57512.
XX PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX PT useful for preventing, diagnosing and/or treating cancers and metastasis.
XX Claim 11; SEQ ID NO 12324; 3071pp + Sequence Listing; English.
XX PS
XX CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
XX CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
XX CC activity, and can be used in gene therapy and vaccine production. (I)
XX CC proteins and polynucleotides may be used in the prevention, diagnosis and
XX CC treatment of diseases associated with inappropriate (I) expression. For
XX CC example, they may be used to treat disorders associated with decreased
XX CC expression by rectifying mutations or deletions in a patient's genome
XX CC that affect the activity of (I) by expressing inactive proteins or to
XX CC supplement the patients own production of (I). Additionally, (I)
XX CC polynucleotides may be used to produce the secreted (I), by inserting the
XX CC nucleic acids into a host cell and culturing the cell to express the
XX CC protein. (I) proteins and polynucleotides may be used to prevent,
XX CC diagnose and treat immune/haematopoietic-related diseases, especially
XX CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
XX CC to AAK87694 represent human immune/haematopoietic antigen genomic
XX CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
XX CC represent sequences used in the exemplification of the present invention
XX SQ Sequence 44 AA;
Query Match 19.3%; Score 40; DB 4; Length 44;
Best Local Similarity 36.7%; Pred. No. 5.9e+02;
Matches 11; Conservative 6; Mismatches 11; Indels 2; Gaps 1;
QY 2 DEPORETLKAHYALNCCGLAGVQFISD 31
DB 10 DTYQXETGNKVNY--QGIGSGGVQIIAN 37
RESULT 34
AAK55688
ID AAY55688 standard; protein; 45 AA.
AC AAY55688;
XX 07-FEB-2000 (first entry)
XX DE M. genitalium ycfB peptide motif 3.
XX KW ycfB polypeptide; gram negative bacteria; gram positive bacteria;
XX KW antibacterial; bacterial infection; bacterial viability; antibiotic.
XX OS Mycoplasma genitalium.
XX PN WO9954462-A2.
XX PD 28-OCT-1999.
XX PF 20-APR-1999; 99WO-EF002638.
XX PR 22-APR-1998; 98GB-00008350.
XX PA (GLAX ) GLAXO GROUP LTD.
XX PI Arigoni F, Edgerton MD, Loferer H, Peitsch MC;
XX WPI; 2000-013249/01.
XX PT Novel bacterial polypeptides used to identify broad spectrum antibiotics.
XX
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PS Claim 3; Fig 2C; 56pp; English.
XX CC The invention discloses a novel family of polypeptides, designated the
XX CC ycfB family, required for the growth of both gram negative and gram
XX CC positive bacteria. The novel polypeptide of ycfB family is defined by:
XX CC (a) a HSP score of greater than or equal to 100 when compared with one of
XX CC the amino acid sequences of the ycfB family members given in the
XX CC specification, when the BLAST algorithm is used with a BLOSUM62 scoring
XX CC matrix; (b) containing a set of amino acid sequences which are positively
XX CC identified when position dependent scoring matrices according to tables 1
XX CC -4 (given in the specification) are used to yield a p-value of less than
XX CC 110-60; or (c) comprising any one of the sequences shown in AAY55710-
XX CC 711. The ycfB polypeptides and polynucleotides can be used in method to
XX CC identify antagonists and antibacterial compounds. These antagonists and
XX CC compounds can be used to treat bacterial infections. The polypeptides of
XX CC the invention are essential proteins for bacterial viability, and
XX CC represent new targets for antibiotics. Sequences AAY55647-709 represent
XX CC different motifs of the ycfB family polypeptides of various bacterial
XX CC species
XX SQ Sequence 45 AA;
Query Match 19.3%; Score 40; DB 3; Length 45;
Best Local Similarity 47.1%; Pred. No. 6e+02;
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 20 GLAGVGEQFISDICKPK 36
DB 11 GLSGGVDVAVSALLKK 27
RESULT 35
ABB41557
ID ABB41557 standard; peptide; 47 AA.
XX AC ABB41557;
XX DT 04-FEB-2002 (first entry)
XX DE Peptide #9063 encoded by human foetal liver single exon probe.
XX KW Human; foetal liver; gene expression; single exon nucleic acid probe.
XX OS Homo sapiens.
XX PN WO200157277-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000669.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483447/52.
XX DR Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human fetal liver.
XX PS Claim 27; SEQ ID NO 34192; 639pp + Sequence Listing; English.
XX CC The invention relates to a single exon nucleic acid probe for measuring
XX CC human gene expression in a sample derived from human foetal liver. The
XX CC single exon nucleic acid probes may be used for predicting, measuring and
```

CC displaying gene expression in samples derived from human fetal liver. The  
CC present sequence is a peptide encoded by a single exon nucleic acid probe  
CC of the invention. Note: The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 47 AA;

Query Match 19.3%; Score 40; DB 4; Length 47;  
Best Local Similarity 50.0%; Pred. No. 6.3e+02;  
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
  
QY 25 VEQFISDICPKKDV 38  
DB 11 VETISTDVCKNRKDV 24  
|| :|| :||  
|| :|| :||

RESULT 36  
AAM35348  
ID ID AAM35348 standard; protein; 47 AA.  
XX AC AAM35348;  
XX 17-OCT-2001 (first entry)  
DT  
XX  
XX Peptide #9385 encoded by probe for measuring placental gene expression.  
DE  
XX  
XX Probe; microarray; human; placenta; antenatal diagnosis;  
KW genetic disorder.  
KW  
XX Homo sapiens.  
OS  
XX WO200157272-A2.  
PN  
XX 09-AUG-2001.  
PD  
XX  
XX 30-JAN-2001; 2001WO-US000663.

XX 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
PA  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2001-48897/53.  
XX  
XX Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human placenta.  
PT  
XX  
XX Claim 27; SEQ ID NO 35617; 654pp; English.  
PS  
XX The present invention relates to single exon nucleic acid probes (SENP:  
CC see AAI31315-AA157546). The present sequence is a peptide encoded by one  
CC such probe. The probes are useful for producing a microarray for  
CC predicting, measuring and displaying gene expression in samples derived  
CC from human placenta. The probes are useful for antenatal diagnosis of  
CC human genetic disorders  
XX  
SQ Sequence 47 AA;

Query Match 19.3%; Score 40; DB 4; Length 47;  
Best Local Similarity 50.0%; Pred. No. 6.3e+02;  
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
  
QY 25 VEQFISDICPKKDV 38  
DB 11 VETISTDVCKNRKDV 24  
|| :|| :||  
|| :|| :||

RESULT 36  
AAM35348  
ID ID AAM35348 standard; protein; 47 AA.  
XX AC AAM35348;  
XX 17-OCT-2001 (first entry)  
DT  
XX  
XX Peptide #9385 encoded by probe for measuring placental gene expression.  
DE  
XX  
XX Probe; microarray; human; placenta; antenatal diagnosis;  
KW genetic disorder.  
KW  
XX Homo sapiens.  
OS  
XX WO200157272-A2.  
PN  
XX 09-AUG-2001.  
PD  
XX  
XX 30-JAN-2001; 2001WO-US000663.

XX 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
PA  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2001-48897/53.  
XX  
XX Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human placenta.  
PT  
XX  
XX Claim 27; SEQ ID NO 35617; 654pp; English.  
PS  
XX The present invention relates to single exon nucleic acid probes (SENP:  
CC see AAI31315-AA157546). The present sequence is a peptide encoded by one  
CC such probe. The probes are useful for producing a microarray for  
CC predicting, measuring and displaying gene expression in samples derived  
CC from human placenta. The probes are useful for antenatal diagnosis of  
CC human genetic disorders  
XX  
SQ Sequence 47 AA;

Query Match 19.3%; Score 40; DB 4; Length 47;  
Best Local Similarity 50.0%; Pred. No. 6.3e+02;  
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
  
QY 25 VEQFISDICPKKDV 38  
DB 11 VETISTDVCKNRKDV 24  
|| :|| :||  
|| :|| :||

## RESULT 37

AAM75236  
ID AAM75236 standard; protein; 47 AA.  
XX

XX AAM75236;  
XX

DT 06-NOV-2001 (first entry)  
XX

DE Human bone marrow expressed probe encoded protein SEQ ID NO: 35542.  
XX  
KW Human; bone marrow expressed exon; gene expression analysis; probe;  
KW microarray; cancer; leukaemia; lymphoma; myeloma.  
XX  
OS Homo sapiens.  
XX

PN WO200157276-A2.  
XX

PD 09-AUG-2001.  
XX

XX 30-JAN-2001; 2001WO-US000668.  
XX

PR 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX

XX (MOLE-) MOLECULAR DYNAMICS INC.  
PA

XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX

XX WPI; 2001-488900/53.  
XX

XX Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human bone marrow.  
PT  
XX  
XX Example 4; SEQ ID NO 35542; 658pp + Sequence Listing; English.  
XX  
CC The present invention provides a number of single exon nucleic acid  
CC probes which are derived from genomic sequences expressed in the human  
CC bone marrow. They can be used to measure gene expression in bone marrow  
CC samples, which may enable the improved diagnosis and treatment of cancers  
CC such as lymphoma, leukaemia and myeloma. The present sequence is a  
CC protein encoded by one of the probes of the invention  
XX  
SQ Sequence 47 AA;

Query Match 19.3%; Score 40; DB 4; Length 47;  
Best Local Similarity 50.0%; Pred. No. 6.3e+02;  
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 25 VEQFISDICPKKDV 38  
DB 11 VETISTDVCKNRKDV 24  
|| :|| :||  
|| :|| :||

## RESULT 38

AAM62428  
ID AAM62428 standard; protein; 47 AA.  
XX

XX AAM62428;  
XX

DT 05-NOV-2001 (first entry)  
XX

DE Human brain expressed single exon probe encoded protein SEQ ID NO: 34533.  
XX  
KW Human; brain expressed exon; gene expression analysis; probe; microarray;  
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.  
XX  
XX

```
OS Homo sapiens.
XX WO200157275-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000667.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains.
XX
XX Example 4; SEQ ID NO 34533; 650pp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX brain. They can be used to measure gene expression in brain cell samples,
XX which may enable the diagnosis and improved treatment of nervous system
XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX epilepsy and cancers. The present sequence is a protein encoded by one of
XX the probes of the invention
XX
XX Sequence 47 AA;
XX
XX Query Match 19.3%; Score 40; DB 4; Length 47;
XX Best Local Similarity 50.0%; Pred. No. 6.3e+02;
XX Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 25 VEQFTSDICPKKDV 38
XX || :||:||||
XX Db 11 VETISTDVCKRQDV 24
XX
XX RESULT 39
XX ABG56998
XX ID ABG56998 standard; peptide; 47 AA.
XX
XX AC ABG56998;
XX
XX DT 25-FEB-2003 (first entry)
XX
XX DE Human liver peptide, SEQ ID No 35646.
XX
XX KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
XX hypercholesterolaemia; coronary heart disease.
XX
XX OS Homo sapiens.
XX
XX PN WO200157273-A2.
XX
XX PD 09-AUG-2001.
XX
XX PF 30-JAN-2001; 2001WO-US000664.
XX
XX PR 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
```

```
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488898/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human adult liver.
XX
XX Claim 27; SEQ ID NO 35646; 658pp; English.
XX
XX The invention relates to a single exon nucleic acid probe (SENP) (I) for
XX measuring human gene expression in a sample derived from human adult
XX liver, comprising one of 13109 defined nucleotide sequences given in the
XX specification (or complements/ fragments). The probe hybridises at high
XX stringency to a nucleic acid molecule expressed in the human adult liver.
XX (I) may be used for predicting, measuring and displaying gene expression
XX in samples derived from human adult liver. The genes identified may be
XX involved in genetic liver diseases such as cirrhosis,
XX hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
XX associated with coronary heart disease. ABG47348-ABG59930 represent human
XX liver single exon encoded peptides of the invention. Note: The sequence
XX information for this patent does not appear in the printed specification
XX but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 47 AA;
XX
XX Query Match 19.3%; Score 40; DB 4; Length 47;
XX Best Local Similarity 50.0%; Pred. No. 6.3e+02;
XX Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 25 VEQFTSDICPKKDV 38
XX || :||:||||
XX Db 11 VETISTDVCKRQDV 24
XX
XX RESULT 40
XX ABG44889
XX ID ABG44889 standard; peptide; 47 AA.
XX
XX AC ABG44889;
XX
XX DT 19-AUG-2002 (first entry)
XX
XX DE Human peptide encoded by genome-derived single exon probe SEQ ID 34554.
XX
XX KW Human; single exon probe; asthma; lung cancer; COPD; ILD;
XX chronic obstructive pulmonary disease; interstitial lung disease;
XX familial idiopathic pulmonary fibrosis; neurofibromatosis;
XX tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
XX Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
XX pulmonary histiocytosis; lymphangiomyomatosis; Karagenen syndrome;
XX pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
XX primary ciliary dyskinesia; pulmonary hypertension;
XX hyaline membrane disease.
XX
XX OS Homo sapiens.
XX
XX PN WO200186003-A2.
XX
XX PD 15-NOV-2001.
XX
XX PF 30-JAN-2001; 2001WO-US000665.
XX
XX PR 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
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PR 04-OCT-2000; 2000GB-00024263.  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2002-114183/15.  
XX  
XX Spatially-addressable set of single exon nucleic acid probes, used to  
PT measure gene expression in human lung samples.  
XX  
XX Claim 27; SEQ ID NO 34554; 634pp; English.  
XX  
XX The invention relates to a spatially-addressable set of single exon  
CC nucleic acid probes for measuring gene expression in a sample derived  
CC from human lung comprising single exon nucleic acid probes having one of  
CC 12614 nucleic acid sequences mentioned in the specification, or their  
CC complements or the 12387 open reading frames derived from the 12614  
CC probes. Also included are a microarray comprising the novel set of probes  
CC ; the novel set of probes which hybridise at high stringency to a nucleic  
CC acid expressed in the human lung; measuring gene expression in a sample  
CC derived from human lung, comprising (a) contacting the array with a  
CC collection of detectably labeled nucleic acids derived from human lung  
CC mRNA, and (b) measuring the label detectably bound to each probe of the  
CC array; identifying exons in a eukaryotic genome, comprising (a)  
CC algorithmically predicting at least one exon from genomic sequences of  
CC the eukaryote; and (b) detecting specific hybridisation of detectably  
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,  
CC having a fragment identical to the predicted exon, the probe is included  
CC in the above mentioned microarray; assigning exons to a single gene,  
CC comprising (a) identifying exons from genomic sequence by the method  
CC above and (b) measuring the expression of each of the exons in several  
CC tissues and/or cell types using hybridisation to a single exon  
CC microarrays having a probe with the exon, where a common pattern of  
CC expression of the exons in the tissues and/or cell types indicates that  
CC the exons should be assigned to a single gene; a peptide comprising one  
CC of 12011 sequences, mentioned in the specification, or encoded by the  
CC probes/open reading frames (ORF). The probes are used for gene expression  
CC analysis, and for identifying exons in a gene, particularly using human  
CC lung derived mRNA and for the study of lung diseases such as asthma, lung  
CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung  
CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,  
CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-  
CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary  
CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,  
CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary  
CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The  
CC present sequence is a peptide/protein encoded by a single exon probe of  
CC the invention. Note: The sequence data for this patent did not form part  
CC of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 47 AA;

Query Match 19.3%; Score 40; DB 5; Length 47;  
Best Local Similarity 50.0%; Pred. No. 6.3e+02;  
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 25 VEQFISDICKDV 38  
|| :|| :||  
Db 11 VETISDVCKRDV 24

Search completed: January 20, 2006, 17:30:38  
Job time : 96.7654 secs

**This Page Blank (uspto)**



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2006, 17:26:44 ; Search time 26.2716 Seconds  
(without alignments)  
119.584 Million cell updates/sec

Title: US-10-619-323-4  
Perfect score: 207  
Sequence: 1 KQEPQETLKAHYALNCCGLAGGVEQFISDICPKDV 38

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 308952

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 50 summaries

Database : Issued Patents AA.\*  
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2: /cgn2\_6/ptodata/1/iaa/6-COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/H-COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/PCUTUS-COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/RE-COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	157	75.8	29	1 US-08-254-493-5	Sequence 5, Appli
2	157	75.8	29	1 US-08-408-222B-5	Sequence 5, Appli
3	50	24.2	29	1 US-08-254-493-6	Sequence 6, Appli
4	50	24.2	29	1 US-08-408-222B-6	Sequence 6, Appli
5	47	22.7	30	1 US-08-254-493-4	Sequence 4, Appli
6	47	22.7	30	1 US-08-408-222B-4	Sequence 4, Appli
7	43	20.8	23	2 US-07-930-593-3	Sequence 3, Appli
8	43	20.8	23	2 US-09-414-872-3	Sequence 3, Appli
9	43	20.8	26	2 US-07-930-593-1	Sequence 1, Appli
10	43	20.8	26	2 US-09-414-872-1	Sequence 1, Appli
11	43	20.8	44	2 US-09-902-540-14873	Sequence 14873, A
12	42	20.3	37	2 US-08-900-230-54	Sequence 54, Appl
13	41.5	20.0	50	2 US-09-004-406C-26	Sequence 26, Appl
14	41	19.8	30	1 US-07-596-081A-33	Sequence 33, Appl
15	41	19.8	32	1 US-07-596-081A-12	Sequence 12, Appl
16	40	19.3	25	1 US-08-406-347A-12	Sequence 12, Appl
17	39.5	19.1	40	2 US-09-493-795B-302	Sequence 302, App
18	39	18.8	45	2 US-09-674-973A-363	Sequence 363, App
19	39	18.8	46	2 US-09-674-973A-364	Sequence 364, App
20	38.5	18.6	26	2 US-09-201-227A-26	Sequence 26, Appl
21	38.5	18.6	26	2 US-09-084-303B-222	Sequence 222, App
22	38.5	18.6	44	1 US-08-747-915-1	Sequence 1, Appli
23	38.5	18.6	44	2 US-09-285-783-1	Sequence 1, Appli
24	38.5	18.6	44	2 US-09-670-537A-1	Sequence 1, Appli
25	38.5	18.6	47	2 US-09-860-503-2	Sequence 2, Appli
26	38.5	18.6	48	2 US-09-219-019-22	Sequence 22, Appl
27	38.5	18.6	49	1 US-08-747-915-5	Sequence 5, Appli

28	38.5	18.6	49	2	US-09-285-783-5	Sequence 5, Appli
29	38	18.4	47	4	PCT-US96-08811-2	Sequence 2, Appli
30	37.5	18.1	26	1	US-08-484-219-3	Sequence 3, Appli
31	37.5	18.1	26	2	US-09-846-149-3	Sequence 3, Appli
32	37.5	18.1	42	1	US-08-278-089A-23	Sequence 23, Appli
33	37.5	18.1	42	1	US-08-838-957A-22	Sequence 22, Appli
34	37.5	18.1	44	2	US-10-729-121-52	Sequence 52, Appli
35	37	17.9	47	1	US-08-849-248-1	Sequence 1, Appli
36	37	17.9	47	1	US-08-849-248-3	Sequence 3, Appli
37	36	17.4	14	1	US-08-564-063-4	Sequence 4, Appli
38	36	17.4	21	2	US-09-493-795B-179	Sequence 179, App
39	36	17.4	28	4	PCT-US96-01720-5	Sequence 5, Appli
40	36	17.4	28	4	PCT-US96-01720-6	Sequence 6, Appli
41	36	17.4	29	2	US-09-471-276-1244	Sequence 1244, Ap
42	36	17.4	32	1	US-08-809-860-6	Sequence 6, Appli
43	36	17.4	35	2	US-09-082-279B-307	Sequence 307, App
44	36	17.4	35	2	US-09-082-279B-308	Sequence 308, App
45	36	17.4	35	2	US-09-082-279B-309	Sequence 309, App
46	36	17.4	35	2	US-09-082-279B-310	Sequence 310, App
47	36	17.4	35	2	US-09-082-279B-311	Sequence 311, App
48	36	17.4	35	2	US-09-315-304B-307	Sequence 307, App
49	36	17.4	35	2	US-09-315-304B-308	Sequence 308, App
50	36	17.4	35	2	US-09-315-304B-309	Sequence 309, App

ALIGNMENTS

RESULT 1  
US-08-254-493-5  
; Sequence 5, Application US/08254493  
; Patent No. 5439886  
; GENERAL INFORMATION:  
; APPLICANT: IKEYAMA, SHUICHI  
; APPLICANT: KOYAMA, MASARU  
; APPLICANT: MIYAKE, MASAYUKI  
; APPLICANT: SENO, MASAHARU  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND  
; PRODUCTION THEREOF  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
; STREET: 130 WATER STREET  
; CITY: BOSTON  
; STATE: MASSACHUSETTS  
; COUNTRY: US  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/254,493  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/865552  
; FILING DATE: 09-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 079996-1991  
; FILING DATE: 12-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 085396-1991  
; FILING DATE: 17-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 022321-1992  
; FILING DATE: 07-FEB-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: RESNICK, DAVID S.  
; REGISTRATION NUMBER: 34235  
; REFERENCE/DOCKET NUMBER: 41777  
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 523-3400  
; TELEFAX: (617) 523-6440  
; TELEX: 200291 STRE UR  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 29 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-254-493-5

Query Match 75.8%; Score 157; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 1.2e-16;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QRETLKAIHYALNCCGLAGGVEQFISDIC 33  
Db 1 QRETLKAIHYALNCCGLAGGVEQFISDIC 29

## RESULT 2

US-08-408-222B-5  
; Sequence 5, Application US/08408222B  
; Patent No. 5776727  
; GENERAL INFORMATION:  
; APPLICANT: Ikeyama, Shuichi  
; APPLICANT: Koyama, Masaru  
; APPLICANT: Miyake, Masayuki  
; APPLICANT: Senoo, Masaharu  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DIKE, Bronstein, Roberts & Cushman  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; FILING DATE: 22-MAR-1995  
; APPLICATION NUMBER: US/08/408,222B  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/254,493  
; FILING DATE: 06-JUN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP-079996-1991  
; FILING DATE: 12-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP-085396-1991  
; FILING DATE: 14-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP-022321-1992  
; FILING DATE: 07-FEB-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Resnick, David S.  
; REGISTRATION NUMBER: 34,235  
; REFERENCE/DOCKET NUMBER: 41777-DIV  
; TELEPHONE: 617-523-3400  
; TELEFAX: 617-523-6440  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 29 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

US-08-408-222B-5

Query Match 75.8%; Score 157; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 1.2e-16;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QRETLKAIHYALNCCGLAGGVEQFISDIC 33  
Db 1 QRETLKAIHYALNCCGLAGGVEQFISDIC 29

## RESULT 3

US-08-254-493-6  
; Sequence 6, Application US/08254493  
; Patent No. 5439886  
; GENERAL INFORMATION:  
; APPLICANT: IKEYAMA, SHUICHI  
; APPLICANT: KOYAMA, MASARU  
; APPLICANT: MIYAKE, MASAYUKI  
; APPLICANT: SENOO, MASAHARU  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND  
; TITLE OF INVENTION: PRODUCTION THEREOF  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
; STREET: 130 WATER STREET  
; CITY: BOSTON  
; STATE: MASSACHUSETTS  
; COUNTRY: US  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/254,493  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/865552  
; FILING DATE: 09-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 079996-1991  
; FILING DATE: 12-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 085396-1991  
; FILING DATE: 17-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 022321-1992  
; FILING DATE: 07-FEB-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: RESNICK, DAVID S.  
; REGISTRATION NUMBER: 34235  
; REFERENCE/DOCKET NUMBER: 41777  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 523-3400  
; TELEFAX: (617) 523-6440  
; TELEX: 200291 STRE UR  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 29 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-254-493-6

Query Match 24.2%; Score 50; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 SDICPKKV 38

Db 1 SDICPKD V 9

RESULT 4  
US-08-408-222B-6  
; Sequence 6, Application US/08408222B  
; Patent No. 5776727  
; GENERAL INFORMATION:  
; APPLICANT: Ikeyama, Shuichi  
; APPLICANT: Koyama, Masaru  
; APPLICANT: Miyake, Masayuki  
; APPLICANT: Senoo, Masaharu  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/408,222B  
; FILING DATE: 22-MAR-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/254,493  
; FILING DATE: 06-JUN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP-079996-1991  
; FILING DATE: 12-APR-1991  
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; APPLICATION NUMBER: JP-085396-1991  
; FILING DATE: 14-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP-022321-1992  
; FILING DATE: 07-FEB-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Resnick, David S.  
; REGISTRATION NUMBER: 34,235  
; REFERENCE/DOCKET NUMBER: 41777-DIV  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-523-3400  
; TELEFAX: 617-523-6440  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 29 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

US-08-408-222B-6

Query Match 24.2%; Score 50; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 SDICPKD V 38  
Db 1 SDICPKD V 9

RESULT 5  
US-08-254-493-4  
; Sequence 4, Application US/08254493  
; Patent No. 5439886  
; GENERAL INFORMATION:  
; APPLICANT: IKEYAMA, SHUICHI

; APPLICANT: KOYAMA, MASARU  
; APPLICANT: MIYAKE, MASAYUKI  
; APPLICANT: SENOO, MASAHARU  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
; STREET: 130 WATER STREET  
; CITY: BOSTON  
; STATE: MASSACHUSETTS  
; COUNTRY: US  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/254,493  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/865552  
; FILING DATE: 09-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 079996-1991  
; FILING DATE: 12-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 085396-1991  
; FILING DATE: 17-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 022321-1992  
; FILING DATE: 07-FEB-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: RESNICK, DAVID S.  
; REGISTRATION NUMBER: 34235  
; REFERENCE/DOCKET NUMBER: 41777  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 523-3400  
; TELEFAX: (617) 523-6440  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 30 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-254-493-4

Query Match 22.7%; Score 47; DB 1; Length 30;  
Best Local Similarity 100.0%; Pred. No. 5;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQEPQRETL 9  
Db 22 KQEPQRETL 30

RESULT 6  
US-08-408-222B-4  
; Sequence 4, Application US/08408222B  
; Patent No. 5776727  
; GENERAL INFORMATION:  
; APPLICANT: Ikeyama, Shuichi  
; APPLICANT: Koyama, Masaru  
; APPLICANT: Miyake, Masayuki  
; APPLICANT: Senoo, Masaharu  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN

STREET: 130 Water Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/408,222B  
FILING DATE: 22-MAR-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/254,493  
FILING DATE: 06-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP-079996-1991  
FILING DATE: 12-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP-085396-1991  
FILING DATE: 14-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP-022321-1992  
FILING DATE: 07-FEB-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Resnick, David S.  
REGISTRATION NUMBER: 34,235  
REFERENCE/DOCKET NUMBER: 41777-DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-408-222B-4

Query Match 22.7%; Score 47; DB 1; Length 30;  
Best Local Similarity 100.0%; Pred. No. 5;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEPQRETL 9  
||| |||||  
Db 22 KDEPQRETL 30

RESULT 7  
US-07-930-593-3  
Sequence 3, Application US/07930593  
Patent No. 6040167  
GENERAL INFORMATION:  
APPLICANT: Gluck, Reinhard  
APPLICANT: Klein, Peter  
TITLE OF INVENTION: SYNTHETIC MEMBRANE VESICLES CONTAINING  
TITLE OF INVENTION: FUNCTIONALLY ACTIVE FUSION PEPTIDES AS DRUG DELIVERY  
TITLE OF INVENTION: SYSTEMS  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen  
STREET: 1180 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-8403  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/930,593  
FILING DATE: 02-NOV-1992  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP92/00089  
FILING DATE: 17-JAN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 91101414.0  
FILING DATE: 02-FEB-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meilman, Edward A.  
REGISTRATION NUMBER: 24,735  
REFERENCE/DOCKET NUMBER: FA-1423 PCT (167-74)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 382-0700  
TELEFAX: (212) 382-0888  
TELEX: 236925  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
ORIGINAL SOURCE:  
ORGANISM: myxovirus, paramyxovirus, rhabdovirus  
US-07-930-593-3

Query Match 20.8%; Score 43; DB 2; Length 23;  
Best Local Similarity 50.0%; Pred. No. 15;  
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 18 CCGLAGGVEQFISD 31  
||| ||| : || :  
Db 2 CCGLFGAIAGFIEN 15

RESULT 8  
US-09-414-872-3  
Sequence 3, Application US/09414872  
Patent No. 6210708  
GENERAL INFORMATION:  
APPLICANT: Witci, Ernst Rudolf  
APPLICANT: Gluck, Reinhard  
APPLICANT: Klein, Peter  
TITLE OF INVENTION: Cationic virosomes as transfer system for genetic  
TITLE OF INVENTION: material  
FILE REFERENCE: 101909.01  
CURRENT APPLICATION NUMBER: US/09/414,872  
CURRENT FILING DATE: 1999-10-18  
EARLIER APPLICATION NUMBER: US 09/171,882  
EARLIER FILING DATE: 1998-12-30  
EARLIER APPLICATION NUMBER: PCT/EP97/02268  
EARLIER FILING DATE: 1997-05-04  
EARLIER APPLICATION NUMBER: EP 96107282.4  
EARLIER FILING DATE: 1996-05-08  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 23  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:  
OTHER INFORMATION: hemagglutinin-type fusogenic peptide  
US-09-414-872-3

Query Match 20.8%; Score 43; DB 2; Length 23;  
Best Local Similarity 50.0%; Pred. No. 15;  
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 18 CCGLAGGVEQFISD 31

```
Db      ||||| : || :
        2 CCGLFGAIGFIEN 15

RESULT 9
US-07-930-593-1
; Sequence 1, Application US/07930593
; Patent No. 6040167
; GENERAL INFORMATION:
; APPLICANT: Gluck, Reinhard
; APPLICANT: Klein, Peter
; APPLICANT: Herrmann, Peter
; TITLE OF INVENTION: SYNTHETIC MEMBRANE VESICLES CONTAINING
; TITLE OF INVENTION: FUNCTIONALLY ACTIVE FUSION PEPTIDES AS DRUG DELIVERY
; TITLE OF INVENTION: SYSTEMS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen
; STREET: 1180 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-8403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/07930,593
; APPLICATION NUMBER: US/07930,593
; FILING DATE: 02-NOV-1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP92/00089
; FILING DATE: 17-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 91101414.0
; FILING DATE: 02-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Weilman, Edward A.
; REGISTRATION NUMBER: 24,735
; REFERENCE/DOCKET NUMBER: FA-1423 PCT (167-74)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 382-0700
; TELEFAX: (212) 382-0888
; TELEX: 236925
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: myxovirus, paramyxovirus, rhabdovirus
US-07-930-593-1

Query Match      20.8%; Score 43; DB 2; Length 26;
Best Local Similarity 50.0%; Pred. No. 17;
Matches      7; Conservative      2; Mismatches      5; Indels      0; Gaps      0;

QY      18 CCGLAGGVEQFISD 31
Db      ||||| : || :
        2 CCGLFGAIGFIEN 15

RESULT 10
US-09-414-872-1
; Sequence 1, Application US/09414872
; Patent No. 6210708
; GENERAL INFORMATION:
; APPLICANT: Witi, Ernst Rudolf
; APPLICANT: Gluck, Reinhard
; APPLICANT: Klein, Peter

; TITLE OF INVENTION: Cationic virosomes as transfer system for genetic
; TITLE OF INVENTION: material
; FILE REFERENCE: 101909.01
; CURRENT APPLICATION NUMBER: US/09/414,872
; CURRENT FILING DATE: 1999-10-18
; EARLIER APPLICATION NUMBER: US 09/171,882
; EARLIER FILING DATE: 1998-12-30
; EARLIER APPLICATION NUMBER: PCT/EP97/02268
; EARLIER FILING DATE: 1997-05-04
; EARLIER APPLICATION NUMBER: EP 96107282.4
; EARLIER FILING DATE: 1996-05-08
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: hemagglutinin-type fusogenic peptide
US-09-414-872-1

Query Match      20.8%; Score 43; DB 2; Length 26;
Best Local Similarity 50.0%; Pred. No. 17;
Matches      7; Conservative      2; Mismatches      5; Indels      0; Gaps      0;

QY      18 CCGLAGGVEQFISD 31
Db      ||||| : || :
        2 CCGLFGAIGFIEN 15

RESULT 11
US-09-902-540-14873
; Sequence 14873, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 14873
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-14873

Query Match      20.8%; Score 43; DB 2; Length 44;
Best Local Similarity 53.3%; Pred. No. 32;
Matches      8; Conservative      2; Mismatches      5; Indels      0; Gaps      0;

QY      17 NCCGLAGGVEQFISD 31
Db      ||||| : || :
        29 DCCGAAGRPVKFILD 43

RESULT 12
US-08-900-230-54
; Sequence 54, Application US/08900230
; Patent No. 6329197
; GENERAL INFORMATION:
; APPLICANT: Bard, Jonathan A.
; TITLE OF INVENTION: DNA ENCODING GALANIN GALR3 RECEPTORS AND
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
```

STREET: 1185 Avenue of The Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 11036

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/900,230  
FILING DATE: 23-JUL-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 52241-C/JPW/ADM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-278-0400  
TELEFAX: 212-391-0525  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 37 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: NO  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-900-230-54

Query Match 20.3%; Score 42; DB 2; Length 37;  
Best Local Similarity 70.0%; Pred. No. 36;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 15 ALNCCGLAGG 24  
DB 21 ACTCCGAAGG 30

## RESULT 13

US-09-004-406C-26  
Sequence 26, Application US/09004406C  
Patent No. 6174706

GENERAL INFORMATION:  
APPLICANT: Vinci, Victor A.  
APPLICANT: Conder, Michael J.  
APPLICANT: McAda, Phyllis C.  
APPLICANT: Reeves, Christopher D.  
APPLICANT: Rambosek, John  
APPLICANT: Davis, Charles Ray  
APPLICANT: Hendrickson, Lee E.  
TITLE OF INVENTION: DNA ENCODING TRIOL POLYKETIDE SYNTHASE  
FILE REFERENCE: 19076PPA  
CURRENT APPLICATION NUMBER: US/09/004,406C  
CURRENT FILING DATE: 1998-01-08  
PRIOR APPLICATION NUMBER: 08/637,640  
PRIOR FILING DATE: 1996-08-23  
PRIOR APPLICATION NUMBER: 08/148,132  
PRIOR FILING DATE: 1993-11-02  
NUMBER OF SEQ ID NOS: 41  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 26  
LENGTH: 50  
TYPE: PRT  
ORGANISM: Rattus norvegicus  
US-09-004-406C-26

Query Match 20.0%; Score 41.5; DB 2; Length 50;  
Best Local Similarity 32.3%; Pred. No. 62;  
Matches 10; Conservative 9; Mismatches 11; Indels 1; Gaps 1;

QY 3 EPQRETLKAIHYALNCCGLAG-GVBOFISDI 32  
DB 4 EAQDLVKAVAHILGIRDLAGINLDSLADL 34

## RESULT 14

US-07-596-081A-33  
Sequence 33, Application US/07596081A  
Patent No. 5194586  
GENERAL INFORMATION:  
APPLICANT: Maeda, Yoshiaki  
APPLICANT: Shiraki, Hiroshi  
APPLICANT: Washitani, Yukiko  
APPLICANT: Kuroda, Naotaka  
APPLICANT: Yamada, Kyoko  
APPLICANT: Oka, Kiichiro  
APPLICANT: Namba, Toshihiro  
TITLE OF INVENTION: Peptides and Use Thereof  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Eric S. Spector  
STREET: P.O. Box 2266 Eads Station  
CITY: Arlington  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22202

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/596,081A  
FILING DATE: 19901011  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 266983/1989  
FILING DATE: 13-OCT-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Spector, Eric S.  
REGISTRATION NUMBER: 22495  
REFERENCE/DOCKET NUMBER: 513904  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-415-1500  
TELEFAX: 703-415-1508  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-596-081A-33

Query Match 19.8%; Score 41; DB 1; Length 30;  
Best Local Similarity 40.0%; Pred. No. 40;  
Matches 8; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 14 YALNCCGLAGGVBOFISDIC 33  
DB 3 YSPSCCTLTIGVSSYHSTPC 22

## RESULT 15

US-07-596-081A-12  
Sequence 12, Application US/07596081A  
Patent No. 5194586

GENERAL INFORMATION:  
APPLICANT: Maeda, Yoshiaki  
APPLICANT: Shiraki, Hiroshi  
APPLICANT: Washitani, Yukiko  
APPLICANT: Kuroda, Naotaka  
APPLICANT: Yamada, Kyoko  
APPLICANT: Oka, Kiichiro

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/041,790
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/583,335
; ATTORNEY/AGENT INFORMATION:
; NAME: Toffenetti, Judith L.
; REGISTRATION NUMBER: 39,048
; REFERENCES/DOCKET NUMBER: 1984/46203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-429-1776
; TELEFAX: 202-429-0796
; INFORMATION FOR SEQ ID NO: 12 :
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-406-347A-12

Query Match 19.1%; Score 40;
Best Local Similarity 58.3%; Pred. No.
Matches 7; Conservative 1; Mismatch

QY 4 PORETLKAHYA 15
DB 10 PNNNTKSIHYA 21

RESULT 17
US-09-493-795B-302
; Sequence 302, Application US/09493795B
; Patent No. 6797808
; GENERAL INFORMATION:
; APPLICANT: Watkins, Wren
; APPLICANT: Oliveira, Balomero M.
; APPLICANT: Hillyard, David R.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Alpha-Conotoxin In Peptid
; FILE REFERENCE: 2314-179 A
; CURRENT APPLICATION NUMBER: US/09/493,795B
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/118,381
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 404
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 302
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Conus arenatus
US-09-493-795B-302

Query Match 19.1%; Score 39.5%
Best Local Similarity 40.0%; Pred. No.
Matches 8; Conservative 3; Mismatch

QY 16 LNCGLAGGVGEQFTSDICPK 35
DB 20 LNCSSIFGWNVEY-KORCSK 38

RESULT 18
US-09-674-973A-363
; Sequence 363, Application US/09674973A
; Patent No. 6759046
; GENERAL INFORMATION:
; APPLICANT: No. 6759046sk Hydros ASA
; TITLE OF INVENTION: Peptides
; FILE REFERENCE: 26625-296
; CURRENT APPLICATION NUMBER: US/09/674,973
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 459
; SOFTWARE: PatentIn version 3.0

```

```

; SEQ ID NO 363
; LENGTH: 45
; TYPE: PRT
; ORGANISM: H
US-09-674-973A-

```

Query Match 18.8%; Score 39; DB 2; Length 45;  
Best Local Similarity 38.1%; Pred. No. 1.3e+02;  
Matches 8; Conservative 4; Mismatches 7; Indels 2; Gaps 1;

Qy 19 CGLA--GGVEQFISDICKD 37  
| | | | | : : : : :  
Db 1 CSLAKDGSTEDTVSSLCGEED 21

## RESULT 19

US-09-674-973A-364  
; Sequence 364, Application US/09674973A  
; Patent No. 6759046

```

; GENETIC INFORMATION:
; APPLICANT: NO. 6759046sk Hydro ASA
; TITLE OF INVENTION: Peptides
; FILE REFERENCES: 26625-236
; CURRENT APPLICATION NUMBER: US/09/674, 973A
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 459
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 364
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-674-973A-364

```

Query Match 18.8%; Score 39; DB 2; Length 46;  
Best Local Similarity 38.1%; Pred. No. 1.3e+02;  
Matches 8; Conservative 4; Mismatches 7; Indels

QY 19 CGLA--GGVEQFISDICKD 37  
| | | | | : : : : :  
Db 2 CSLAKDGSTEDTVSSLCGEED 22

## RESULT 20

```

US-09-201-227A-26
; Sequence 26, Application US/09201227A
; Patent No. 6468770
; GENERAL INFORMATION:
; APPLICANT: Keyes, Linda N.
; APPLICANT: Doberstein, Stephen K.
; APPLICANT: Buchman, Andrew R.
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF D. MELANOGASTER INSULIN-LIKE
; FILE REFERENCE: 7326-066
; CURRENT APPLICATION NUMBER: US/09/201,227A
; CURRENT FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-227A-26

```

Query Match 18.6%; Score 38.5; DB 2; Length 26;  
Best Local Similarity 37.5%; Pred. No. 81;  
Matches 9; Conservative 5; Mismatches 9; Indels

Qy	11	AIHYALNCCGLAGGVEQFISD	34
		:   :   :   :   :   :	
Db	3	ATNPARHCC-LSGCTRODLLTL	25

RESULT 21

US-09-084-303B-222  
; Sequence 222, Application US/09084303B  
; Patent No. 6627746  
; GENERAL INFORMATION:

INVENTOR: Doreen, Stephen  
 APPLICANT: Reddy, Bindu  
 APPLICANT: Platt, Darren  
 APPLICANT: Ferguson, Kimberly  
 TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEIN  
 TITLE OF INVENTION: THEREOF  
 FILE REFERENCE: 7326-069-999  
 CURRENT APPLICATION NUMBER: US/09/084,303B  
 CURRENT FILING DATE: 1998-05-26  
 NUMBER OF SEQ ID NOS: 302  
 SOFTWARE: Patent In version 3.1

RESULT 22

```

US-08-747-915-1
; Sequence 1, Application US/08747915
; Patent No. 5942492
; GENERAL INFORMATION:
; APPLICANT: Jones, Terence R.
; APPLICANT: Haney, David N.
; APPLICANT: Varga, Janos
; TITLE OF INVENTION: CYCLIC PEPTIDES THAT BIND TO
; NUMBER OF INVENTION: UKONINASE-TYPE PLASMINOGEN ACTIVATOR RECEPTOR
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,915
; FILING DATE: 12-NOV-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 32904-20001.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030 MRSNFOERSMWSH
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 44 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-747-915-1

```



```
Query Match      18.6%; Score 38.5; DB 1; Length 44;
Best Local Similarity 40.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 3; Mismatches 6; Indels 7; Gaps 2;

QY 17 NCCGLAGGV---EQFISDI----CPKK 36
   |||||
Db 10 NCDCLNGGTCVSNKYFSNIHWNCPCPK 36

RESULT 23
US-09-285-783-1
; Sequence 1, Application US/09285783
; Patent No. 6514710
; GENERAL INFORMATION:
; APPLICANT: Jones, Terence R.
;           Haney, David N.
;           Varga, Janos
; TITLE OF INVENTION: CYCLIC PEPTIDES THAT BIND TO
;                     UROKINASE-TYPE PLASMINOGEN ACTIVATOR RECEPTOR
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RADER, FISHMAN & GRAUER
; STREET: 1233 20TH STREET NW, SUITE 501
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/285,783
; FILING DATE: 05-Apr-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: LIVNAT, SHMUEL
; REGISTRATION NUMBER: 33,949
; REFERENCE/DOCKET NUMBER: ANG-001/DIV (80144-0007)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 955-8787
; TELEFAX: (202) 955-3751
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 44 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-285-783-1

Query Match      18.6%; Score 38.5; DB 2; Length 44;
Best Local Similarity 40.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 3; Mismatches 6; Indels 7; Gaps 2;

QY 17 NCCGLAGGV---EQFISDI----CPKK 36
   |||||
Db 10 NCDCLNGGTCVSNKYFSNIHWNCPCPK 36

RESULT 24
US-09-670-537A-1
; Sequence 1, Application US/09670537A
; Patent No. 6896870
; GENERAL INFORMATION:
; APPLICANT: MAZAR, Andrew P.
; APPLICANT: JONES, Terence R.
; TITLE OF INVENTION: DIAGNOSTIC PROBES AND THERAPEUTICS TARGETING UPA AND UPAR
; FILE REFERENCE: 38369-169219
; CURRENT APPLICATION NUMBER: US/09/670,537A
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 60/157,012

Query Match      18.6%; Score 38.5; DB 1; Length 44;
Best Local Similarity 40.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 3; Mismatches 6; Indels 7; Gaps 2;

QY 17 NCCGLAGGV---EQFISDI----CPKK 36
   |||||
Db 10 NCDCLNGGTCVSNKYFSNIHWNCPCPK 36

RESULT 25
US-09-880-503-2
; Sequence 2, Application US/09880503
; Patent No. 6833357
; GENERAL INFORMATION:
; APPLICANT: CINES, Douglas B
; APPLICANT: HIGAZI, Abd Al-Roof
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
; FILE REFERENCE: 9596-331
; CURRENT APPLICATION NUMBER: US/09/880,503
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/212,847
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-503-2

Query Match      18.6%; Score 38.5; DB 2; Length 47;
Best Local Similarity 40.7%; Pred. No. 1.6e+02;
Matches 11; Conservative 3; Mismatches 6; Indels 7; Gaps 2;

QY 17 NCCGLAGGV---EQFISDI----CPKK 36
   |||||
Db 10 NCDCLNGGTCVSNKYFSNIHWNCPCPK 36

RESULT 26
US-09-219-019-22
; Sequence 22, Application US/09219019
; Patent No. 6268341
; GENERAL INFORMATION:
; APPLICANT: ROSENBERG, STEVEN
; APPLICANT: STRATTON-THOMAS, JENNIFER R.
; TITLE OF INVENTION: EXPRESSION OF UROKINASE PLASMINOGEN ACTIVATOR
; FILE REFERENCE: 23533-0005
; CURRENT APPLICATION NUMBER: US/09/219,019
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 08/438,263
; PRIOR FILING DATE: 1995-05-10
; PRIOR APPLICATION NUMBER: 08/280,288
; PRIOR FILING DATE: 1994-07-26
; PRIOR APPLICATION NUMBER: 08/070,153
; PRIOR FILING DATE: 1993-06-01
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 22
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-09-219-019-22

Query Match 18.6%; Score 38.5; DB 2; Length 48;  
Best Local Similarity 40.7%; Pred. No. 1.7e+02;  
Matches 11; Conservative 3; Mismatches 6; Indels 7; Gaps 2;

QY 17 NCCLAGGV---EQFISDI-----CPKK 36  
||| ||| :|:| |||  
Db 10 NCDCLNGGTCVSNKYFSNIHWCNCPKK 36

RESULT 27

US-08-747-915-5  
; Sequence 5, Application US/08747915  
; Patent No. 5942492  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Terence R.  
; APPLICANT: Haney, David N.  
; APPLICANT: Varga, Janos  
; TITLE OF INVENTION: CYCLIC PEPTIDES THAT BIND TO  
; UROKINASE-TYPE PLASMINOGEN ACTIVATOR RECEPTOR  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 2000 PENNSYLVANIA AVENUE, NW  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1812  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/747,915  
; FILING DATE: 12-NOV-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURASHIGE, KATE H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 32904-20001.00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 887-1500  
; TELEFAX: (202) 887-0763  
; TELEX: 90-4030 MRSNFOERSWSH  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 49 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Disulfide-bond  
; LOCATION: group(11..19, 13..31, 33..42)  
US-08-747-915-5

Query Match 18.6%; Score 38.5; DB 1; Length 49;  
Best Local Similarity 40.7%; Pred. No. 1.7e+02;  
Matches 11; Conservative 3; Mismatches 6; Indels 7; Gaps 2;

QY 17 NCCLAGGV---EQFISDI-----CPKK 36  
||| ||| :|:| |||  
Db 10 NCDCLNGGTCVSNKYFSNIHWCNCPKK 36

RESULT 28

US-09-285-783-5  
; Sequence 5, Application US/09285783  
; Patent No. 6514710  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Terence R.  
; APPLICANT: Haney, David N.

Varga, Janos  
; TITLE OF INVENTION: CYCLIC PEPTIDES THAT BIND TO  
; UROKINASE-TYPE PLASMINOGEN ACTIVATOR RECEPTOR  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: RADER, FISHMAN & GRAUER  
; STREET: 1233 20TH STREET NW, SUITE 501  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/285,783  
; FILING DATE: 05-Apr-1999  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LIVNAT, SHMUEL  
; REGISTRATION NUMBER: 33,949  
; REFERENCE/DOCKET NUMBER: ANG-001/DIV (80144-0007)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 955-8787  
; TELEFAX: (202) 955-3751  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 49 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Disulfide-bond  
; LOCATION: group(11..19, 13..31, 33..42)  
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-285-783-5

Query Match 18.6%; Score 38.5; DB 2; Length 49;  
Best Local Similarity 40.7%; Pred. No. 1.7e+02;  
Matches 11; Conservative 3; Mismatches 6; Indels 7; Gaps 2;

QY 17 NCCLAGGV---EQFISDI-----CPKK 36  
||| ||| :|:| |||  
Db 10 NCDCLNGGTCVSNKYFSNIHWCNCPKK 36

RESULT 29

PCT-US96-08811-2  
; Sequence 2, Application PC/TUS9608811  
; GENERAL INFORMATION:  
; APPLICANT: VERNON, Leo P., RAEI, Eppie D. and  
; APPLICANT: GASANOV, Sardar E.  
; TITLE OF INVENTION: Pyruvate thionin containing  
; immunotoxins and immunotoxin-like compounds  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MADSON & METCALF  
; STREET: 950 First Interstate Building, 170 South  
; STREET: Main Street  
; CITY: Salt Lake City  
; STATE: Utah  
; COUNTRY: USA  
; ZIP: 84101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage  
; COMPUTER: IBM  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORDPERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/08811  
; FILING DATE:







```
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Alpha-Conotoxin Peptides
; FILE REFERENCE: 2314-179.A
; CURRENT APPLICATION NUMBER: US/09/493,795B
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/118,381
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 404
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 179
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Conus arenatus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (7)..(13)
; OTHER INFORMATION: Xaa at residue 7 is Pro or hydroxy-Pro; Xaa at
; OTHER INFORMATION: residue 10 is Trp (D or L) or halo-Trp; Xaa at
; OTHER INFORMATION: residue 12 is Glu or gamma-carboxy-Glu; Xaa at
; OTHER INFORMATION: residue 13 is Tyr, nor-Tyr, mono-halo-Tyr,
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (13)..(19)
; OTHER INFORMATION: di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or
; OTHER INFORMATION: nitro-Tyr; Xaa at residues 14 and 19 is Lys,
; OTHER INFORMATION: N-methyl-Lys, N,N-dimethyl-Lys or
; OTHER INFORMATION: N,N,N-trimethyl-Lys.
; US-09-493-795B-179

Query Match 17.4%; Score 36; DB 2; Length 21;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 16 LNCCLAG 23
DB 1 LNCCLAG 8

RESULT 39
PCT-US96-01720-5
; Sequence 5, Application PC/TUS9601720
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: MODIFIED-AFFINITY STREPTAVIDIN
; NUMBER OF SEQUENCES: 11
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/01720
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/387,055
; FILING DATE: 09-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 16336-5PC
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-01720-5

Query Match 17.4%; Score 36; DB 4; Length 28;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 18 CCGLAGG 24
DB 8 CCGGAGG 14

Search completed: January 20, 2006, 17:35:32
Job time : 27.2716 secs
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QY 18 CCGLAGG 24
DB 8 CCGGAGG 14

RESULT 40
PCT-US96-01720-6
; Sequence 6, Application PC/TUS9601720
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: MODIFIED-AFFINITY STREPTAVIDIN
; NUMBER OF SEQUENCES: 11
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/01720
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/387,055
; FILING DATE: 09-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 16336-5PC
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-01720-6

Query Match 17.4%; Score 36; DB 4; Length 28;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 18 CCGLAGG 24
DB 8 CCGGAGG 14

Search completed: January 20, 2006, 17:35:32
Job time : 27.2716 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:27:09 ; Search time 72.716 Seconds  
(without alignments)  
218.350 Million cell updates/sec

Title: US-10-619-323-4

Perfect score: 207

Sequence: 1 KDEPQRETLLKAIHYALNCCGLAGGVEQFISDICPKKDV 38

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 549595

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

Published Applications\_AA\_Main:\*

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2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*

3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*

4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*

6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	207	100.0	38	4	US-10-619-323-4
2	128	61.8	30	5	US-10-473-127-1717
3	60	29.0	22	4	US-10-619-323-7
4	45	21.7	32	6	US-11-111-953-658
5	44	21.3	33	3	US-09-798-889-81
6	44	21.3	33	4	US-10-633-680-81
7	44	21.3	44	4	US-10-072-602B-490
8	44	21.3	44	6	US-11-097-315-490
9	42.5	20.5	47	4	US-10-425-115-188223
10	42.5	20.5	50	4	US-10-074-024-339
11	42	20.3	37	2	US-08-900-230-54
12	42	20.3	40	4	US-10-424-599-232491
13	42	20.3	42	4	US-10-424-599-165084
14	41.5	20.0	32	4	US-10-072-602B-39
15	41.5	20.0	32	6	US-11-097-315-39
16	41	19.8	40	4	US-10-425-115-259736
17	41	19.8	40	3	US-09-864-761-36105
18	41	19.8	44	4	US-10-106-698-5684
19	41	19.8	44	4	US-10-425-115-206370
20	41	19.8	46	4	US-10-424-599-233026
21	41	19.8	49	4	US-10-425-115-200533
22	40.5	19.6	32	4	US-10-072-602B-42
23	40.5	19.6	32	4	US-10-072-602B-553
24	40.5	19.6	32	6	US-11-097-315-42
25	40.5	19.6	32	6	US-11-097-315-553
26	40	19.3	44	4	US-10-424-599-283568
27	40	19.3	47	3	US-09-864-761-45041

28	40	19.3	47	4	US-10-425-115-220604	Sequence 220604,
29	40	19.3	49	4	US-10-424-599-234805	Sequence 234805,
30	39.5	19.1	22	4	US-10-072-602B-554	Sequence 554, App
31	39.5	19.1	32	6	US-11-097-315-554	Sequence 554, App
32	39.5	19.1	40	5	US-10-895-372-302	Sequence 302, App
33	39.5	19.1	43	4	US-10-425-115-355346	Sequence 355346,
34	39	18.8	28	3	US-09-866-066-31	Sequence 31, Appl
35	39	18.8	28	5	US-10-969-677-31	Sequence 31, Appl
36	39	18.8	45	3	US-09-864-761-38744	Sequence 38744, A
37	39	18.8	45	5	US-10-776-224-363	Sequence 363, App
38	39	18.8	46	4	US-10-424-599-216516	Sequence 216516,
39	39	18.8	46	4	US-10-425-115-300697	Sequence 300697,
40	39	18.8	46	5	US-10-776-224-364	Sequence 364, App
41	39	18.8	47	4	US-10-424-599-191877	Sequence 191877,
42	39	18.8	49	4	US-10-425-115-266792	Sequence 266792,
43	39	18.8	50	4	US-10-425-115-202414	Sequence 202414,
44	39	18.8	50	4	US-10-425-115-248925	Sequence 248925,
45	38.5	18.6	26	4	US-10-339-740-222	Sequence 222, App
46	38.5	18.6	27	4	US-10-196-394-54	Sequence 54, Appl
47	38.5	18.6	37	4	US-10-425-115-256841	Sequence 256841,
48	38.5	18.6	40	4	US-10-437-963-152437	Sequence 152437,
49	38.5	18.6	44	4	US-10-349-543-1	Sequence 1, Appli
50	38.5	18.6	44	4	US-10-744-527-8	Sequence 8, Appli

#### ALIGNMENTS

##### RESULT 1

US-10-619-323-4

; Sequence 4, Application US/10619323

; Publication No. US20040136985A1

; GENERAL INFORMATION:

; APPLICANT: Jennings, Lisa K.

; APPLICANT: Longhurst, Celia M.

; APPLICANT: Bao, Jianxiong

; APPLICANT: Zhang, Chunxiang

; APPLICANT: White, Melanie M.

; APPLICANT: Crossno, Jr., Joseph T.

; APPLICANT: Lu, Yi

; TITLE OF INVENTION: METHODS OF MODIFYING BEHAVIOR OF CD9-EXPRESSING CELLS

; FILE REFERENCE: 20609/241

; CURRENT APPLICATION NUMBER: US/10/619,323

; CURRENT FILING DATE: 2003-07-14

; PRIOR APPLICATION NUMBER: 60/395,864

; PRIOR FILING DATE: 2002-07-12

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 4

; LENGTH: 38

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: CD9 peptide

US-10-619-323-4

Query Match 100.0%; Score 207; DB 4; Length 38;

Best Local Similarity 100.0%; Pred. No. 2.4e-22;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEPQRETLLKAIHYALNCCGLAGGVEQFISDICPKKDV 38

Db 1 KDEPQRETLLKAIHYALNCCGLAGGVEQFISDICPKKDV 38

##### RESULT 2

US-10-473-127-1717

; Sequence 1717, Application US/10473127

; Publication No. US20040236091A1

; GENERAL INFORMATION:

; APPLICANT: Zycos Inc.

; TITLE OF INVENTION: TRANSLATIONAL PROFILING

; FILE REFERENCE: 08191-026WO1  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; PRIOR FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1717  
; LENGTH: 30  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1717

Query Match 61.8%; Score 128; DB 5; Length 30;  
Best Local Similarity 100.0%; Pred. No. 5.2e-11; Indels 0; Gaps 0;  
Matches 23; Conservative 0; Mismatches 0;

QY 16 LNCCLAGGVEQFISDICPKDV 38  
|||||  
Db 1 LNCCLAGGVEQFISDICPKDV 23

RESULT 3  
US-10-619-323-7  
; Sequence 7, Application US/10619323  
; Publication No. US20040136985A1  
; GENERAL INFORMATION:  
; APPLICANT: Jennings, Lisa K.  
; APPLICANT: Longhurst, Celia M.  
; APPLICANT: Cook, George A.  
; APPLICANT: Bao, Jianxiong  
; APPLICANT: Zhang, Chunxiang  
; APPLICANT: White, Melanie M.  
; APPLICANT: Crossno, Jr., Joseph T.  
; APPLICANT: Lu, Yi  
; TITLE OF INVENTION: METHODS OF MODIFYING BEHAVIOR OF CD9-EXPRESSING CELLS  
; FILE REFERENCE: 20609/241  
; CURRENT APPLICATION NUMBER: US/10/619,323  
; CURRENT FILING DATE: 2003-07-14  
; PRIOR APPLICATION NUMBER: 60/395,864  
; PRIOR FILING DATE: 2002-07-12  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 22  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: CD9 peptide  
US-10-619-323-7

Query Match 29.0%; Score 60; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.26;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAI 12  
|||||  
Db 11 KDEPQRETLKAI 22

RESULT 4  
US-11-111-953-658  
; Sequence 658, Application US/11111953

; Publication No. US20050214844A1  
; GENERAL INFORMATION:  
; APPLICANT: Moore et al.  
; TITLE OF INVENTION: 86 Human Secreted Proteins  
; FILE REFERENCE: PZ008P1C2  
; CURRENT APPLICATION NUMBER: US/11/111,953  
; CURRENT FILING DATE: 2005-04-22  
; PRIOR APPLICATION NUMBER: 10/219,793  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: 09/209,462  
; PRIOR FILING DATE: 1998-12-11  
; PRIOR APPLICATION NUMBER: PCT/US98/12125  
; PRIOR FILING DATE: 1998-06-11  
; PRIOR APPLICATION NUMBER: 60/049,547  
; PRIOR FILING DATE: 1997-06-13  
; PRIOR APPLICATION NUMBER: 60/049,548  
; PRIOR FILING DATE: 1997-06-13  
; PRIOR APPLICATION NUMBER: 60/049,549  
; PRIOR FILING DATE: 1997-06-13  
; PRIOR APPLICATION NUMBER: 60/049,550  
; PRIOR FILING DATE: 1997-06-13  
; PRIOR APPLICATION NUMBER: 60/049,566  
; PRIOR FILING DATE: 1997-06-13  
; PRIOR APPLICATION NUMBER: 60/049,606  
; PRIOR FILING DATE: 1997-06-13  
; PRIOR APPLICATION NUMBER: 60/049,607  
; PRIOR FILING DATE: 1997-06-13  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 737  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 658  
; LENGTH: 32  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-111-953-658

Query Match 21.7%; Score 45; DB 6; Length 32;  
Best Local Similarity 36.8%; Pred. No. 60;  
Matches 7; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 2 DEPQRETLKAIHYALNCCG 20  
| : : : : : : : : : :  
Db 4 DMKRCETPEILHHQIKCG 22

RESULT 5  
US-09-798-889-81  
; Sequence 81, Application US/09798889  
; Publication No. US20030004324A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 31 Human secreted proteins  
; FILE REFERENCE: PZ026P1  
; CURRENT APPLICATION NUMBER: US/09/798,889  
; CURRENT FILING DATE: 2001-03-06  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/393,022  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-09  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/077,714  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-12  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/077,686  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-12  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/077,687  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-12  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/077,696  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-12  
; NUMBER OF SEQ ID NOS: 185  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 81  
; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE



; LOCATION: (19)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-798-889-81

Query Match 21.3%; Score 44; DB 3; Length 33;  
Best Local Similarity 42.9%; Pred. No. 86;  
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 10 KAIHYALNCCGLAG 23  
| : : ||| : :  
Db 16 KVVXFGGLACGVSG 29

## RESULT 6

US-10-633-680-81  
; Sequence 81, Application US/10633680  
; Publication No. US20040030115A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 31 Human secreted proteins  
; FILE REFERENCE: P2026P1C2  
; CURRENT APPLICATION NUMBER: US/10/633,680  
; CURRENT FILING DATE: 2003-08-05  
; PRIOR FILING DATE: 2001-03-06  
; PRIOR APPLICATION NUMBER: 09/787,889  
; PRIOR FILING DATE: 1999-09-09  
; PRIOR APPLICATION NUMBER: PCT/US99/05721  
; PRIOR FILING DATE: 1999-03-11  
; PRIOR APPLICATION NUMBER: 60/077,714  
; PRIOR FILING DATE: 1998-03-12  
; PRIOR APPLICATION NUMBER: 60/077,686  
; PRIOR FILING DATE: 1998-03-12  
; PRIOR APPLICATION NUMBER: 60/077,687  
; PRIOR FILING DATE: 1998-03-12  
; PRIOR APPLICATION NUMBER: 60/077,696  
; PRIOR FILING DATE: 1998-03-12  
; NUMBER OF SEQ ID NOS: 185  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 81  
; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (19)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-10-633-680-81

Query Match 21.3%; Score 44; DB 4; Length 33;  
Best Local Similarity 42.9%; Pred. No. 86;  
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 10 KAIHYALNCCGLAG 23  
| : : ||| : :  
Db 16 KVVXFGGLACGVSG 29

## RESULT 7

US-10-072-602B-490  
; Sequence 490, Application US/10072602B  
; Publication No. US20030109670A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Cognetix, Inc.  
; APPLICANT: Olivera, Baldomero M.  
; APPLICANT: McIntosh, J, Michael  
; APPLICANT: Watkins, Maren  
; APPLICANT: Garrett, James E.  
; APPLICANT: Cruz, Lourdes J.  
; APPLICANT: Grilley, Michelle  
; APPLICANT: Schoenfeld, Robert M.  
; APPLICANT: Walker, Craig

; APPLICANT: Shetty, Reshma  
; APPLICANT: Jones, Robert M.  
; TITLE OF INVENTION: Cone Snail Peptides  
; FILE REFERENCE: 2314-249  
; CURRENT APPLICATION NUMBER: US/10/072,602B  
; CURRENT FILING DATE: 2002-02-11  
; PRIOR APPLICATION NUMBER: US 60/267,408  
; PRIOR FILING DATE: 2001-02-09  
; NUMBER OF SEQ ID NOS: 638  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 490  
; LENGTH: 44  
; TYPE: PRT  
; ORGANISM: Conus radiatus  
US-10-072-602B-490

Query Match 21.3%; Score 44; DB 4; Length 44;  
Best Local Similarity 37.5%; Pred. No. 1.2e+02;  
Matches 9; Conservative 1; Mismatches 12; Indels 2; Gaps 1;

Qy 14 YALNCCGLAGGVEQFISDI--CPK 35  
| | | | | : | | | |  
Db 1 YGLGCAGTCGSSNCVRDYCDCPK 24

## RESULT 8

US-11-097-315-490  
; Sequence 490, Application US/11097315  
; Publication No. US20050214213A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Cognetix, Inc.  
; APPLICANT: Olivera, Baldomero M.  
; APPLICANT: McIntosh, J, Michael  
; APPLICANT: Watkins, Maren  
; APPLICANT: Garrett, James E.  
; APPLICANT: Cruz, Lourdes J.  
; APPLICANT: Grilley, Michelle  
; APPLICANT: Schoenfeld, Robert M.  
; APPLICANT: Walker, Craig  
; APPLICANT: Shetty, Reshma  
; APPLICANT: Jones, Robert M.  
; TITLE OF INVENTION: Cone Snail Peptides  
; FILE REFERENCE: 2314-293  
; CURRENT APPLICATION NUMBER: US/11/097,315  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: US 10/072,602  
; PRIOR FILING DATE: 2002-02-11  
; PRIOR APPLICATION NUMBER: US 60/267,408  
; NUMBER OF SEQ ID NOS: 638  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 490  
; LENGTH: 44  
; TYPE: PRT  
; ORGANISM: Conus radiatus  
US-11-097-315-490

Query Match 21.3%; Score 44; DB 6; Length 44;  
Best Local Similarity 37.5%; Pred. No. 1.2e+02;  
Matches 9; Conservative 1; Mismatches 12; Indels 2; Gaps 1;

Qy 14 YALNCCGLAGGVEQFISDI--CPK 35  
| | | | | : | | | |  
Db 1 YGLGCAGTCGSSNCVRDYCDCPK 24

## RESULT 9

US-10-425-115-188223  
; Sequence 188223, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.





Query Match 19.8%; Score 41; DB 3; Length 44;  
Best Local Similarity 47.4%; Pred. No. 3.2e+02;  
Matches 9: Conservative 2; Mismatches 8; Indels

Qy 1 KDEPQRETLKAHYALNCC 19  
|||:|:|:|:|:|:|  
Db 10 KDRAQSOTLQKIYCGNGC 28

## RESULT 18

```

US-10-106-698-5684
; Sequence 5684, Application US/10106698
; Publication No. US20030109690A1
GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 5684
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (34)_
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC FEATURE
; LOCATION: (38)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-5684

```

```
Query Match      19.8%; Score 41; DB 4; Length 44;
Best Local Similarity 35.0%; Pred. No. 3.2e+02;
Matches 7: Conservative 3; Mismatches 10; Indels 0; Gaps 0;
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Qy 17 NCCGLAGVEQFISDICK 36  
|| : : ||||  
Db 3 NCITVTNEILSLLSICK 22

RESULT 19

```

US-10-425-115-206370
; Sequence 206370, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 206370
; LENGTH: 44
; TYPE: ERT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRF4577_119792C.1.pep
US-10-425-115-206370

```

Query Match 19.8%; Score 41; DB 4; Length 44;

```

RESULT 17
US-09-864-761-36105
; Sequence 36105, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aemica-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 36105
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC008925.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 6.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 6.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 5.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 6.4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 6
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 5.7
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 5.4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 5
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 5.9
; OTHER INFORMATION: EST_HUMAN HIT: BE081896.1, EVALUATE 1.00e-11
US-09-864-761-36105

```

Best Local Similarity 24.2%; Pred. No. 3.2e+02; Indels 10; Gaps 1;  
Matches 8; Conservative 9; Mismatches 6;  
QY 6 RETLKAIHYALNCCGLAGVEQFISDIPCKDV 38  
Db 3 REVWKLVPF-----VEAFVNLCSRRRV 25

RESULT 20  
US-10-424-599-233026  
; Sequence 233026, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 233026  
; LENGTH: 46  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_52447C.1.pep  
US-10-424-599-233026

Query Match 19.8%; Score 41; DB 4; Length 46;  
Best Local Similarity 36.7%; Pred. No. 3.4e+02;  
Matches 11; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 7 ETLKAIHYALNCCGLAGVEQFISDIPCK 36  
Db 4 ERIADIQLHMTLLSGTVERVHLLCPK 33

RESULT 21  
US-10-425-115-200533  
; Sequence 200533, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 200533  
; LENGTH: 49  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_114474C.1.pep  
US-10-425-115-200533

Query Match 19.8%; Score 41; DB 4; Length 49;  
Best Local Similarity 33.3%; Pred. No. 3.6e+02;  
Matches 7; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 13 HYALNCCGLAGVEQFISDIC 33  
Db 4 HHFMCLVLTSLKFLADIC 24

RESULT 22

US-10-072-602B-42  
; Sequence 42, Application US/10072602B  
; Publication No. US20030109670A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Cognetix, Inc.  
; APPLICANT: Olivera, Baldomero M.  
; APPLICANT: McIntosh, J, Michael  
; APPLICANT: Watkins, Maren  
; APPLICANT: Garrett, James E.  
; APPLICANT: Cruz, Lourdes J.  
; APPLICANT: Grilley, Michelle  
; APPLICANT: Schoenfeld, Robert M.  
; APPLICANT: Walker, Craig  
; APPLICANT: Shetty, Reshma  
; APPLICANT: Jones, Robert M.  
; TITLE OF INVENTION: Cone Snail Peptides  
; FILE REFERENCE: 2314-249  
; CURRENT APPLICATION NUMBER: US/10/072,602B  
; CURRENT FILING DATE: 2002-02-11  
; PRIOR APPLICATION NUMBER: US 60/267,408  
; PRIOR FILING DATE: 2001-02-09  
; NUMBER OF SEQ ID NOS: 638  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 42  
; LENGTH: 32  
; TYPE: PRT  
; ORGANISM: Conus arenatus  
; FEATURE:  
; NAME/KEY: PSPTIDE  
; LOCATION: (1)..(31)  
; OTHER INFORMATION: Xaa at residues 7, 8, 11, 13, 14 and 21 is Glu or gamma-carboxy-  
; OTHER INFORMATION: Glu; Xaa at residue 25 is Pro or hydroxy-Pro  
US-10-072-602B-42

Query Match 19.6%; Score 40.5; DB 4; Length 32;  
Best Local Similarity 41.2%; Pred. No. 2.7e+02;  
Matches 7; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 17 NCCGLAGVEQFISDIC 33  
Db 16 HCCGLXNG-OXFCARLC 31

RESULT 23  
US-10-072-602B-553  
; Sequence 553, Application US/10072602B  
; Publication No. US20030109670A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Cognetix, Inc.  
; APPLICANT: Olivera, Baldomero M.  
; APPLICANT: McIntosh, J, Michael  
; APPLICANT: Watkins, Maren  
; APPLICANT: Garrett, James E.  
; APPLICANT: Cruz, Lourdes J.  
; APPLICANT: Grilley, Michelle  
; APPLICANT: Schoenfeld, Robert M.  
; APPLICANT: Walker, Craig  
; APPLICANT: Shetty, Reshma  
; APPLICANT: Jones, Robert M.  
; TITLE OF INVENTION: Cone Snail Peptides  
; FILE REFERENCE: 2314-249  
; CURRENT APPLICATION NUMBER: US/10/072,602B  
; CURRENT FILING DATE: 2002-02-11  
; PRIOR APPLICATION NUMBER: US 60/267,408  
; PRIOR FILING DATE: 2001-02-09  
; NUMBER OF SEQ ID NOS: 638  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 553  
; LENGTH: 32  
; TYPE: PRT  
; ORGANISM: Conus arenatus

US-10-072-602B-553

Query Match 19.6%; Score 40.5; DB 4; Length 32;  
Best Local Similarity 43.8%; Pred. No. 2.7e+02;  
Matches 7; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 18 CCGLAGGVQPFISDIC 33  
||||| : : : : :  
DB 17 CCGLENG-QPFCAPVC 31

RESULT 24

US-11-097-315-42  
; Sequence 42, Application US/11097315  
; Publication No. US20050214213A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Cognetix, Inc.  
; APPLICANT: Olivera, Baldomero M.  
; APPLICANT: McIntosh, J, Michael  
; APPLICANT: Watkins, Maren  
; APPLICANT: Garrett, James E.  
; APPLICANT: Cruz, Lourdes J.  
; APPLICANT: Grilley, Michelle  
; APPLICANT: Schoenfeld, Robert M.  
; APPLICANT: Walker, Craig  
; APPLICANT: Shetty, Reshma  
; APPLICANT: Jones, Robert M.  
; TITLE OF INVENTION: Cone Snail Peptides  
; FILE REFERENCE: 2314-293  
; CURRENT APPLICATION NUMBER: US/11/097,315  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: US 10/072,602  
; PRIOR FILING DATE: 2002-02-11  
; PRIOR APPLICATION NUMBER: US 60/267,408  
; PRIOR FILING DATE: 2001-02-09  
; NUMBER OF SEQ ID NOS: 638  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 42  
; LENGTH: 32  
; TYPE: PRT  
; ORGANISM: Conus arenatus  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (1)..(31)  
; OTHER INFORMATION: Xaa at residues 7, 8, 11, 13, 14 and 21 is Glu or gamma-carboxy-  
; OTHER INFORMATION: Glu; Xaa at residue 25 is Pro or hydroxy-Pro  
US-11-097-315-42

Query Match 19.6%; Score 40.5; DB 6; Length 32;  
Best Local Similarity 41.2%; Pred. No. 2.7e+02;  
Matches 7; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 17 NCCGLAGGVQPFISDIC 33  
||||| : : : : :  
DB 16 HCCGLXNG-QXFCARLC 31

RESULT 25

US-11-097-315-553  
; Sequence 553, Application US/11097315  
; Publication No. US20050214213A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Cognetix, Inc.  
; APPLICANT: Olivera, Baldomero M.  
; APPLICANT: McIntosh, J, Michael  
; APPLICANT: Watkins, Maren  
; APPLICANT: Garrett, James E.  
; APPLICANT: Cruz, Lourdes J.  
; APPLICANT: Grilley, Michelle  
; APPLICANT: Schoenfeld, Robert M.  
; APPLICANT: Walker, Craig

; APPLICANT: Shetty, Reshma  
; APPLICANT: Jones, Robert M.  
; TITLE OF INVENTION: Cone Snail Peptides  
; FILE REFERENCE: 2314-293  
; CURRENT APPLICATION NUMBER: US/11/097,315  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: US 10/072,602  
; PRIOR FILING DATE: 2002-02-11  
; PRIOR APPLICATION NUMBER: US 60/267,408  
; PRIOR FILING DATE: 2001-02-09  
; NUMBER OF SEQ ID NOS: 638  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 553  
; LENGTH: 32  
; TYPE: PRT  
; ORGANISM: Conus arenatus  
US-11-097-315-553

Query Match 19.6%; Score 40.5; DB 6; Length 32;  
Best Local Similarity 43.8%; Pred. No. 2.7e+02;  
Matches 7; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 18 CCGLAGGVQPFISDIC 33  
||||| : : : : :  
DB 17 CCGLENG-QPFCAPVC 31

RESULT 26

US-10-424-599-283568  
; Sequence 283568, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 283568  
; LENGTH: 44  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_98084C.1.pep  
US-10-424-599-283568

Query Match 19.3%; Score 40; DB 4; Length 44;  
Best Local Similarity 63.6%; Pred. No. 4.5e+02;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 9 LKAIHYALNCC 19  
||| : |||||  
DB 29 LKIVHVALNSC 39

RESULT 27

US-09-864-761-45041  
; Sequence 45041, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: Aeomica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23



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; CURRENT APPLICATION NUMBER: US/10/072,602B
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 554
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Conus arenatus
US-10-072-602B-554

Query Match      19.1%; Score 39.5; DB 4; Length 32;
Best Local Similarity 41.2%; Pred. No. 3.7e+02;
Matches 7; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 17 NCCGLAGGVQFISDIC 33
      ||||| : | : |
Db 16 HCCGLENG-QPFCARLC 31

RESULT 31
US-11-097-315-554
; Sequence 554, Application US/11097315
; Publication No. US20050214213A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J, Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-293
; CURRENT APPLICATION NUMBER: US/11/097,315
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: US 10/072,602
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 554
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Conus arenatus
US-11-097-315-554

Query Match      19.1%; Score 39.5; DB 6; Length 32;
Best Local Similarity 41.2%; Pred. No. 3.7e+02;
Matches 7; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 17 NCCGLAGGVQFISDIC 33
      ||||| : | : |
Db 16 HCCGLENG-QPFCARLC 31

RESULT 32
US-10-895-372-302
; Sequence 302, Application US/10895372
; Publication No. US20050032705A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Hillvard, David R.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Jones, Robert M.

; TITLE OF INVENTION: Alpha-Conotoxin Peptides
; FILE REFERENCE: 2314-286
; CURRENT APPLICATION NUMBER: US/10/895,372
; CURRENT FILING DATE: 2004-07-21
; PRIOR APPLICATION NUMBER: US 09/493,795
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/118,381
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 404
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 302
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Conus arenatus
US-10-895-372-302

Query Match      19.1%; Score 39.5; DB 5; Length 40;
Best Local Similarity 40.0%; Pred. No. 4.8e+02;
Matches 8; Conservative 3; Mismatches 8; Indels 1; Gaps 1;

QY 16 LNCCLAGGVQFISDICPK 35
      ||||| : | : |
Db 20 LNCSSIPGCWNEY-KDRCSK 38

RESULT 33
US-10-425-115-355346
; Sequence 355346, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 355346
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_87242C.1.pep
US-10-425-115-355346

Query Match      19.1%; Score 39.5; DB 4; Length 43;
Best Local Similarity 38.5%; Pred. No. 5.2e+02;
Matches 10; Conservative 3; Mismatches 12; Indels 1; Gaps 1;

QY 2 DEPORETLKAIHVALNCCGLAGGVEQ 27
      | : | : | ||| |||
Db 18 DQAGRDRCETRH-CLNCTSLGPGYQ 42

RESULT 34
US-09-866-066-31
; Sequence 31, Application US/09866066
; Publication No. US20030113888A1
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Christopher
; APPLICANT: Berberds, Steve
; APPLICANT: Ruble, Cara
; APPLICANT: Gotow, Lisa
; APPLICANT: Karnovsky, Alla
; TITLE OF INVENTION: Human Ion Channels
; FILE REFERENCE: 00229.US1
; CURRENT APPLICATION NUMBER: US/09/866,066
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,152
; PRIOR FILING DATE: 2000-05-26
```



; PRIOR APPLICATION NUMBER: 60/207,257  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/207,119  
; PRIOR FILING DATE: 2000-05-26  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 31  
; LENGTH: 28  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-866-066-31

Query Match 18.8%; Score 39; DB 3; Length 28;  
Best Local Similarity 35.7%; Pred. No. 3.8e+02;  
Matches 10; Conservative 3; Mismatches 13; Indels 2; Gaps 1;

Qy 1 KDEPQRETLKAIHYALNCCGLAGGVEQF 28  
Db 3 KNSQQHIKKLIHY--NQVFGISGMDWF 28

## RESULT 35

US-10-969-677-31  
; Sequence 31, Application US/10969677  
; Publication No. US20050176098A1  
; GENERAL INFORMATION:  
; APPLICANT: Benjamin, Christopher  
; APPLICANT: Roberts, Steve  
; APPLICANT: Rubie, Cara  
; APPLICANT: Gotow, Lisa  
; APPLICANT: Karnovsky, Alla  
; TITLE OF INVENTION: Human Ion Channels  
; FILE REFERENCE: 00229 US1  
; CURRENT APPLICATION NUMBER: US/10/969,677  
; CURRENT FILING DATE: 2004-10-20  
; PRIOR APPLICATION NUMBER: US/09/866,066  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/207,152  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/207,257  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/207,119  
; PRIOR FILING DATE: 2000-05-26  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 31  
; LENGTH: 28  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-969-677-31

Query Match 18.8%; Score 39; DB 5; Length 28;  
Best Local Similarity 35.7%; Pred. No. 3.8e+02;  
Matches 10; Conservative 3; Mismatches 13; Indels 2; Gaps 1;

Qy 1 KDEPQRETLKAIHYALNCCGLAGGVEQF 28  
Db 3 KNSQQHIKKLIHY--NQVFGISGMDWF 28

## RESULT 36

US-09-864-761-38744  
; Sequence 38744, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wenheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: Aescmca-x-1  
; CURRENT APPLICATION NUMBER: US/09/864,761

; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 38744  
; LENGTH: 45  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO Z98884.11  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.9  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.4  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.7  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.9  
; OTHER INFORMATION: SWISSPROT HIT: O70361, EVALU6 6.00e-13  
US-09-864-761-38744

Query Match 18.8%; Score 39; DB 3; Length 45;  
Best Local Similarity 63.6%; Pred. No. 6.4e+02;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TLKAIHYALNC 18  
Db 20 TLDALNVALRC 30

## RESULT 37

US-10-776-224-363  
; Sequence 363, Application US/10776224  
; Publication No. US20050074849A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaudernack, Gustav  
; APPLICANT: Erickson, Jon Amund  
; APPLICANT: Moller, Mona  
; APPLICANT: Gjertsen, Marianne Klemp  
; APPLICANT: Saeterdal, Ingvil

```
; TITLE OF INVENTION: Peptides
; FILE REFERENCE: 01702.4015LO
; CURRENT APPLICATION NUMBER: US/10/776,224
; CURRENT FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: US 09/674,973
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 459
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 363
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-776-224-363

Query Match      18.8%; Score 39; DB 5; Length 45;
Best Local Similarity 38.1%; Pred. No. 6.4e+02;
Matches 8; Conservative 4; Mismatches 7; Indels 2; Gaps 1;

QY      19  CGLA--GGVEQFISDICPKD 37
Db      1  CSLAKDGTEDTVSSLCGEED 21

RESULT 38
US-10-424-599-216516
; Sequence 216516, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 216516
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_37542C.1.pep
US-10-424-599-216516

Query Match      18.8%; Score 39; DB 4; Length 46;
Best Local Similarity 36.4%; Pred. No. 6.6e+02;
Matches 8; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY      2  DEPORETLKAIHYALNCCGLAG 23
Db      23  BECVKAALIAVTLSLPCCSIG 44

RESULT 39
US-10-425-115-300697
; Sequence 300697, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 300697
; LENGTH: 46
; TYPE: PRT
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; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_37305C.1.pep
US-10-425-115-300697

Query Match      18.8%; Score 39; DB 4; Length 46;
Best Local Similarity 29.4%; Pred. No. 6.6e+02;
Matches 10; Conservative 8; Mismatches 14; Indels 2; Gaps 1;

QY      4  PORETLKAIHYALNCCGLAGVEQFISDICPKD 37
Db      10  PQSYILGYINYCLVLCQLI--IKPCVNDLGRSN 41

RESULT 40
US-10-776-224-364
; Sequence 364, Application US/10776224
; Publication No. US20050074849A1
; GENERAL INFORMATION:
; APPLICANT: Gaudernack, Gustav
; APPLICANT: Ericksen, Jon Amund
; APPLICANT: Moller, Mona
; APPLICANT: Gjertsen, Marianne Klemp
; APPLICANT: Saeterdal, Ingvil
; TITLE OF INVENTION: Peptides
; FILE REFERENCE: 01702.4015LO
; CURRENT APPLICATION NUMBER: US/10/776,224
; CURRENT FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: US 09/674,973
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 459
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 364
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-776-224-364

Query Match      18.8%; Score 39; DB 5; Length 46;
Best Local Similarity 38.1%; Pred. No. 6.6e+02;
Matches 8; Conservative 4; Mismatches 7; Indels 2; Gaps 1;

QY      19  CGLA--GGVEQFISDICPKD 37
Db      2  CSLAKDGTEDTVSSLCGEED 22

Search completed: January 20, 2006, 17:38:18
Job time : 73.716 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw\_model

Run on: January 20, 2006, 17:30:50 ; Search time 6.5679 Seconds  
(without alignments)  
58.632 Million cell updates/sec

Title: US-10-619-323-4

Perfect score: 207

Sequence: 1 KDSQRETLKAIHYALNCCGLAGVEQFISDIPKDV 38

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 70606 seqs, 10133881 residues

Total number of hits satisfying chosen parameters: 41278

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : Published Applications AA New:  
1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB pep:.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB pep:.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB pep:.\*  
4: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB pep:.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US05\_NEW\_PUB pep:.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB pep:.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB pep:.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB pep:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37.5	18.1	44	6	US-10-957-887B-193
2	37.5	18.1	44	6	US-10-729-121-52
3	36.5	17.6	45	6	US-10-957-887B-243
4	35	17.4	47	7	US-11-123-896-372
5	35.5	17.1	30	6	US-10-467-657-3382
6	35	16.9	31	7	US-11-145-035-45
7	34	16.4	47	7	US-11-038-501-4
8	34	16.4	47	7	US-11-059-633-7
9	32.5	15.7	20	7	US-11-106-415-285
10	32	15.5	46	7	US-11-068-783-111
11	31	15.0	15	7	US-11-045-024-13448
12	31	15.0	21	6	US-10-939-890-535
13	31	15.0	24	7	US-11-198-847-180
14	31	15.0	24	7	US-11-198-847-282
15	31	15.0	31	7	US-11-033-039-631
16	31	15.0	36	6	US-10-957-351-184
17	30.5	14.7	21	6	US-10-939-890-537
18	30.5	14.7	49	6	US-10-467-657-2116
19	30	14.5	15	7	US-11-045-024-13229
20	30	14.5	15	7	US-11-045-024-13251
21	30	14.5	20	7	US-11-106-415-284
22	30	14.5	21	7	US-11-198-847-323
23	30	14.5	25	7	US-11-198-847-177
24	30	14.5	25	7	US-11-198-847-281
25	30	14.5	35	6	US-10-467-657-5682

26	30	14.5	35	6	US-10-467-657-7098	Sequence 7098, Ap
27	30	14.5	35	6	US-10-467-657-8030	Sequence 8030, Ap
28	30	14.5	35	6	US-10-957-351-20	Sequence 20, Appl
29	30	14.5	40	6	US-10-979-871-10	Sequence 10, Appl
30	30	14.5	40	6	US-10-979-871-12	Sequence 12, Appl
31	30	14.5	47	7	US-11-123-896-390	Sequence 390, App
32	30	14.5	47	7	US-11-123-896-393	Sequence 393, App
33	29.5	14.3	31	7	US-11-043-590-43	Sequence 43, Appl
34	29.5	14.3	36	6	US-10-467-657-6618	Sequence 6618, Ap
35	29	14.0	10	6	US-10-859-843-628	Sequence 628, App
36	29	14.0	10	7	US-11-097-864-628	Sequence 628, App
37	29	14.0	10	7	US-11-097-912-628	Sequence 628, App
38	29	14.0	11	7	US-11-045-024-2377	Sequence 2377, Ap
39	29	14.0	11	7	US-11-045-024-4816	Sequence 4816, Ap
40	29	14.0	14	6	US-10-939-890-86	Sequence 86, Appl
41	29	14.0	15	7	US-11-045-024-13207	Sequence 13207, A
42	29	14.0	20	7	US-11-133-465A-6	Sequence 6, Appli
43	29	14.0	26	7	US-11-114-813-3	Sequence 3, Appli
44	29	14.0	26	7	US-11-115-003-3	Sequence 3, Appli
45	29	14.0	27	7	US-11-110-274-299	Sequence 299, App
46	29	14.0	34	7	US-11-121-301-12	Sequence 12, Appl
47	29	14.0	34	7	US-11-121-301-14	Sequence 14, Appl
48	29	14.0	38	6	US-10-957-351-89	Sequence 89, Appl
49	29	14.0	39	6	US-10-632-150-66	Sequence 66, Appl
50	29	14.0	39	7	US-11-027-111-3	Sequence 3, Appli

#### ALIGNMENTS

##### RESULT 1

US-10-957-887B-193  
; Sequence 193, Application US/10957887B  
; Publication No. US20050272677A1  
; GENERAL INFORMATION:  
; APPLICANT: Friesen, Robert H. E.  
; APPLICANT: Leenhouts, Cornelius J.  
; APPLICANT: Hektor, Harm  
; APPLICANT: van Bach, Johannes H.  
; APPLICANT: Heeres, Andre

; TITLE OF INVENTION: DELIVERY OF A SUBSTANCE TO A PRE-DETERMINED SITE  
; FILE REFERENCE: 2183-6668US  
; CURRENT APPLICATION NUMBER: US/10/957,887B  
; CURRENT FILING DATE: 2004-10-04  
; PRIOR APPLICATION NUMBER: PCT/NL/00256  
; PRIOR FILING DATE: 2003-04-04  
; NUMBER OF SEQ ID NOS: 309  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 193  
; LENGTH: 44  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-957-887B-193

Query Match 18.1%; Score 37.5; DB 6; Length 44;

Best Local Similarity 44.1%; Pred. No. 27;

Matches 15; Conservative 3; Mismatches 11; Indels 5; Gaps 3;

Qy 1 KDSQRETLKAIHYALN-CCGLAG--GVQFISD 31

Db 1 KDIQEGDTLNAI--ALQYCTVADIKRVNLLISD 32

##### RESULT 2

US-10-729-121-52

; Sequence 52, Application US/10729121

; Publication No. US20040144397A1

; GENERAL INFORMATION:

; APPLICANT: Conkling, Mark

; TITLE OF INVENTION: MODIFYING NICOTINE AND NITROSAMINE

; FILE REFERENCE: VTOB.033C1

; CURRENT APPLICATION NUMBER: US/10/729,121

; CURRENT FILING DATE: 2003-12-04  
; PRIOR APPLICATION NUMBER: 60/297,154  
; PRIOR FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: PCTUS02/18040  
; PRIOR FILING DATE: 2002-06-06  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 52  
; LENGTH: 44  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
US-10-729-121-52

Query Match 18.1%; Score 37.5; DB 6; Length 44;  
Best Local Similarity 36.8%; Pred. No. 27;  
Matches 7; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 13 HVALNCCGLAGGVGEQFISD 31  
| | | | | : | : | : |  
Db 11 HFLLE-CGLNDNLEFYLCD 28

RESULT 3  
US-10-957-887B-243  
; Sequence 243, Application US/10957887B  
; Publication No. US20050272677A1  
; GENERAL INFORMATION:  
; APPLICANT: Friesen, Robert H. E.  
; APPLICANT: Leenhouts, Cornelius J.  
; APPLICANT: Hektor, Harm  
; APPLICANT: van Esch, Johannes H.  
; APPLICANT: Heeres, Andre  
; TITLE OF INVENTION: DELIVERY OF A SUBSTANCE TO A PRE-DETERMINED SITE  
; FILE REFERENCE: 2183-6668US  
; CURRENT APPLICATION NUMBER: US/10/957,887B  
; CURRENT FILING DATE: 2004-10-04  
; PRIOR APPLICATION NUMBER: PCT/NL/00256  
; PRIOR FILING DATE: 2003-04-04  
; NUMBER OF SEQ ID NOS: 309  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 243  
; LENGTH: 45  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-957-887B-243

Query Match 17.6%; Score 36.5; DB 6; Length 45;  
Best Local Similarity 41.2%; Pred. No. 40;  
Matches 14; Conservative 4; Mismatches 11; Indels 5; Gaps 3;

QY 1 KDEPQRETLKAHYALN-CCGLAG--GVEQFISD 31  
| | : | | : | | : | | : | |  
Db 2 KDIQEGDTLNAV--ALQVCCTVADIKRVNLI 33

RESULT 4  
US-11-123-896-372  
; Sequence 372, Application US/11123896  
; Publication No. US20050273881A1  
; GENERAL INFORMATION:  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Navarro Acevedo, Pedro A.  
; APPLICANT: Harvell, Leslie  
; APPLICANT: Cahoon, Rebecca  
; APPLICANT: McCutchen, Billy Fred  
; APPLICANT: Lu, Albert  
; APPLICANT: Herrmann, Rafael  
; APPLICANT: Wong, James  
; TITLE OF INVENTION: Defensin Polynucleotides and Methods of Use  
; FILE REFERENCE: 35718/246703  
; CURRENT APPLICATION NUMBER: US/11/123,896  
; CURRENT FILING DATE: 2005-05-06

; PRIOR APPLICATION NUMBER: 60/300,152  
; PRIOR FILING DATE: 2001-06-22  
; PRIOR APPLICATION NUMBER: 60/300,241  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 469  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 372  
; LENGTH: 47  
; TYPE: PRT  
; ORGANISM: Vernonia mespilifolia  
US-11-123-896-372

Query Match 17.4%; Score 36; DB 7; Length 47;  
Best Local Similarity 35.5%; Pred. No. 50;  
Matches 11; Conservative 1; Mismatches 19; Indels 0; Gaps 0;

QY 3 EPORETLKAHYALNCCGLAGGVGEQFISD 33  
| | | | | : | | | | |  
Db 4 ESQSHGFKGRCMNNNCGLVCRNEGPAAGGIC 34

RESULT 5  
US-10-467-657-3382  
; Sequence 3382, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 3382  
; LENGTH: 30  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-3382

Query Match 17.1%; Score 35.5; DB 6; Length 30;  
Best Local Similarity 39.1%; Pred. No. 36;  
Matches 9; Conservative 1; Mismatches 4; Indels 9; Gaps 1;

QY 12 IHVALNCCGLAGGVGEQFISD 34  
| | | | | : | | | | |  
Db 3 IHVSLN-----NFIQDFIP 16

RESULT 6  
US-11-145-035-45  
; Sequence 45, Application US/11145035  
; Publication No. US20050287122A1  
; GENERAL INFORMATION:  
; APPLICANT: Bartlett et al.  
; TITLE OF INVENTION: AAV VECTORS AND METHODS  
; FILE REFERENCE: 28335/41335  
; CURRENT APPLICATION NUMBER: US/11/145,035  
; CURRENT FILING DATE: 2005-06-03  
; PRIOR APPLICATION NUMBER: US 10/038,972  
; PRIOR FILING DATE: 2002-01-04  
; PRIOR APPLICATION NUMBER: US 60/260,124  
; PRIOR FILING DATE: 2001-01-05  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 45  
; LENGTH: 31  
; TYPE: PRT



```
RESULT 11
US-11-045-024-13448
; Sequence 13448, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13448
; LENGTH: 15
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-13448
Query Match 15.0%; Score 31; DB 7; Length 15;
Best Local Similarity 38.5%; Pred. No. 78;
Matches 5; Conservative 4; Mismatches 4; Indels 4; Gaps 0;

QY 26 EQFISDIPCQDV 38
:|:|:|:|:|
Db 2 DQILIEIGKKAI 14

RESULT 12
US-10-939-890-535
; Sequence 535, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Buesat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
```

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; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 535
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Library Isolate
US-10-939-890-535
Query Match 15.0%; Score 31; DB 6; Length 21;
Best Local Similarity 41.7%; Pred. No. 11e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 15 ALNCCGLAGGVE 26
:|:|:|:|:|
Db 2 SFNACGFEEGLE 13

RESULT 13
US-11-198-847-180
; Sequence 180, Application US/11198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847
; CURRENT FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US 10/058,053
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 180
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Conus parius
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(24)
; OTHER INFORMATION: Xaa at residues 1, 2, 15, 16 and 20 may be Pro or hydroxy-Pro; X
; OTHER INFORMATION: a at residue 24 may be Glu or Gla
US-11-198-847-180
Query Match 15.0%; Score 31; DB 7; Length 24;
```

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; NAME/KEY: MOD RES
; LOCATION: (5)---(5)
; OTHER INFORMATION: Ava
US-11-033-039-631

Query Match      15.0%; Score 31; DB 7; Length 31;
Best Local Similarity 42.9%; Pred. No. 1.8e+02;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 7 ETLKAIHYALNCCG 20
Db 11 ETLSEINGSVTCFG 24

RESULT 16
US-10-957-351-184
; Sequence 184, Application US/10957351
; Publication No. US2006008844A1
; GENERAL INFORMATION:
; APPLICANT: Stemmer, Willem P. C.
; APPLICANT: Perlroth, D. Victor
; APPLICANT: Satyal, Sanjeev
; APPLICANT: Avidia Research Institute
; TITLE OF INVENTION: c-Met Kinase Binding Proteins
; FILE REFERENCE: 022013-001400US
; CURRENT APPLICATION NUMBER: US/10/957,351
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: US 10/871,602
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 471
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 184
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human LDL-receptor class A domain
US-10-957-351-184

Query Match      15.0%; Score 31; DB 6; Length 36;
Best Local Similarity 39.1%; Pred. No. 2.1e+02;
Matches 9; Conservative 3; Mismatches 5; Indels 6; Gaps 2;

Qy 19 CGLAGGV---EQFISDI--CPK 35
Db 7 CGVAPGLCLTPEQLCDGIPDCPQ 29

RESULT 17
US-10-939-890-537
; Sequence 537, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjeppan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
```

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; NAME/KEY: MOD RES
; LOCATION: (5)---(5)
; OTHER INFORMATION: Ava
US-11-033-039-631

Query Match      15.0%; Score 31; DB 7; Length 24;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 17 NCCGLAGG 24
Db 4 SCAGLRGG 11

RESULT 14
US-11-198-847-282
; Sequence 282, Application US/11198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847
; CURRENT FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US 10/058,053
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 282
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Conus parius
; OTHER INFORMATION:
US-11-198-847-282

Query Match      15.0%; Score 31; DB 7; Length 24;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 17 NCCGLAGG 24
Db 4 SCAGLRGG 11

RESULT 15
US-11-033-039-631
; Sequence 631, Application US/11033039
; Publication No. US2006002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 631
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: hybrid peptide
; FEATURE:
```

```
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 537
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Library Isolate
; US-10-939-890-537

Query Match      14.7%   Score 30.5; DB 6; Length 21;
Best Local Similarity 33.3%; Pred. No. 1.4e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 5; Gaps 1;

QY  16  LNCCLAGGVEQFISDIC 33
      :|||  |||  :|
      4  MNC-----GAEGLESIC 16

Db

RESULT 18
US-10-467-657-2116
; Sequence 2116, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 2116
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
; US-10-467-657-2116

Query Match      14.7%   Score 30.5; DB 6; Length 49;
Best Local Similarity 47.1%; Pred. No. 3.5e+02;
Matches 8; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY  3  EPORETIKATH-YALNC 18
      :|||  |||  |||
      26  QARRNFLKSITKTVANN 42

Db

RESULT 19
US-11-045-024-13229
; Sequence 13229, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Greenwood, Scott
; US-11-045-024-13229

Query Match      14.5%   Score 30; DB 7; Length 15;
Best Local Similarity 45.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY  26  EGFISDICPKK 36
      :|||  :|||
      5  DQILIEICGK 15

Db

RESULT 20
US-11-045-024-13251
; Sequence 13251, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
```



; PRIOR APPLICATION NUMBER: US 08/159,184  
; PRIOR FILING DATE: 1993-11-29  
; PRIOR APPLICATION NUMBER: US 08/159,339  
; PRIOR FILING DATE: 1993-11-29  
; PRIOR APPLICATION NUMBER: US 08/205,713  
; PRIOR FILING DATE: 1994-03-04  
; PRIOR APPLICATION NUMBER: US 08/347,610  
; PRIOR FILING DATE: 1994-12-01  
; NUMBER OF SEQ ID NOS: 14528  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13251  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-13251

Query Match 14.5%; Score 30; DB 7; Length 15;  
Best Local Similarity 58.3%; Pred. No. 1.1e+02;  
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 9 LKAIHYALNCG 20  
|:|:|:|:  
Db 4 LQAIHLALQDSG 15

RESULT 21  
US-11-106-415-284  
; Sequence 284, Application US/11106415  
; Publication No. US20050287153A1  
; GENERAL INFORMATION:  
; APPLICANT: MARK S. DENNIS  
; TITLE OF INVENTION: Serum Albumin Binding Peptides for Tumor Targeting  
; FILE REFERENCE: P1774R1P2  
; CURRENT APPLICATION NUMBER: US/11/106,415  
; CURRENT FILING DATE: 2005-04-13  
; PRIOR APPLICATION NUMBER: US 10/186,229  
; PRIOR FILING DATE: 2002-06-28  
; NUMBER OF SEQ ID NOS: 425  
; SEQ ID NO 284  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: sequence is synthesized  
US-11-106-415-284

Query Match 14.5%; Score 30; DB 7; Length 20;  
Best Local Similarity 62.5%; Pred. No. 1.1e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 26 EQFLSDIC 33  
|:|:|:|:  
Db 1 EGFLGDIC 8

RESULT 22  
US-11-198-847-323  
; Sequence 323, Application US/11198847  
; Publication No. US20050271589A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Cognetix, Inc.  
; APPLICANT: Jones, Robert M.  
; APPLICANT: Garrett, James E.  
; APPLICANT: Watkins, Maren  
; APPLICANT: Olivera, Baldomero M.  
; TITLE OF INVENTION: B-Superfamily Conotoxins  
; FILE REFERENCE: 2314-296  
; CURRENT APPLICATION NUMBER: US/11/198,847  
; CURRENT FILING DATE: 2005-08-08  
; PRIOR APPLICATION NUMBER: US 10/838,226  
; PRIOR FILING DATE: 2004-05-05  
; PRIOR APPLICATION NUMBER: US 10/058,053

; PRIOR FILING DATE: 2000-01-29  
; PRIOR APPLICATION NUMBER: US 60/264323  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 340  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 323  
; LENGTH: 21  
; TYPE: PRT  
; ORGANISM: Conus purpurascens  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (1)..(21)  
; OTHER INFORMATION: Xaa may be Trp (D or L)  
US-11-198-847-323

Query Match 14.5%; Score 30; DB 7; Length 21;  
Best Local Similarity 38.5%; Pred. No. 1.6e+02;  
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 22 AGGVEQFISDIP 34  
|:|:|:|:  
Db 2 SNGVEICMKKVC 14

RESULT 23  
US-11-198-847-177  
; Sequence 177, Application US/11198847  
; Publication No. US20050271589A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Cognetix, Inc.  
; APPLICANT: Jones, Robert M.  
; APPLICANT: Garrett, James E.  
; APPLICANT: Watkins, Maren  
; APPLICANT: Olivera, Baldomero M.  
; TITLE OF INVENTION: B-Superfamily Conotoxins  
; FILE REFERENCE: 2314-296  
; CURRENT APPLICATION NUMBER: US/11/198,847  
; CURRENT FILING DATE: 2005-08-08  
; PRIOR APPLICATION NUMBER: US 10/838,226  
; PRIOR FILING DATE: 2004-05-05  
; PRIOR APPLICATION NUMBER: US 10/058,053  
; PRIOR FILING DATE: 2000-01-29  
; PRIOR APPLICATION NUMBER: US 60/264323  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 340  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 177  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: Conus parius  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (1)..(25)  
; OTHER INFORMATION: Xaa at residues 1, 3, 15, 16 and 20 may be Pro or hydroxy-Pro  
US-11-198-847-177

Query Match 14.5%; Score 30; DB 7; Length 25;  
Best Local Similarity 62.5%; Pred. No. 2e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 17 NCCGLAGG 24  
|:|:|:|:  
Db 4 SCSGLRGG 11

RESULT 24  
US-11-198-847-281  
; Sequence 281, Application US/11198847  
; Publication No. US20050271589A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Cognetix, Inc.

```
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847
; CURRENT FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US 10/058,053
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 281
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Conus parius
; US-11-198-847-281

Query Match      14.5%; Score 30; DB 7; Length 25;
Best Local Similarity 62.5%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 17 NCCGLAGG 24
Db 4 SCGSLRGG 11

RESULT 25
US-10-467-657-5682
; Sequence 5682, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5682
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
; US-10-467-657-5682

Query Match      14.5%; Score 30; DB 6; Length 35;
Best Local Similarity 33.3%; Pred. No. 2.9e+02;
Matches 6; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 5 QRETLKAHVALNCCGLA 22
Db 5 RREVKALSDMVSCKIA 22

RESULT 26
US-10-467-657-7098
; Sequence 7098, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega

; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7098
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
; US-10-467-657-7098

Query Match      14.5%; Score 30; DB 6; Length 35;
Best Local Similarity 42.9%; Pred. No. 2.9e+02;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 18 CCGLAGGVQFISD 31
Db 14 CRSLDGDFDAGVSD 27

RESULT 27
US-10-467-657-8030
; Sequence 8030, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8030
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
; US-10-467-657-8030

Query Match      14.5%; Score 30; DB 6; Length 35;
Best Local Similarity 42.9%; Pred. No. 2.9e+02;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 18 CCGLAGGVQFISD 31
Db 14 CRSLDGDFDAGVSD 27

RESULT 28
US-10-957-351-20
; Sequence 20, Application US/10957351
; Publication No. US2006000844A1
; GENERAL INFORMATION:
; APPLICANT: Stemmer, Willem P. C.
; APPLICANT: Perlroth, D. Victor
; APPLICANT: Satyal, Sanjeev
; APPLICANT: Avidia Research Institute
; TITLE OF INVENTION: c-Met Kinase Binding Proteins
; FILE REFERENCE: 022013-001400US
; CURRENT APPLICATION NUMBER: US/10/957,351
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: US 10/871,602
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 471
```

```
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human LDL-receptor class A domain
US-10-957-351-20

Query Match      14.5%; Score 30; DB 6; Length 35;
Best Local Similarity 46.2%; Pred. No. 2.9e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy      8 TLKAIHYALNCCG 20
Db      10 TGKCLNYSLVCDG 22

RESULT 29
US-10-979-871-10
; Sequence 10, Application US/10979871
; Publication No. US20050267071A1
; GENERAL INFORMATION:
; APPLICANT: Freire, Ernesto
; APPLICANT: Bacha, Usman
; APPLICANT: Barrila, Jennifer
; APPLICANT: Leavitt, Stephanie A.
; APPLICANT: Vellazquez-Campoy, Adrian
; APPLICANT: Xiao, Yingxin
; APPLICANT: Ottenbrite, Raphael
; TITLE OF INVENTION: INHIBITORS OF CORONAVIRUS PROTEASE AND METHODS OF USE THEREOF
; FILE REFERENCE: 03173/1200093-US1
; CURRENT APPLICATION NUMBER: US/10/979,871
; CURRENT FILING DATE: 2004-11-01
; PRIOR APPLICATION NUMBER: 60/516,008
; PRIOR FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 40
; TYPE: PRT
; ORGANISM: BCV Quebec
US-10-979-871-10

Query Match      14.5%; Score 30; DB 6; Length 40;
Best Local Similarity 41.2%; Pred. No. 3.3e+02;
Matches 7; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy      19 CGLAGGVEQFISDICPK 35
Db      23 CGSCGSGVYVIMGDCVK 39

RESULT 30
US-10-979-871-12
; Sequence 12, Application US/10979871
; Publication No. US20050267071A1
; GENERAL INFORMATION:
; APPLICANT: Freire, Ernesto
; APPLICANT: Bacha, Usman
; APPLICANT: Barrila, Jennifer
; APPLICANT: Leavitt, Stephanie A.
; APPLICANT: Vellazquez-Campoy, Adrian
; APPLICANT: Xiao, Yingxin
; APPLICANT: Ottenbrite, Raphael
; TITLE OF INVENTION: INHIBITORS OF CORONAVIRUS PROTEASE AND METHODS OF USE THEREOF
; FILE REFERENCE: 03173/1200093-US1
; CURRENT APPLICATION NUMBER: US/10/979,871
; CURRENT FILING DATE: 2004-11-01
; PRIOR APPLICATION NUMBER: 60/516,008
; PRIOR FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.2
```

```
; SEQ ID NO 12
; LENGTH: 40
; TYPE: PRT
; ORGANISM: BCV Mebus
US-10-979-871-12

Query Match      14.5%; Score 30; DB 6; Length 40;
Best Local Similarity 41.2%; Pred. No. 3.3e+02;
Matches 7; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy      19 CGLAGGVEQFISDICPK 35
Db      23 CGSCGSGVYVIMGDCVK 39

RESULT 31
US-11-123-896-390
; Sequence 390, Application US/11123896
; Publication No. US20050273881A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Harvell, Leslie
; APPLICANT: Cahoon, Rebecca
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Lu, Albert
; APPLICANT: Herrmann, Rafael
; APPLICANT: Wong, James
; TITLE OF INVENTION: Defensin Polynucleotides and Methods of
; FILE REFERENCE: 35718/246703
; CURRENT APPLICATION NUMBER: US/11/123,896
; CURRENT FILING DATE: 2005-05-06
; PRIOR APPLICATION NUMBER: 60/300,152
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/300,241
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 390
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Licania michauxii
US-11-123-896-390

Query Match      14.5%; Score 30; DB 7; Length 47;
Best Local Similarity 29.0%; Pred. No. 4e+02;
Matches 9; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

Qy      3 EPORETAKAIHYALNCCGLAGGVEQFISDIC 33
Db      4 ESQSHGFKGMCVRDHNCAWVCRVEGFGGIC 34

RESULT 32
US-11-123-896-393
; Sequence 393, Application US/11123896
; Publication No. US20050273881A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Harvell, Leslie
; APPLICANT: Cahoon, Rebecca
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Lu, Albert
; APPLICANT: Herrmann, Rafael
; APPLICANT: Wong, James
; TITLE OF INVENTION: Defensin Polynucleotides and Methods of
; FILE REFERENCE: 35718/246703
; CURRENT APPLICATION NUMBER: US/11/123,896
; CURRENT FILING DATE: 2005-05-06
; PRIOR APPLICATION NUMBER: 60/300,152
```

```
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/300,241
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 393
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Chrysobalanus icaco
US-11-123-896-393

Query Match      14.5%; Score 30; DB 7; Length 47;
Best Local Similarity 29.0%; Pred. No. 4e+02;
Matches 9; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

QY 3 EPQRETLKATHYALNCCGLAGGVEQFISDIC 33
    | | | | | | | | | | | | | | | |
Db 4 ESQSHGFKGCMRDHNCAMVCRVEGFGGIC 34

RESULT 33
US-11-043-590-43
; Sequence 43, Application US/11043590
; Publication No. US20050277156A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: Novel Brain Natriuretic Peptide Variants and Methods of use there
; FILE REFERENCE: 1847.1011
; CURRENT APPLICATION NUMBER: US/11/043,590
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 43
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-043-590-43

Query Match      14.3%; Score 29.5; DB 7; Length 31;
Best Local Similarity 30.0%; Pred. No. 3e+02;
Matches 6; Conservative 6; Mismatches 5; Indels 3; Gaps 1;

QY 20 GLAGGVE---QFISDICPKK 36
    | | | | | : | | | |
Db 5 GSSGGLDSSNERNVLTCCPKR 24

RESULT 34
US-10-467-657-6618
; Sequence 6618, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6618
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6618

Query Match      14.3%; Score 29.5; DB 6; Length 36;

; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/300,241
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 393
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Chrysobalanus icaco
US-11-123-896-393

Query Match      14.5%; Score 30; DB 7; Length 47;
Best Local Similarity 29.0%; Pred. No. 4e+02;
Matches 9; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

QY 3 EPQRETLKATHYALNCCGLAGGVEQFISDIC 33
    | | | | | | | | | | | | | | | |
Db 4 ESQSHGFKGCMRDHNCAMVCRVEGFGGIC 34

RESULT 33
US-11-043-590-43
; Sequence 43, Application US/11043590
; Publication No. US20050277156A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: Novel Brain Natriuretic Peptide Variants and Methods of use there
; FILE REFERENCE: 1847.1011
; CURRENT APPLICATION NUMBER: US/11/043,590
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 43
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-043-590-43

Query Match      14.3%; Score 29.5; DB 7; Length 31;
Best Local Similarity 30.0%; Pred. No. 3e+02;
Matches 6; Conservative 6; Mismatches 5; Indels 3; Gaps 1;

QY 20 GLAGGVE---QFISDICPKK 36
    | | | | | : | | | |
Db 5 GSSGGLDSSNERNVLTCCPKR 24

RESULT 34
US-10-467-657-6618
; Sequence 6618, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6618
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6618

Query Match      14.3%; Score 29.5; DB 6; Length 36;

Best Local Similarity 40.0%; Pred. No. 3.5e+02;
Matches 8; Conservative 1; Mismatches 4; Indels 7; Gaps 1;

QY 24 GVEQFISD-----ICPKK 36
    | | | | | | | | | | | | | | | |
Db 9 GCKDFIEDVGHVVFRICPKK 28

RESULT 35
US-10-859-643-628
; Sequence 628, Application US/10859643
; Publication No. US20060002993A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 511582006203
; CURRENT APPLICATION NUMBER: US/10/859,643
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 628
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-859-643-628

Query Match      14.0%; Score 29; DB 6; Length 10;
Best Local Similarity 62.5%; Pred. No. 99;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 KAIHYALN 17
    | | | | |
Db 3 KRLHYAKN 10

RESULT 36
US-11-097-864-628
; Sequence 628, Application US/11097864
; Publication No. US20050265924A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
; FILE REFERENCE: 511582006205
; CURRENT APPLICATION NUMBER: US/11/097,864
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 628
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-864-628

Query Match      14.0%; Score 29; DB 7; Length 10;
```

```
Best Local Similarity 62.5%; Pred. No. 99;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 10 KAIHYALN 17
Db 3 KRLHYAKN 10

RESULT 37
US-11-097-912-628
; Sequence 628, Application US/11097912
; Publication No. US20050265921A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B
; TITLE REFERENCE: 51158206204
; CURRENT APPLICATION NUMBER: US/11/097,912
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 628
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-912-628

Query Match 14.0%; Score 29; DB 7; Length 10;
Best Local Similarity 62.5%; Pred. No. 99;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 10 KAIHYALN 17
Db 3 KRLHYAKN 10

RESULT 38
US-11-045-024-2377
; Sequence 2377, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4816
; LENGTH: 11
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-4816

Query Match 14.0%; Score 29; DB 7; Length 11;
Best Local Similarity 63.6%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2377
; LENGTH: 11
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-2377

Query Match 14.0%; Score 29; DB 7; Length 11;
Best Local Similarity 63.6%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 11 AIHYALNCCGL 21
Db 1 AIHLAQDSGL 11

RESULT 39
US-11-045-024-4816
; Sequence 4816, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4816
; LENGTH: 11
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-4816

Query Match 14.0%; Score 29; DB 7; Length 11;
Best Local Similarity 63.6%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

QY 11 AIHYALNCCGL 21  
|||  
Db 1 AIHLALQDSGL 11

## RESULT 40

US-10-939-890-86  
; Sequence 86, Application US/10939890  
; Publication No. US20050250700A1  
; GENERAL INFORMATION:  
; APPLICANT: Sato, Aaron K.  
; APPLICANT: Sexton, Daniel J.  
; APPLICANT: Dransfield, Daniel T.  
; APPLICANT: Ledner, Robert C.  
; APPLICANT: Arbogast, Christophe  
; APPLICANT: Bussat, Philippe  
; APPLICANT: Fan, Hong  
; APPLICANT: Khurana, Sudha  
; APPLICANT: Linder, Karen E.  
; APPLICANT: Marinelli, Edmund R.  
; APPLICANT: Nanjappan, Palaniappa  
; APPLICANT: Nunn, Adrian D.  
; APPLICANT: Pillai, Radhakrishna  
; APPLICANT: Pochon, Sibylle  
; APPLICANT: Ramalingam, Kondareddiar  
; APPLICANT: Shrivastava, Ajay  
; APPLICANT: Song, Bo  
; APPLICANT: Swenson, Rolf E.  
; APPLICANT: Von Wronski, Mathew A.  
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES  
; FILE REFERENCE: D0617, 70014US00  
; CURRENT APPLICATION NUMBER: US/10/939,890  
; CURRENT FILING DATE: 2004-09-13  
; PRIOR APPLICATION NUMBER: US 10/661,156  
; PRIOR FILING DATE: 2003-09-11  
; PRIOR APPLICATION NUMBER: US 10/382,082  
; PRIOR FILING DATE: 2003-03-03  
; PRIOR APPLICATION NUMBER: PCT/US03/06731  
; PRIOR FILING DATE: 2003-03-03  
; PRIOR APPLICATION NUMBER: US 60/440,411  
; PRIOR FILING DATE: 2003-01-15  
; PRIOR APPLICATION NUMBER: US 60/360,851  
; PRIOR FILING DATE: 2002-03-01  
; NUMBER OF SEQ ID NOS: 883  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 86  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Library Isolate  
US-10-939-890-86

Query Match 14.0%; Score 29; DB 6; Length 14;  
Best Local Similarity 57.1%; Pred.No. 1.4e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 12 IHYALNC 18  
:|  
Db 5 MHYGLGC 11

Search completed: January 20, 2006, 17:38:43  
Job time : 7.5679 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run On: January 20, 2006, 17:23:49 ; Search time 14.0741 Seconds  
(without alignments)  
259.785 Million cell updates/sec

Title: US-10-619-323-4

Perfect score: 207

Sequence: 1 KDEPQRETLKAIHYALNCCLAGGVEQFISDICPKDV 38

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 11837

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 50 summaries

Database : PIR\_80.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	19.3	33	2 I46600	myosin - pig (frag
2	39.5	19.1	48	2 AD2809	hypothetical prote
3	39	18.8	38	2 S33484	hypothetical prote
4	38	18.4	12	2 PH1481	T-cell receptor be
5	38	18.4	47	1 A24074	pyruvate thionin
6	38	18.4	50	2 A82772	hypothetical prote
7	37.5	18.1	48	2 S29216	neurotoxin Tx2 - a
8	36.5	17.6	33	2 I22565	R-phycocerythrin ga
9	36	17.4	33	1 S66586	hypothetical prote
10	35.5	17.1	33	2 A05136	neurotoxin IX - sc
11	35.5	17.1	48	2 T16032	hypothetical prote
12	35	16.9	20	2 I46940	6-phosphofructo-2-
13	34	16.4	34	2 JQ1620	hypothetical 4.3K
14	33.5	16.2	33	2 C82390	hypothetical prote
15	33.5	16.2	44	2 B85569	hypothetical prote
16	33	15.9	16	4 I79565	hypothetical TGL3/
17	33	15.9	40	2 T16014	hypothetical prote
18	33	15.9	41	2 T18202	hypothetical prote
19	33	15.9	46	2 B81717	hypothetical prote
20	32.5	15.7	37	2 A59487	parabutoxin 2 - Pa
21	32.5	15.7	48	2 JV0019	hypothetical prote
22	32	15.5	41	2 B49910	probable tyrosine
23	32	15.5	42	2 T01991	hypothetical prote
24	32	15.5	42	2 T07324	hypothetical prote
25	32	15.5	48	2 I50819	MHC class I protei
26	32	15.5	48	2 AC1046	entericidin B prec
27	32	15.5	48	2 H86110	hypothetical prote
28	31.5	15.2	36	2 A59486	parabutoxin 10 - p
29	31.5	15.2	46	2 H71262	hypothetical prote

30	31.5	15.2	47	2 C26534	hypothetical prote
31	31.5	15.2	49	2 T37008	hypothetical prote
32	31.5	15.2	50	2 B60718	phospholipase A2 h
33	31	15.0	34	2 S77646	hypothetical prote
34	31	15.0	35	2 JX0200	gummarin - Gymnema
35	31	15.0	36	2 PH1751	Ig heavy chain V r
36	31	15.0	36	2 S04184	fixC protein - Bra
37	31	15.0	37	2 A49591	spike protein - po
38	31	15.0	37	2 PS0131	H-2 class I histoc
39	31	15.0	39	2 C37264	E2 glycoprotein -
40	31	15.0	45	2 S77773	probable thymidine
41	31	15.0	46	2 B45174	eye cell developme
42	31	15.0	48	2 D82817	hypothetical prote
43	31	15.0	50	2 T08019	hypothetical prote
44	30.5	14.7	30	2 B81346	hypothetical prote
45	30.5	14.7	37	2 C60580	growth hormone-rel
46	30.5	14.7	44	2 T21578	hypothetical prote
47	30.5	14.7	47	2 B58319	gamma-zeathionin 2
48	30	14.5	30	2 G71359	hypothetical prote
49	30	14.5	33	2 I46601	myosin - pig (frag
50	30	14.5	36	2 S70092	hypothetical prote

#### ALIGNMENTS

##### RESULT 1

I46600

myosin - pig (fragment)

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 09-Jul-2004

C;Accession: I46600

R;Bement, W.M.; Haseoon, T.; Wirth, J.A.; Cheney, R.E.; Mooseker, M.S.

Proc. Natl. Acad. Sci. U.S.A. 91, 6549-6553, 1994

A;Title: Identification and overlapping expression of multiple unconventional myosin ge

A;Reference number: A55758; MUID:94294418; PMID:8022818

A;Accession: I46600

A;Status: preliminary; translated from GB/EMBL/DBD

A;Molecule type: mRNA

A;Residues: 1-33 <BEM>

A;Cross-references: UNIPROT:Q29066; UNIPARC:UPI0000087769; GB:L29135; NID:9457345; PIDN

C;Superfamily: myosin heavy chain 95F; myosin motor domain homology

Query Match 19.3% Score 40; DB 2; Length 33;

Best Local Similarity 55.0%; Pred.No. 1.1e+02;

Matches 11; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

Qy 12 IHY--ALNCCGLAGGVEQFI 29

Db 7 IHULTALSQKPGASGVEQII 26

##### RESULT 2

AD2809

hypothetical protein Atul1894 [imported] - Agrobacterium tumefaciens (strain C58, Dupont

C;Species: Agrobacterium tumefaciens

C;Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004

C;Accession: AD2809

R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo,

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuttyavin, T.; Levy, R.; Li, M.; McGlel

; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Kraspan, W.; Perry, M.; Gordon-Kamm,

ster, E.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Reference number: AB2577; MUID:21608550; PMID:11743193

A;Accession: AD2809

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-48 <KUR>

A;Cross-references: UNIPROT:Q8UE67; UNIPARC:UPI00000D1CF5; GB:AE008688; PIDN:AAL42890.1

A;Experimental source: strain C58 (Dupont)

C;Genetics:

A;Gene: Atul894

A;Map position: circular chromosome

Query Match 19.1%; Score 39.5; DB 2; Length 48;

Best Local Similarity 45.0%; Pred. No. 1.9e+02;

Matches 9; Conservative 2; Mismatches 6; Indels 3; Gaps 1;

Qy 18 CCGLAGGVEQFIS---DIPC 34

Db 12 CCGSCGGVQFPTGGIGICP 31

RESULT 3

S33484

hypothetical protein 38 - Xanthomonas campestris phage phi-Lf

C;Species: Xanthomonas campestris phage phi-Lf

C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004

C;Accession: S33484

R;Wen, F.S.; Tseng, Y.H.

submitted to the EMBL Data Library, February 1993

A;Description: Single e-stranded DNA binding protein and major coat protein of filamentous

A;Reference number: S33482

A;Accession: S33484

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-38 <WEN>

A;Cross-references: UNIPROT:Q07484; UNIPARC:UPI0000127C91; EMBL:X70331; NID:g3111543; PID

Query Match 18.8%; Score 39; DB 2; Length 38;

Best Local Similarity 28.9%; Pred. No. 1.8e+02;

Matches 11; Conservative 5; Mismatches 10; Indels 12; Gaps 2;

Qy 4 PORETLKAIHYALNCCG-----LAGGVEQFISD 31

Db 2 PSQE--DAVWSTGCCGLVIVFWVLGRLAGSVAGMFND 37

RESULT 4

PH1481

T-cell receptor beta chain (clone A24/PEG2) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 15-Mar-2004

C;Accession: PH1481

R;Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; K

J. Exp. Med. 177, 811-820, 1993

A;Title: T cell receptor selection by and recognition of two class I major histocompatib

A;Reference number: PH1430; MUID:93171821; PMID:8436911

A;Accession: PH1481

A;Molecule type: mRNA

A;Residues: 1-12 <CAS>

A;Cross-references: UNIPARC:UPI000017C79D

A;Experimental source: cytolytic T-lymphocyte

A;Note: the authors translated the codon GGT for residue 2 as Ala and GCT for residue 3

C;Keywords: receptor; T-cell

Query Match 18.4%; Score 38; DB 2; Length 12;

Best Local Similarity 70.0%; Pred. No. 81;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 19 CGLAGGVEQF 28

Db 1 CGAEGAEQF 10

RESULT 5

A24074

pyricularia thionin - oil nut

C;Species: Pyricularia pubera (oil nut, buffalo nut)

C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 31-Dec-2004

C;Accession: A24074

R;Vernon, L.P.; Evtett, G.E.; Zeikus, R.D.; Gray, W.R.

Arch. Biochem. Biophys. 238, 18-29, 1985

A;Title: A toxic thionin from Pyricularia pubera: purification, properties, and amino acid

A;Reference number: A24074; MUID:85173323; PMID:3985614

A;Accession: A24074

A;Molecule type: protein

A;Residues: 1-47 <VER>

A;Cross-references: UNIPROT:P07504; UNIPARC:UPI0000136EC3

C;Superfamily: hordothionin precursor

Query Match 18.4%; Score 38; DB 1; Length 47;

Best Local Similarity 38.5%; Pred. No. 2.9e+02;

Matches 10; Conservative 4; Mismatches 6; Indels 6; Gaps 2;

Qy 14 YALNC---CGLAGGVEQFISDIPC 36

Db 8 WARNCYNVCRLPGTISR---EICAKK 30

RESULT 6

A82772

hypothetical protein XF0722 [imported] - Xylella fastidiosa (strain 9a5c)

C;Species: Xylella fastidiosa

C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004

C;Accession: A82772

R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequ

Nature 406, 151-157, 2000

A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A;Reference number: A82515; MUID:20365717; PMID:10910347

A;Note: for a complete list of authors see reference number A59328 below

A;Accession: A82772

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-50 <SIM>

A;Cross-references: UNIPROT:Q9PF88; UNIPARC:UPI00000C24E3; GB:AE003849; N

R;Simpson, A.J.G.; Reinach, P.C.; Arruda, P.; Abreu, P.A.; Acencio, M.; Alvarenga, R.;

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carreir,

as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froh

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuranae, E.E.; Laig

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins,

A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasa

M.; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silve

M.; Tshuko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;

A;Reference number: A59328

A;Contents: annotation

C;Genetics:

A;Gene: XF0722

Query Match 18.4%; Score 38; DB 2; Length 50;

Best Local Similarity 29.6%; Pred. No. 3.1e+02;

Matches 8; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

Qy 7 ETIKAIHYALNCCGLAGGVEQFISD 33

Db 22 OOLGGTHRAVSCGFSLAFLLSVTDIC 48

RESULT 7

S29216

neurotoxin Tx2 - spider (Phoneutria nigriventer)

C;Species: Phoneutria nigriventer

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004

C;Accession: S29216

R;do Nascimento Cordeiro, M.; Ribeiro Diniz, C.; do Carmo Valentim, A.; von Eickstedt,

FESS Lett. 310, 153-156, 1992

A;Title: The purification and amino acid sequences of four Tx2 neurotoxins from the ven

A;Reference number: S29214; MUID:93011905; PMID:1397265

A;Accession: S29216

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-48 <COR>



A;Cross-references: UNIPROT:P29425; UNIPARC:UPI00001766CE  
C;Superfamily: curtatoxin

Query Match	18.1%	Score	37.5;	DB 2;	Length	48;			
Best Local Similarity	34.8%	Pred. No.	3.5e+02;						
Matches	8;	Conservative	4;	Mismatches	4;	Indels	7;	Gaps	1;

QY 1 KDEPQRETAKAIHYALNCCGLAG 23  
:|:|:|:|:|:|  
Db 6 QDQPCKE-T-----CDCCGERG 21

## RESULT 8

I22565  
R-phycoerythrin gamma-D chain - red alga (Gastrocloonium coulteri) (fragment)  
C;Species: Gastrocloonium coulteri  
C;Date: 07-Mar-1988 #sequence\_revision 07-Mar-1988 #text\_change 09-Jul-2004  
C;Accession: I22565  
J;Klotz, A.V.; Glazer, A.N.  
J. Biol. Chem. 260, 4856-4863, 1985  
A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.  
A;Reference number: A22565; MUID:85182601; PMID:3886644  
A;Accession: I22565  
A;Molecule type: protein  
A;Residues: 1-33 <KLO>

A; Cross-references: UNIPROT:Q7M269; UNIPARC:UPI00001792E6  
C; Superfamily: Aglaothamnion neglectum R-phycoerythrin ga

Query Match 17.6%; Score 36.5; DB 2; Length 33;  
Best Local Similarity 38.5%; Pred. No. 3.4e+02;  
Matches 10; Conservative 3; Mismatches 12; Indels 1; Gaps 1;

**Qy**      2 DEPQRETLKAIHYALNCCGLAGVEQ 27  
          | | : | | | : | | |  
**Dd**      9 DFPVAPSL-AGHYSLTNCGPSPGASK 33

## RESULT 9

S66586  
hypothetical protein 33 - Escherichia coli cryptic lambdoid prophage DLP12  
C:Species: Escherichia coli  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: S66586  
R:Mahdi, A.A.; Sharples, G.J.; Mandal, T.N.; Lloyd, R.G.  
J. Mol. Biol. 257, 561-573, 1996  
A:Title: Holliday junction resolvases encoded by homologous *rusA* genes in *Escherichia coli*  
A:Reference number: S66579; MUID:96196428; PMID:8648624  
A:Accession: S66586  
A:Molecule type: DNA  
A:Residues: 1-33 <MAH>  
A:Cross-references: UNIPROT:Q47268; UNIPARC:UPI000013B802; EMBL:X92587; NID:gl051136; PT  
C:Genetics:  
A:Map position: 12 min  
A:Genome: prophage  
C:Superfamily: phage 82 hypothetical protein 33

```
Query Match      17.4%; Score 36; DB 1; Length 33;
Best Local Similarity 37.5%; Pred. No. 3.9e+02;
Matches 6; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
```

```
QY      5 QRETLKAHYALNCCG 20
      | : | : | : | : |
Db     15 QKCTCNSLHLAFDLCG 30
```

## RESULT 10

A05136  
neurotoxin IX - scorpion (Buthus occitanus) (fragment)  
C-Species: Buthus occitanus tunetanus  
C-Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 09-Jul-2004  
C-Accession: A05136  
R:Martin, M.F.; Rochat, H.  
Toxicon 22, 279-291, 1984

A;Title: Purification of thirteen toxins active on mice  
A;Reference number: A94316; MUID:84224814; PMID:6729843  
A;Accession: A05136  
A;Molecule type: protein  
A;Residues: 1-33 <VAR>  
A;Cross-references: UNIPROT:P04099; UNIPARC:UPI000001356  
C;Superfamily: scorpion neurotoxin  
C;Keywords: neurotoxin

Query Match 17.1%; Score 35.5; DB 2;  
Best Local Similarity 36.0%; Pred. No. 4.6e+02;  
Matches 9; Conservative 4; Mismatches 5; Indels

Qy		12 IHVALNC---CGLAGGVEQFISDIC 33
Db	: : :	10 IVYPNNCVYHCGL----DPYCNDLC 30

**RESULT 11**

T16032  
 Hypothetical protein F11D5.6 - *Caenorhabditis elegans*  
 C:Species: *Caenorhabditis elegans*  
 C:date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
 C:Accession: T16032  
 R:Nhan, M.  
 submitted to the EMBL Data Library, November 1995  
 A:Description: The sequence of C. elegans cosmid F11D5.  
 A:Reference number: Z18449

A;Reference number: Z18495  
A;Accession: T16032  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-48 <NHA>  
A;Cross-references: UNIPROT:Q9GYP8, UNIPARC:UPI000007E1  
C;Genetics:  
A;Gene: CESP:F1D5.6  
A;Introns: 30/1

Query Match 17.1%; Score 35.5; DB 2; Length 48;  
Best Local Similarity 47.1%; Pred. No. 6.6e+02;  
Matches 8; Conservative 2; Mismatches 6; Indels

Qy	3	EPQRET	KA	IHYA	LNCC	19
			:	:	:	:
Db	7	ENQKET	-AYI	HFIY	YCC	22

## RESULT 12

6-phosphofructo-2-kinase (EC 2.7.1.105) / fructose-2,6-bisphosphate 2-phosphatase (EC 3.1.3.16)  
 C:Species: *Bos primigenius taurus* (cattle)  
 C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 09-Jul-2004  
 C:Accession: I46940  
 R:Sakata, J.; Uyeda, K.  
 Biochem. Biophys. Res. Commun. 180, 470-474, 1991  
 A:Title: Characterization of two isozymic forms of heart fructose 6-phosphate, 2-kinase  
 A:Reference number: I46940; MUID:92062062; PMID:1659398  
 A:Accession: I46940  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-20 <S>  
 A:Cross-references: UNIPROT:Q28830; UNIPARC:UPI00000876C7; GB:S62278; NID:G237973; PIDN  
 C:Superfamily: 6-phosphofructo-2-kinase / fructose-2,6-bisphosphate 2-phosphatase; phosphotransferase  
 C:Keywords: phosphoric monoester hydrolase; phosphotransferase

Query Match 16.9%; Score 35; DB 2; Length 20;  
... Best Local Similarity 46.2%; Pred. No. 3.4e+02;  
Matches 6; Conservative 3; Mismatches 4; Indels

Qy	1	KDEPQRETLKAIH	13
		: :      :	
Db	6	RDKPTAETSRAAH	18



RESULT 18

TI8202

hypothetical protein - Bacillus sp. (fragment)

C/Species: Bacillus sp.

C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C/Accession: TI8202

R/van Waasbergen, L.G.; Hildebrand, M.; Tebo, B.M.

J. Bacteriol. 178, 3517-3530, 1996

A/Title: Identification and characterization of a gene cluster involved in manganese oxidation

A/Reference number: Z18825; MUID:96256605; PMID:8655549

A/Accession: TI8202

A/Status: preliminary; translated from GB/EMBL/DBDB

A/Molecule type: DNA

A/Residues: 1-41 <V>

A/Cross-references: UNIPROT:P70956; UNIPARC:UPI00000B345A; EMBL:U31081; NID:g942616; NID:18825

Query Match 15.9%; Score 33; DB 2; Length 41;

Best Local Similarity 35.7%; Pred. No. 1.2e+03;

Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 4 PORETLKAHYALN 17

| | | | |

Db 9 PHRTISGIYWTYN 22

RESULT 19

B81717

hypothetical protein TC0307 [imported] - Chlamydia muridarum (strain Nigg)

C/Species: Chlamydia muridarum, Chlamydia trachomatis MoPn

C/Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004

C/Accession: B81717

R/Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, S.L.; et al. Nucleic Acids Res. 28, 1397-1406, 2000

A/Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.

A/Reference number: A81500; MUID:20150255; PMID:10684935

A/Accession: B81717

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-46 <T>

A/Cross-references: UNIPROT:Q9P0L1; UNIPARC:UPI0000057893; GB:AE002298; GB:AE002160; NID:18825

A/Experimental source: strain Nigg (MoPn)

C/Genetics:

A/Gene: TC0307

Query Match 15.9%; Score 33; DB 2; Length 46;

Best Local Similarity 75.0%; Pred. No. 1.4e+03;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 15 ALNCCGLA 22

| | | | |

Db 37 ALNCSGVA 44

RESULT 20

A59487

parabutoxin 2 - Parabuthus villosus

C/Species: Parabuthus villosus

C/Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 02-Jun-2003

C/Accession: A59487

R/Tytgat, J.

submitted to the Protein Sequence Database, April 2003

A/Description: Acidic short chain K+ channel toxins from Parabuthus venom.

A/Reference number: A59487

A/Accession: A59487

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-37 <Y>

A/Note: potassium channel toxin

F/8-27/Disulfide bonds: #Status predicted

F/13-33/Disulfide bonds: #Status predicted

F/17-35/Disulfide bonds: #Status predicted







Matches 7; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 4 PORETKAIHYALNCCGLAGG 24  
| | | | | | | | | |  
Db 7 PNRITVRALLGAMITLGFMSG 27

## RESULT 39

C37264  
E2 glycoprotein - Barmah Forest virus (fragment)  
C;Species: Barmah Forest virus  
C;Date: 30-Aug-1991 #sequence\_revision 30-Jan-1993 #text\_change 31-Dec-2004  
C;Accession: C37264  
R;Bell, J.R.; Kinney, R.M.; Trent, D.W.; Strauss, E.G.; Strauss, J.H.  
Proc. Natl. Acad. Sci. U.S.A. 81, 4702-4706, 1984  
A;Title: An evolutionary tree relating eight alphaviruses, based on amino-terminal sequences  
A;Reference number: A21774; MUID:84272701; PMID:6087344  
A;Accession: C37264  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-39 <BEL>  
A;Cross-references: UNIPROT:P89946; UNIPARC:UPI000017855E  
C;Keywords: glycoprotein

Query Match 15.0%; Score 31; DB 2; Length 39;  
Best Local Similarity 43.8%; Pred. No. 2.2e+03;  
Matches 7; Conservative 0; Mismatches 1; Indels 8; Gaps 1;

Qy 19 CGLAGGVEQFIISDIP 34  
| | | | | | | | | |  
Db 21 CGLAGS-----CP 28

## RESULT 40

S77773  
Probable thymidine kinase - Mycoplasma capricolum (fragment)  
N;Alternate names: protein MC375  
C;Species: Mycoplasma capricolum  
C;Date: 09-Oct-1997 #sequence\_revision 24-Oct-1997 #text\_change 09-Jul-2004  
C;Accession: S77773; S48624  
R;Bork, P.; Ouzounis, C.; Casari, G.; Schneider, R.; Sander, C.; Dolan, M.; Gilbert, W.;  
Mol. Microbiol. 16, 955-967, 1995  
A;Title: Exploring the Mycoplasma capricolum genome: a minimal cell reveals its physiology  
A;Reference number: S77739; MUID:96059641; PMID:7476192  
A;Accession: S77773  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-45 <BOR>  
A;Cross-references: UNIPROT:Q49069; UNIPARC:UPI000000AF9FF; EMBL:Z33279; NID:9541724; PID:  
A;Experimental source: ATCC 27343  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994  
C;Genetics:  
A;Genetic code: SGC3  
C;Superfamily: thymidine kinase  
C;Keywords: ATP; phosphotransferase

Query Match 15.0%; Score 31; DB 2; Length 45;  
Best Local Similarity 54.5%; Pred. No. 2.5e+03;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 19 CGLAGGVEQFI 29  
| | | | | | | | | |  
Db 26 CMFAGKTEEFI 36

Search completed: January 20, 2006, 17:34:26  
Job time : 16.0741 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:22:44 ; Search time 82.5679 Seconds  
(without alignments)  
324.703 Million cell updates/sec

Title: US-10-619-323-4

Perfect score: 207

Sequence: 1 KDPQRETLKAIHYALNCCGLAGVEQFISDIPKXDV 38

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 90886

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 50 summaries

Database : Uniprot\_05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	22.2	36	2	Q5P857_AZOSE
2	45.5	22.0	45	2	Q5WG86_BACSK
3	45	21.7	37	2	Q72VY5_BACCL
4	45	21.7	37	2	Q81KH9_BACAN
5	43.5	21.0	39	2	Q9BF50_CONAE
6	43	20.8	35	2	Q5C273_SCHJA
7	43	20.8	44	2	Q4X8W4_PLACH
8	42	20.3	44	2	Q5BZF7_SCHJA
9	41	19.8	19	2	Q86DB6_HALRO
10	41	19.8	41	2	Q4R921_WACFA
11	41	19.8	46	1	SF12_SEGFL
12	40	19.3	33	2	Q29066_PIG
13	40	19.3	33	2	Q9W7N9_MORSA
14	39.5	19.1	48	2	Q8UE67_AGRTS
15	39	18.8	36	2	Q4YB36_PLABE
16	39	18.8	38	1	COAT3_BPPLH
17	39	18.8	38	1	COAT3_XANCP
18	39	18.8	38	2	Q4UUG6_XANCP
19	39	18.8	44	1	YDAG_ECOLI
20	39	18.8	50	2	Q51AA2_ENTHI
21	38.5	18.6	36	2	Q4Z513_PLABE
22	38	18.4	37	2	Q5C5J9_SCHJA
23	38	18.4	42	2	Q4X2T4_PLACH
24	38	18.4	42	2	Q4Y419_PLACH
25	38	18.4	43	2	Q6J506_PIG
26	38	18.4	43	1	LEBCE_VIPLE
27	38	18.4	47	1	THN_PYRPU
28	38	18.4	48	2	Q4RC82_TETNG
29	38	18.4	50	2	Q7N8J8_PHOHL
30	38	18.4	50	2	Q9PFE8_XYLFA
31	37	17.9	30	2	Q86DN6_9CAEN

32	37	17.9	44	2	Q9WMD8_9FLAV	Q9wmd8 gb virus c/
33	37	17.9	49	2	Q5C4E6_SCHJA	Q5c4e6 schistosoma
34	37	17.9	50	2	Q787S5_9FLAV	Q787s5 gb virus c/
35	37	17.9	50	2	Q787T7_9FLAV	Q787t7 gb virus c/
36	37	17.9	50	2	Q787R8_9FLAV	Q787r8 gb virus c/
37	37	17.9	50	2	Q9WA37_9FLAV	Q9wa37 gb virus c/
38	37	17.9	50	2	Q9YIK7_9FLAV	Q9yik7 gb virus c/
39	37	17.9	50	2	Q9Z039_9FLAV	Q9z039 gb virus c/
40	36.5	17.6	33	2	Q7M269_GASCO	Q7m269 gastrocloni
41	36.5	17.6	34	2	Q71798_9HIVI	Q71798 human immun
42	36.5	17.6	35	2	Q9IPX9_9HIVI	Q9ipx9 human immun
43	36.5	17.6	35	2	Q9IPY1_9HIVI	Q9ipy1 human immun
44	36.5	17.6	47	1	TX32_PHORI	P83904 phoneutria
45	36.5	17.6	49	2	Q8CIW8_MOUSE	Q8ciw8 mus musculus
46	36	17.4	25	2	Q7Z6N6_HUMAN	Q7z6n6 homo sapien
47	36	17.4	30	1	CX2A_CONBE	P58625 conus betul
48	36	17.4	33	1	YLCH_ECOLI	Q47288 escherichia
49	36	17.4	33	2	Q9NGN0_STRPU	Q9ngn0 strongyloce
50	36	17.4	37	2	Q81RS9_BACAN	Q81rs9 bacillus an

#### ALIGNMENTS

##### RESULT 1

Q5P857\_AZOSE  
ID Q5P857\_AZOSE PRELIMINARY; PRT; 36 AA.  
AC Q5P857\_AZOSE PRELIMINARY; PRT; 36 AA.  
DT 01-FEB-2005 (TrEMBLrel. 29, Created)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
DE Hypothetical protein.  
GN OrderedLocusNames=AZOSEA03820; ORFNames=eBA749;  
OS Azocarcus sp. (strain EbN1).  
OC Bacteria; Proteobacteria; Betaproteobacteria; Rhodocyclales;  
OC Rhodocyclaceae; Azocarcus.  
OX NCBI\_TaxID=76114;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=EbN1.  
RX PubMed=15551059; DOI=10.1007/s00203-004-0742-9;  
RA Rabus R., Kube M., Heider J., Beck A., Heitmann K., Widdel F., Reinhardt R.;  
RT "The genome sequence of an anaerobic aromatic-degrading denitrifying bacterium, strain EbN1."  
RL Arch. Microbiol. 183:27-36(2005).  
DR EMBL; CR555306; CA06504.1; -; Genomic DNA.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 36 AA; 4153 MW; 38E2D62BA024C649 CRC64;

Query Match 22.2%; Score 46; DB 2; Length 36;  
Best Local Similarity 47.8%; Pred. No. 56;

Matches 10; Conservative 2; Mismatches 7; Indels 2; Gaps 1;

QY 2 DEPQRETLKAIHYALNCC--CG 20

Db 16 DEPQRETLKAIHYALNCCGCG 36

##### RESULT 2

Q5WG86\_BACSK  
ID Q5WG86\_BACSK PRELIMINARY; PRT; 45 AA.  
AC Q5WG86\_BACSK PRELIMINARY; PRT; 45 AA.  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Hypothetical protein.  
GN OrderedLocusNames=ABC2084;  
OS Bacillus clausii (strain KSM-K16).  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=66692;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.

```
RC STRAIN=KSM-K16;
RA Takaki Y., Kageyama Y., Shimamura S., Suzuki H., Nishi S., Hatada Y.,
RA Kawai S., Ito S., Horikoshi K.;
RT "The complete genome sequence of the alkaliphilic Bacillus clausii
RT KSM-K16.";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP006627; BAB64619.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 45 AA; 5293 MW; 783D494D2BCDA185 CRC64;

Query Match 22.0%; Score 45.5; DB 2; Length 45;
Best Local Similarity 31.2%; Pred. No. 84;
Matches 10; Conservative 10; Mismatches 7; Indels 5; Gaps 1;

QY 1 KDSQRETLKAIHYALNCCGLAGVQFISDI 32
Db 12 EDDPRREVEAMTESIFC-----AIEQEIDEI 38

RESULT 3
Q72YV5_BACCI1 PRELIMINARY; PRT; 37 AA.
AC Q72YV5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=BCE4915;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=222523;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14960714; DOI=10.1093/nar/gkh259;
RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis px01.";
RL Nucleic Acids Res. 32:977-988(2004).
DR EMBL; AE017279; AAS43816.1; -; Genomic_DNA.
DR TIGR; BCE4915; -.
KW Complete proteome.
SQ SEQUENCE 37 AA; 4309 MW; 3A33382F140D7DEC CRC64;

Query Match 21.7%; Score 45; DB 2; Length 37;
Best Local Similarity 34.6%; Pred. No. 81;
Matches 9; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 5 QRETLKAIHYALNCCGLAGVQFIS 30
Db 5 KQKEINSIHLYNCVILLGITRNI 30

RESULT 4
Q81KH9_BACAN PRELIMINARY; PRT; 37 AA.
AC Q81KH9; O6KIX6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=BA5018, GBAA5018;
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1392;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ames / isolate Porton;
RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
RA Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
```

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RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzaple E.K., Okstad O.A., Helgason E., Ristone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R.T., Redmond C., Thwaitte J.E., White O.,
RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,
RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria.";
RN Nature 423:81-86(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ames / isolate 0581;
RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
RA Fraser C.M.;
RT "Bacillus anthracis comparative genomics.";
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017039; AAP28698.1; -; Genomic_DNA.
DR EMBL; AE017334; AAT35445.1; -; Genomic_DNA.
DR TIGR; BA5018; -.
DR TIGR; GBAA5018; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 37 AA; 4335 MW; 3A3338340EBCDC CRC64;

Query Match 21.7%; Score 45; DB 2; Length 37;
Best Local Similarity 34.6%; Pred. No. 81;
Matches 9; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 5 QRETLKAIHYALNCCGLAGVQFIS 30
Db 5 KQKEINSIHLYNCVILLGITRNI 30

RESULT 5
Q9BP50_CONAE PRELIMINARY; PRT; 39 AA.
AC Q9BP50;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Conotoxin scaffold VI/VII (Fragment).
OS Conus arenatus (Sand-dusted cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hyposogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89451;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21105969; PubMed=11158371;
RA Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
RA Fainzilber M.;
RT "Mechanisms for evolving hypervariability: the case of conopeptides.";
RL Mol. Biol. Evol. 18:120-131(2001).
DR EMBL; AF215107; AAG60528.1; -; mRNA.
FT NON_TER 1 1
SQ SEQUENCE 39 AA; 4551 MW; 1C4D2343C0BC115E CRC64;

Query Match 21.0%; Score 43.5; DB 2; Length 39;
Best Local Similarity 56.2%; Pred. No. 1.4e+02;
Matches 9; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

QY 18 CCGIAGGVQFISDIC 33
Db 23 CCGLENG-QPFCSRIC 37

RESULT 6
Q5C273_SCHJA PRELIMINARY; PRT; 35 AA.
ID Q5C273_SCHJA
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AC Q5C273;  
DT 10-MAY-2005 (TReMBLrel. 30, Created)  
DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)  
DE 10-MAY-2005 (TReMBLrel. 30, Last annotation update)  
DE Hypothetical protein.  
OS Schistosoma japonicum (Blood fluke).  
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;  
OC Schistosomatidae; Schistosomatidae; Schistosoma.  
OX NCBI\_TaxID=6182;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Han Z.;  
RL Submitted (MAR-2005) to the EMBL/GenBank/DBSJ databases.  
DR EMBL; AY810363; AAX26252.1; -, mRNA.  
KW Hypothetical protein.  
SQ SEQUENCE 35 AA; 3872 MW; 6D7F796482D9952B CRC64;  
  
Query Match 20.8%; Score 43; DB 2; Length 35;  
Best Local Similarity 33.3%; Pred. No. 1.5e+02;  
Matches 9; Conservative 5; Mismatches 13; Indels 0; Gaps 0;  
  
QY 12 IHVALNCCGLAGGVQFISDICPKDV 38  
DB 2 IQSAFNYKLSGLDVTQNVVPTKV 28  
  
RESULT 7  
ID Q4X8W4\_PLACH PRELIMINARY; PRT; 44 AA.  
AC Q4X8W4;  
DT 13-SEP-2005 (TReMBLrel. 31, Created)  
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)  
DE Hypothetical protein (Fragment).  
GN ORFNames=PC404818.00.0;  
OS Plasmodium chabaudi.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.  
OX NCBI\_TaxID=5825;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Hall N., Karras M., Raine J.D., Carlton J.M., Koolij T.W.A.,  
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,  
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,  
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,  
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,  
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.,  
RA "A comprehensive survey of the Plasmodium life cycle by genomic,  
RT transcriptomic, and proteomic analyses."  
RL Science 307:82-86(2005).  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBSJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; CAAY01008748; CAH86662.1; -, Genomic\_DNA.  
KW Hypothetical protein.  
FT NON TER 1  
FT NON TER 44  
SQ SEQUENCE 44 AA; 4905 MW; D77C3404234DDF50 CRC64;  
  
Query Match 20.8%; Score 43; DB 2; Length 44;  
Best Local Similarity 37.0%; Pred. No. 1.9e+02;  
Matches 10; Conservative 4; Mismatches 13; Indels 0; Gaps 0;  
  
QY 8 TLKAIHYALNCCGLAGGVQFISDICP 34  
DB 6 TIPITENAINCLFSLISIEFTFSIIP 32  
  
RESULT 8  
ID Q5BZF7\_SCHJA PRELIMINARY; PRT; 44 AA.  
AC Q5BZF7;  
DT 10-MAY-2005 (TReMBLrel. 30, Created)  
DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)

DT 10-MAY-2005 (TReMBLrel. 30, Last annotation update)  
DE Hypothetical protein.  
OS Schistosoma japonicum (Blood fluke).  
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;  
OC Schistosomatidae; Schistosomatidae; Schistosoma.  
OX NCBI\_TaxID=6182;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Han Z.;  
RL Submitted (MAR-2005) to the EMBL/GenBank/DBSJ databases.  
DR EMBL; AY811329; AAX27218.1; -, mRNA.  
KW Hypothetical protein.  
SQ SEQUENCE 44 AA; 5266 MW; 4EBCF906ED28BD18 CRC64;  
  
Query Match 20.3%; Score 42; DB 2; Length 44;  
Best Local Similarity 46.7%; Pred. No. 2.7e+02;  
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
  
QY 2 DEPORETLKAIHYAL 16  
DB 10 DQPTQEMVKNLHFAL 24  
  
RESULT 9  
ID Q86DB6\_HALRO PRELIMINARY; PRT; 19 AA.  
AC Q86DB6;  
DT 01-JUN-2003 (TReMBLrel. 24, Created)  
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
DE Homeobox protein Otx (Fragment).  
GN Name=Hroth;  
OS Halocynthia roretzi (Sea squirt).  
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;  
OC Stolidobranchia; Pyuridae; Halocynthia.  
OX NCBI\_TaxID=7729;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22586101; PubMed=12701103; DOI=10.1002/dvdy.10295;  
RA Oda-Ishii I., Saiga H.;  
RT "Genomic organization and promoter and transcription regulatory  
RT regions for the expression in the anterior brain (sensory vesicle) of  
RT Hroth, the otx homologue of the ascidian, Halocynthia roretzi.";  
RL Dev. Dyn. 227:104-113(2003).  
DR EMBL; AB104851; BAC76068.1; -, Genomic\_DNA.  
DR GO; GO:0005634; C:nucleus; IEA.  
KW Nuclear protein.  
FT NON TER 19  
FT NON TER 19  
SQ SEQUENCE 19 AA; 2041 MW; 2D9CAB7036EAF8D CRC64;  
  
Query Match 19.8%; Score 41; DB 2; Length 19;  
Best Local Similarity 61.5%; Pred. No. 1.5e+02;  
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
  
QY 9 LKAIHYALNCCGL 21  
DB 4 LKSHYAMNGLGL 16  
  
RESULT 10  
ID Q4R921\_MACFA PRELIMINARY; PRT; 41 AA.  
AC Q4R921;  
DT 13-SEP-2005 (TReMBLrel. 31, Created)  
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)  
DE Testis cDNA clone: QtaA-10904, similar to human tudor domain  
DE containing 6 protein (LOC388929).  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
OC Cercopithecidae; Cercopithecinae; Macaca.  
OX NCBI\_TaxID=9541;

```

RN NUCLEOTIDE SEQUENCE.
RP International consortium for macaque cDNA sequencing, analysis;
RA "DNA sequences of macaque genes expressed in brain or testis and its
RT evolutionary implications.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN NUCLEOTIDE SEQUENCE.
RP Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,
RA Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hashimoto K.;
RT Substitution rate and structural divergence of 5'UTR evolution:
RT Comparative analysis between human and cynomolgus monkey cDNAs.";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB168276; BAB00400.1; -; mRNA.
SQ SEQUENCE 41 AA; 4624 MW; EBD6FE0E219C7FD2 CRC64;

Query Match 19.8%; Score 41; DB 2; Length 41;
Best Local Similarity 50.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 24 GVEQFISDICKP 35
Db 28 GIERFFSSCPQ 39

RESULT 11
SF12 SEGFL STANDARD; PRT; 46 AA.
AC P61096;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Toxin SFI 2 (F5.7).
OS Segestria florentina (tube-web spider).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Haplogynae; Dyderoidea; Segestriidae; Segestria.
OX NCBI_TaxID=31925;
RN NUCLEOTIDE SEQUENCE, PROTEIN SEQUENCE OF 1-18, MASS SPECTROMETRY, AND
RP LETHAL DOSE.
RA TISSUE=Venom, and Venom gland;
RX PubMed=11689233; DOI=10.1016/S0041-0101(01)00181-7;
RA Lipkin A., Kozlov S., Nosyreva E., Blake A., Windass J.D., Grishin E.;
RT "Novel insecticidal toxins from the venom of the spider Segestria
RT florentina.";
RL Toxinon 40:125-130(2002).
CC -1- FUNCTION: Causes complete flaccid paralysis on H.virescens larvae
CC and death with larger doses. Is inactive on mice.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -1- PTM: Contains four disulfide bonds (probable).
CC -1- MASS SPECTROMETRY: MW=4993; METHOD=MALDI; RANGE=1-46; NOTE=Ref.1.
CC -1- TOXIC DOSE: LD(50) is 7 mg/kg on H.virescens larvae.
CC -1- SIMILARITY: Belongs to the spider toxin SFI family.
CC -1- CAUTION: Mass spectrometry experiment was done on the entire
CC protein whose the sequence known is incomplete (sequence of 1-18).
CC The difference between measured (4993) and calculated (5136) mass
CC resides in the fact that the sequence of this entire protein is
CC maybe not identical to the sequence shown.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
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CC InterPro: IPR012633; Toxin_28.
DR Pfam: PF08115; Toxin_28; 1.
KW Direct protein sequencing; Multigene family; Toxin.
SQ SEQUENCE 46 AA; 5136 MW; CBFC66F6292D8F6 CRC64;

Query Match 19.8%; Score 41; DB 1; Length 46;
Best Local Similarity 57.1%; Pred. No. 4e+02;


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Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 7 ETLKAIHYALNCCG 20
Db 7 ETVCIYIHNHNNCCG 20

RESULT 12
Q29066_PIG PRELIMINARY; PRT; 33 AA.
ID Q29066_PIG PRELIMINARY; PRT; 33 AA.
AC Q29066;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Myosin (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC SUB_TaxID=9823;
OX NCBI_TaxID=9823;
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Kidney;
RX MEDLINE=94294418; PubMed=8022818;
RA Benet W.M., Hasson T., Wirth J.A., Cheney R.E., Mooseker M.S.;
RT "Identification and overlapping expression of multiple unconventional
RT myosin genes in vertebrate cell types.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:6549-6553(1994).
DR EMBL; L29135; AAA20920.1; -; mRNA.
DR PIR; I46600; I46600. 1
FT NON_TER 1 33
SQ SEQUENCE 33 AA; 3448 MW; 2EAD4B56F22A40C7 CRC64;

Query Match 19.3%; Score 40; DB 2; Length 33;
Best Local Similarity 55.0%; Pred. No. 3.8e+02;
Matches 11; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

Qy 12 IHV--ALNCCGLAGGVEQFI 29
Db 7 IHHLTALSQKGFASGVEQII 26

RESULT 13
Q9W7N9_MORSA PRELIMINARY; PRT; 33 AA.
ID Q9W7N9_MORSA PRELIMINARY; PRT; 33 AA.
AC Q9W7N9;
DT 01-NOV-1999 (T-EMBLrel. 12, Created)
DT 01-NOV-1999 (T-EMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Class 9A myosin (Striped bass).
OS Morone saxatilis (Striped bass).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Moronidae; Morone.
OX NCBI_TaxID=34816;
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=RPE;
RA Hillman D.W., Best-Usinger L., Cheng J., Burnside B.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF002868; AAD41449.1; -; mRNA.
FT NON_TER 1 33
SQ SEQUENCE 33 AA; 3476 MW; 2EBFFCA6F22A40C7 CRC64;

Query Match 19.3%; Score 40; DB 2; Length 33;
Best Local Similarity 55.0%; Pred. No. 3.8e+02;
Matches 11; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

Qy 12 IHV--ALNCCGLAGGVEQFI 29
Db 7 IHHLTALSQKGFASGVEQII 26


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Db 7 IHHLTALSQRGFASGVBEQII 26
RESULT 14
Q8UE67 AGRT5
ID Q8UE67_AGR5 PRELIMINARY; PRT; 48 AA.
AC Q8UE67;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein Atu1894.
GN OrderedLocuNames=Atu1894;
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Dupont;
RX MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Clendenning J., Decherage G., Gillet W., Grant C.,
RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58."
RL Science 294:2317-2323(2001).
DR EMBL; AE009143; AAL42890.1; -; Genomic_DNA.
DR FIR; AD2809; AD2809.
SQ Complete proteome; Hypothetical protein.
KW SEQUENCE 48 AA; 5156 MW; F14474E058E50D58 CRC64;

Query Match 19.1%; Score 39.5; DB 2; Length 48;
Best Local Similarity 45.0%; Pred. No. 6.9e+02;
Matches 9; Conservative 2; Mismatches 6; Indels 3; Gaps 1;

QY 18 CCGAGGVQFIS---DIPC 34
||| : | : | : |||
Db 12 CCGCSQGVQFPFGGIGICP 31

RESULT 15
Q4YB36 PLABE
ID Q4YB36_PLABE PRELIMINARY; PRT; 36 AA.
AC Q4YB36;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PB107877.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriam M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses."
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
```







vi  
oc



CC animal cells. They seem to exert their toxic effect at the level  
CC of the cell membrane. Their precise function is not known.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC  
CC -1- SIMILARITY: Belongs to the plant thionin (TC 1.C.44) family.  
CC  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC  
CC PIR; A24074; A24074.  
DR HSP; P01538; IED0.  
DR InterPro; IPR001010; Thionin.  
DR Pfam; PF00321; Thionin; 1.  
DR PRINTS; PR00287; THIONIN.  
DR PROSITE; PS00271; THIONIN; 1.  
KW Direct protein sequencing; Plant defense; Plant toxin; Thionin; Toxin.  
FT DISULFID 3 41 By similarity.  
FT DISULFID 4 31 By similarity.  
FT DISULFID 16 27 By similarity.  
FT SQ SEQUENCE 47 AA; 5288 MW; 87E10460DBE4C6E1 CRC64;  
SQ  
Query Match 18.4%; Score 38; DB 1; Length 47;  
Best Local Similarity 38.5%; Pred. No. 1.1e+03;  
Matches 10; Conservative 4; Mismatches 6; Indels 6; Gaps 2;  
QY 14 YALNC---CGLAGGVQFISDICPK 36  
DB 8 WARNCYNVCKLPGTISR---EICAK 30  
RESULT 28  
Q4RC82 TETNG  
ID Q4RC82\_TETNG PRELIMINARY; PRT; 48 AA.  
AC Q4RC82;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Chromosome undetermined SCAP19550, whole genome shotgun sequence.  
DE (Fragment).  
GN ORFNames=GSTENG00038161001;  
OS Tetraodon nigroviridis (Green puffer).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
OC Tetraodontidae; Tetraodontidae; Tetraodon.  
OX NCBI\_TaxID=99883;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,  
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
RA Basilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,  
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,  
RA Craud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,  
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,  
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,  
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.;  
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
RT the early vertebrate proto-karyotype."  
RL Nature 431:946-957(2004).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RG Genoscope; Whitehead Institute Centre for Genome Research;  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
CC -1- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
CC  
CC EMBL; CAAE01019550; CAG14001.1; -; Genomic\_DNA.

FT NON TER 1 1  
SQ SEQUENCE 48 AA; 5445 MW; 778C266C74DAC92B CRC64;  
Query Match 18.4%; Score 38; DB 2; Length 48;  
Best Local Similarity 28.6%; Pred. No. 1.1e+03;  
Matches 8; Conservative 6; Mismatches 14; Indels 0; Gaps 0;  
QY 6 RETLKAHYALNCCGLAGGVQFISDIC 33  
DB 8 RUPHRLPSFWLNVLAAGNVERWIAPAC 35  
RESULT 29  
Q7N8J8 PHOLL  
ID Q7N8J8\_PHOLL PRELIMINARY; PRT; 50 AA.  
AC Q7N8J8;  
DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Similarities with unknown protein.  
GN OrderedLocusNames=plu0724;  
OS Photorhabdus luminescens (subsp. laumondii).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Photorhabdus.  
OX NCBI\_TaxID=141679;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=TT01;  
RX MEDLINE=22957627; PubMed=14528314; DOI=10.1038/nbt886;  
RA Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A.,  
RA Taourit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-F.,  
RA Dassa E., Derose R., Derzelle S., Freyssinet G., Gaudriault S.,  
RA Medigue C., Lanois A., Powell K., Sigvier P., Vincent R., Wingate V.,  
RA Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.;  
RT "The genome sequence of the entomopathogenic bacterium Photorhabdus  
RT luminescens";  
RL Nat. Biotechnol. 21:1307-1313(2003).  
DR EMBL; BX571861; CAE13019.1; -; Genomic\_DNA.  
DR PhotoList; plu0724; -;  
KW Complete proteome.  
SQ SEQUENCE 50 AA; 5429 MW; 1B964C7A0DB14253 CRC64;  
Query Match 18.4%; Score 38; DB 2; Length 50;  
Best Local Similarity 41.2%; Pred. No. 1.2e+03;  
Matches 7; Conservative 3; Mismatches 5; Indels 2; Gaps 1;  
QY 17 NCCGLAGG--VEQFISD 31  
DB 14 SCCALKGGTAINFVRD 30  
RESULT 30  
Q9PF8 XYLFA  
ID Q9PF8\_XYLFA PRELIMINARY; PRT; 50 AA.  
AC Q9PF8;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Hypothetical protein.  
GN OrderedLocusNames=Xf0722;  
OS Xylella fastidiosa.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;  
OC Xanthomonadaceae; Xylella.  
OX NCBI\_TaxID=2371;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=9a5C;  
RX MEDLINE=20365717; PubMed=10910347; DOI=10.1038/35018003;  
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,  
RA Alvares R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,  
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,  
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,  
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,

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Qy 20 GLAGVGEQFISDIPCK 35
   ||:|:|:|:|
Db 8 GIVRDLVDIAIDVCPK 23

RESULT 32
ID Q9WMD8_9FLAV PRELIMINARY; PRT; 44 AA.
AC Q9WMD8;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Polyprotein (fragment).
OS GB virus C/Hepatitis G virus.
SC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC GBV-C/HGV group.
OX NCBI_TaxID=54290;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=38154923; PubMed=9495537; DOI=10.1016/S0168-1702(97)00123-8;
RA Kondo Y., Mizokami M., Nakano T., Kato T., Ohba K., Orito E., Ueda R.,
RA Mukaide M., Hikiji K., Oyunsuren T., Cookeley W.G.;
RT "Genotype of GB virus C/hepatitis G virus by molecular evolutionary
RT analysis."; 52:221-230(1997).
RL virus Res. 52:221-230(1997).
DR EMBL; AB006146; BAA35134.1; -; Genomic_RNA.
KW Polyprotein.
FT NON TER 44 44
SQ SEQUENCE 44 AA; 4558 MW; 34C6C10975CCE306 CRC64;

Query Match 17.9%; Score 37; DB 2; Length 44;
Best Local Similarity 29.2%; Pred. No. 1.5e+03;
Matches 7; Conservative 7; Mismatches 8; Indels 2; Gaps 1;

Qy 15 ALNCCGLAGVGEQFISDIPCKDV 38
   ||:|:|:|:|:|:|:|:|:|
Db 19 ATHACGANG--QYFLTNCCALEDI 40

RESULT 33
ID Q5CAE6 SCHJA PRELIMINARY; PRT; 49 AA.
AC Q5CAE6;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX Han Z.;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY809590; AAX25479.1; -; mRNA.
DR InterPro; IPR000471; Interferon_abd.
KW Hypothetical protein.
SQ SEQUENCE 49 AA; 5479 MW; 1491391F97B9E9FA CRC64;

Query Match 17.9%; Score 37; DB 2; Length 49;
Best Local Similarity 26.3%; Pred. No. 1.6e+03;
Matches 10; Conservative 4; Mismatches 14; Indels 10; Gaps 1;

Qy 1 KDEPQRETLKAIHYALNCCGLAGVGEQFISDIPCKDV 38
   |||:|:|:|:|:|:|:|:|:|
Db 3 KDPDTEELFDVWNSLVCCSL-----ICLGNDI 30

RESULT 34
ID Q787R5_9FLAV PRELIMINARY; PRT; 50 AA.
DT Q787R5_9FLAV

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DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Polypeptide (Fragment).
OS GB virus C/Hepatitis G virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC GBV-C/HGV group.
OX NCBI_TaxID=54290;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98154925; PubMed=9495537; DOI=10.1016/S0168-1702(97)00123-8;
RA Kondo Y., Mizokami M., Nakano T., Oba K., Orito E., Ueda R.,
RA Mukaide M., Hikiji K., Oyunsuren T., Cooksley W.G.;
RT "Genotype of GB virus C/Hepatitis G virus by molecular evolutionary
RT analysis.";
RL Virus Res. 52:221-230(1997).
DR EMBL; AB003545; BAA36157.1; -; Genomic_RNA.
KW Polypeptide.
FT NON_TER 50
SQ SEQUENCE 50 AA; 5083 MW; C77B505F1A2CE4C6 CRC64;

Query Match 17.9%; Score 37; DB 2; Length 50;
Best Local Similarity 29.2%; Pred. No. 1.7e+03;
Matches 7; Conservative 7; Mismatches 8; Indels 2; Gaps 1;

QY 15 ALNCCGLAGGVEQFISDIPCKDV 38
DB 19 ATHACGANG--QYFLTNCCALEDI 40

RESULT 35
Q787R7_9FLAV
ID Q787R7_9FLAV PRELIMINARY; PRT; 50 AA.
AC Q787R7_2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Polypeptide (Fragment).
OS GB virus C/Hepatitis G virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC GBV-C/HGV group.
OX NCBI_TaxID=54290;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kondo Y., Mizokami M., Nakano T., Ueda R., Mukaide M., Hikiji K.,
RA Kato T., Oyunsuren T., Rukibakiev R., Cooksley W.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB003538; BAA36188.1; -; Genomic_RNA.
KW Polypeptide.
FT NON_TER 50
SQ SEQUENCE 50 AA; 5083 MW; C77B505F1A2CE4C6 CRC64;

Query Match 17.9%; Score 37; DB 2; Length 50;
Best Local Similarity 29.2%; Pred. No. 1.7e+03;
Matches 7; Conservative 7; Mismatches 8; Indels 2; Gaps 1;

QY 15 ALNCCGLAGGVEQFISDIPCKDV 38
DB 19 ATHACGANG--QYFLTNCCALEDI 40

RESULT 36
Q787R8_9FLAV
ID Q787R8_9FLAV PRELIMINARY; PRT; 50 AA.
AC Q787R8_2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Polypeptide (Fragment).
OS GB virus C/Hepatitis G virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC GBV-C/HGV group.
OX NCBI_TaxID=54290;

Query Match 17.9%; Score 37; DB 2; Length 50;
Best Local Similarity 29.2%; Pred. No. 1.7e+03;
Matches 7; Conservative 7; Mismatches 8; Indels 2; Gaps 1;

QY 15 ALNCCGLAGGVEQFISDIPCKDV 38
DB 19 ATHACGANG--QYFLTNCCALEDI 40
```

```
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kondo Y., Mizokami M., Nakano T., Ueda R., Mukaide M., Hikiji K.,
RA Kato T., Oyunsuren T., Rukibakiev R., Cooksley W.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB003535; BAA36185.1; -; Genomic_RNA.
KW Polypeptide.
FT NON_TER 50
SQ SEQUENCE 50 AA; 5117 MW; C77B5877B8AE4C6 CRC64;

Query Match 17.9%; Score 37; DB 2; Length 50;
Best Local Similarity 29.2%; Pred. No. 1.7e+03;
Matches 7; Conservative 7; Mismatches 8; Indels 2; Gaps 1;

QY 15 ALNCCGLAGGVEQFISDIPCKDV 38
DB 19 ATHACGANG--QYFLTNCCALEDI 40

RESULT 37
Q9WA37_9FLAV
ID Q9WA37_9FLAV PRELIMINARY; PRT; 50 AA.
AC Q9WA37_2004 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE Polypeptide (Fragment).
OS GB virus C/Hepatitis G virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC GBV-C/HGV group.
OX NCBI_TaxID=54290;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kondo Y., Mizokami M., Nakano T., Ueda R., Mukaide M., Hikiji K.,
RA Kato T., Oyunsuren T., Rukibakiev R., Cooksley W.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB003537; BAA36187.1; -; Genomic_RNA.
KW Polypeptide.
FT NON_TER 50
SQ SEQUENCE 50 AA; 5117 MW; C77B5877B8AE4C6 CRC64;

Query Match 17.9%; Score 37; DB 2; Length 50;
Best Local Similarity 29.2%; Pred. No. 1.7e+03;
Matches 7; Conservative 7; Mismatches 8; Indels 2; Gaps 1;

QY 15 ALNCCGLAGGVEQFISDIPCKDV 38
DB 19 ATHACGANG--QYFLTNCCALEDI 40

RESULT 38
Q9YIK7_9FLAV
ID Q9YIK7_9FLAV PRELIMINARY; PRT; 50 AA.
AC Q9YIK7_2004 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE Polypeptide (Fragment).
OS GB virus C/Hepatitis G virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC GBV-C/HGV group.
OX NCBI_TaxID=54290;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kondo Y., Mizokami M., Nakano T., Ueda R., Mukaide M., Hikiji K.,
RA Kato T., Oyunsuren T., Rukibakiev R., Cooksley W.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB003539; BAA36189.1; -; Genomic_RNA.
KW Polypeptide.
FT NON_TER 50
SQ SEQUENCE 50 AA; 5083 MW; C77B505F1A2CE4C6 CRC64;

Query Match 17.9%; Score 37; DB 2; Length 50;
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2006, 17:21:43 ; Search time 62.3457 Seconds  
(without alignments)  
176.187 Million cell updates/sec

Title: US-10-619-323-5

Perfect score: 132

Sequence: 1 PKQVLETFVKSCPDPAKEVFDNK 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 1130394

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

A\_Geneseq\_21.\*  
1: Geneseq19808.\*  
2: Geneseq19908.\*  
3: Geneseq20008.\*  
4: Geneseq20018.\*  
5: Geneseq20028.\*  
6: Geneseq20038a.\*  
7: Geneseq20038b.\*  
8: Geneseq20048.\*  
9: Geneseq20058.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	132	100.0	25	8	ADJ57562 Human CD9
2	95	72.0	18	8	ADJ57563 Human CD9
3	61	46.2	30	6	ABU05051 Human exp
4	49	37.1	10	6	ABU03385 Human exp
5	46	34.8	44	4	AAM83184 Human imm
6	39	29.5	41	4	AAU20329 Human nov
7	38	28.8	46	9	ADY51925 Phage SPO
8	36	27.3	33	4	ABR39440 Peptide #
9	36	27.3	33	4	AAM32967 Peptide #
10	36	27.3	33	4	AAM72739 Human bon
11	36	27.3	33	4	AAM60125 Human bra
12	36	27.3	33	4	ABG54437 Human liv
13	36	27.3	33	5	ABG42563 Human pep
14	36	27.3	34	3	AAY92549 Finger 2
15	36	27.3	34	3	AAB02778 Human TGF
16	36	27.3	36	2	AAB030357 Fragment
17	36	27.3	36	3	AAB09511 Human TGF
18	36	27.3	39	7	ADJ81051 INSP010 p
19	36	27.3	46	8	ADS06580 Staphyloc
20	35.5	26.9	39	3	AAY56422 Mycoplasma
21	35.5	26.9	41	4	AAM65372 Human bra
22	35.5	26.9	41	4	ABG59698 Human liv
23	35.5	26.9	42	8	ADJ97737 Protein e
24	35.5	26.9	43	4	ABB66998 Drosophil

25	35	26.5	28	4	AAM64295	Aam64295 Human bra
26	35	26.5	33	4	AAM18282	Aam18282 Peptide #
27	35	26.5	33	4	ABB37316	Abb37316 Peptide #
28	35	26.5	33	4	AAM30772	Aam30772 Peptide #
29	35	26.5	33	4	ABB32066	Abb32066 Peptide #
30	35	26.5	33	4	ABB22608	Abb22608 Protein #
31	35	26.5	33	4	AAM70450	Aam70450 Human bon
32	35	26.5	33	4	AAM58010	Aam58010 Human bra
33	35	26.5	33	4	ABG52136	Abg52136 Human liv
34	35	26.5	33	4	AAM05895	Aam05895 Peptide #
35	35	26.5	33	5	ABG40088	Abg40088 Human pep
36	35	26.5	38	4	ABB42598	Abb42598 Peptide #
37	35	26.5	38	4	AAM36414	Aam36414 Peptide #
38	35	26.5	38	4	AAM76304	Aam76304 Human bon
39	35	26.5	38	4	AAM63489	Aam63489 Human bra
40	35	26.5	38	4	ABG58014	Abg58014 Human liv
41	35	26.5	38	5	ABG45607	Abg45607 Human pep
42	35	26.5	50	2	AAR66211	Aar66211 Phi 29 in
43	34.5	26.1	18	7	ADC29648	Adc29648 Antioxi
44	34.5	26.1	35	4	AAM17469	Aam17469 Peptide #
45	34.5	26.1	35	4	ABB36490	Abb36490 Peptide #
46	34.5	26.1	35	4	AAM29988	Aam29988 Peptide #
47	34.5	26.1	35	4	ABB31285	Abb31285 Peptide #
48	34.5	26.1	35	4	ABB21834	Abb21834 Protein #
49	34.5	26.1	35	4	AAM69654	Aam69654 Human bon
50	34.5	26.1	35	4	AAM57255	Aam57255 Human bra

ALIGNMENTS

RESULT 1

ADJ57562

ID ADJ57562 standard; peptide; 25 AA.

AC ADJ57562;

DT 06-MAY-2004 (first entry)

DE Human CD9 fibronectin-binding domain peptide fragment.

XX Human; CD9; antithrombotic; antiarteriosclerotic; vasotropic;

XX haemostatic; angiogenic; cytostatic.

XX Homo sapiens.

XX WO2004007685-A2.

PN 22-JAN-2004.

PD 14-JUL-2003; 2003WO-US022050.

PF 12-JUL-2002; 2002US-0395864P.

PR (UYTE-) UNIV TENNESSEE RES FOUND.

PA Jennings LX, Longhurst CM, Cook GA, Bao J, Zhang C, White MW;

PI Crossno JT, Lu Y,

XX WPI; 2004-122924/12.

DR Interfering with CD9 binding to fibronectin by binding a fibronectin-binding domain of the CD9 protein or polypeptide, useful in treating thrombosis, atherosclerosis, restenosis, bleeding disorders, angiogenesis and cancers.

XX Claim 7; SEQ ID NO 5; 126pp; English.

XX The present sequence is that of a peptide fragment from the fibronectin-binding domain of human CD9 ADJ57558. The peptide, or an antibody that binds to it, is used in claimed methods for: interfering with CD9 binding to fibronectin; modifying adhesion, motility or spreading of a CD9-expressing cell on fibronectin; inhibiting proliferation or survival of

CC CD9-expressing cells; modifying pericellular fibronectin matrix assembly;  
 CC modifying invasiveness of a cell through a collagen and/or laminin matrix  
 CC ; and modifying cell-to-cell interaction. The methods are based on the  
 CC finding that increased CD9 expression is implicated in (i) decreased  
 CC adhesiveness of cells to extracellular matrix (via alpha5-beta-1  
 CC integrin) and/or decreased cell invasiveness and/or decreased  
 CC pericellular fibronectin matrix assembly, and/or (ii) increased cell  
 CC motility, spreading, proliferation, cell survival against apoptosis,  
 CC and/or cell-to-cell contacts. Conditions or disease states involving  
 CC proliferation or survival of CD9-expressing cells can be treated, e.g.  
 CC thrombosis, atherosclerosis, vein graft failure, restenosis, transplant  
 CC arteriopathy, bleeding disorders, angiogenesis, and primary and  
 CC metastatic cancers including breast cancer, prostate cancer, colon  
 CC cancer, melanoma, ovarian cancer, neuroblastoma, glioma and glioblastoma.  
 XX  
 SQ Sequence 25 AA;

Query Match 100.0%; Score 132; DB 8; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-13;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQDVLETFVKSCPDAIKEVFDNK 25  
 |||||  
 DB 1 PKQDVLETFVKSCPDAIKEVFDNK 25

RESULT 2  
 ADJ57563  
 ID ADJ57563 standard; peptide; 18 AA.  
 XX  
 AC ADJ57563;

XX DT 06-MAY-2004 (first entry)  
 XX DE Human CD9 fibronectin-binding domain peptide fragment.  
 XX Human; CD9; antithrombotic; antiarteriosclerotic; vasotropic;  
 KW haemostatic; antiangiogenic; cytostatic.  
 KW  
 XX Homo sapiens.

XX PN WO2004007685-A2.  
 XX DT 22-JAN-2004.  
 XX PF 14-JUL-2003; 2003WO-US022050.  
 XX PR 12-JUL-2002; 2002US-0395864P.  
 XX PA (UYTE-) UNIV TENNESSEE RES FOUND.  
 XX PI Jennings LK, Longhurst CM, Cook GA, Bao J, Zhang C, White MW,  
 PI Crossano JT, Lu Y;  
 XX WPI; 2004-122924/12.

XX Interfering with CD9 binding to fibronectin by binding a fibronectin-  
 PT binding domain of the CD9 protein or polypeptide, useful in treating  
 PT thrombosis, atherosclerosis, restenosis, bleeding disorders, angiogenesis  
 PT and cancers.

XX PS Claim 7; SEQ ID NO 6; 126pp; English.

XX The present sequence is that of a peptide fragment from the fibronectin-  
 CC binding domain of human CD9 ADJ57563. The peptide, or an antibody that  
 CC binds to it, is used in claimed methods for: interfering with CD9 binding  
 CC to fibronectin; modifying adhesion, motility or spreading of a CD9-  
 CC expressing cell on fibronectin; inhibiting proliferation or survival of  
 CC CD9-expressing cells; modifying pericellular fibronectin matrix assembly;  
 CC modifying invasiveness of a cell through a collagen and/or laminin matrix  
 CC ; and modifying cell-to-cell interaction. The methods are based on the  
 CC finding that increased CD9 expression is implicated in (i) decreased  
 CC adhesiveness of cells to extracellular matrix (via alpha5-beta-1

CC integrin) and/or decreased cell invasiveness and/or decreased  
 CC pericellular fibronectin matrix assembly, and/or (ii) increased cell  
 CC motility, spreading, proliferation, cell survival against apoptosis,  
 CC and/or cell-to-cell contacts. Conditions or disease states involving  
 CC proliferation or survival of CD9-expressing cells can be treated, e.g.  
 CC thrombosis, atherosclerosis, vein graft failure, restenosis, transplant  
 CC arteriopathy, bleeding disorders, angiogenesis, and primary and  
 CC metastatic cancers including breast cancer, prostate cancer, colon  
 CC cancer, melanoma, ovarian cancer, neuroblastoma, glioma and glioblastoma.  
 XX  
 SQ Sequence 18 AA;

Query Match 72.0%; Score 95; DB 8; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 8.8e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQDVLETFVKSCPDAI 18  
 |||||  
 DB 1 PKQDVLETFVKSCPDAI 18

RESULT 3  
 ABU05051  
 ID ABU05051 standard; protein; 30 AA.  
 XX  
 AC ABU05051;

XX DT 29-JAN-2003 (first entry)  
 XX DE Human expressed protein tag (EPT) #1717.  
 XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
 KW protease; protease inhibitor; transporter; cytoskeletal protein;  
 KW receptor; transcription factor; cancer; MHC;  
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX OS Homo sapiens.

XX PN WO200278524-A2.

XX PD 10-OCT-2002.

XX PF 28-MAR-2002; 2002WO-US009671.

XX PR 28-MAR-2001; 2001US-0279495P.

XX PR 21-MAY-2001; 2001US-0292544P.

XX PR 08-AUG-2001; 2001US-0310801P.

XX PR 01-OCT-2001; 2001US-0326370P.

XX PR 04-DEC-2001; 2001US-0336780P.

XX PR 20-FEB-2002; 2002US-0358985P.

XX PA (ZYCO-) ZYCOS INC.

XX PI Chicx RM, Tomlinson AJ, Urban RG;

XX WPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
 PT cytoskeletal proteins, receptors or transcription factors), useful for  
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
 PT leukemia.

XX PS Example 2; SEQ ID NO 1717; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a  
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
 CC transporter, cytoskeletal protein, receptor or transcription factor. The  
 CC polypeptide is useful as an immunogenic composition for eliciting in a  
 CC mammal an immunogenic response directed against any of the purified  
 CC polypeptide. The purified polypeptide, or the antibody that binds to this  
 CC polypeptide, is useful for treating cancer. The polypeptide is also  
 CC useful for identifying compounds that binds to a naturally processed

CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 30 AA;

Query Match 46.2%; Score 61; DB 6; Length 30;  
Best Local Similarity 100.0%; Pred. No. 0.04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 PKDVLFTFTVK 12  
| | | | | | | |  
Db 19 PKDVLFTFTVK 30

RESULT 4  
ABU03385  
ID ABU03385 standard; protein; 10 AA.

XX AC ABU03385;

XX DT 29-JAN-2003 (first entry)

XX DE Human expressed protein tag (EPT) #165.

XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX OS Homo sapiens.

XX PN WO200278524-A2.

XX PD 10-OCT-2002.

XX PF 28-MAR-2002; 2002WO-US009671.

XX PR 28-MAR-2001; 2001US-0279495P.

XX PR 21-MAY-2001; 2001US-0292544P.

XX PR 08-AUG-2001; 2001US-0310801P.

XX PR 01-OCT-2001; 2001US-0326370P.

XX PR 04-DEC-2001; 2001US-0336780P.

XX PR 20-FEB-2002; 2002US-0358985P.

XX PA (ZYCO-) ZYCOS INC.

XX PI Chicx RM, Tomlinson AJ, Urban RG;

XX DR WPI; 2003-040607/03.

XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
XX cytoskeletal proteins, receptors or transcription factors), useful for  
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
XX leukemia.

XX PS Claim 10; SEQ ID NO 165; 134pp; English.

XX CC The invention describes a purified polypeptide, which comprises a  
XX fragment of a kinase, phosphatase, protease, protease inhibitor,  
XX transporter, cytoskeletal protein, receptor or transcription factor. The  
XX polypeptide is useful as an immunogenic composition for eliciting in a  
XX mammal an immunogenic response directed against any of the purified  
XX polypeptide. The purified polypeptide, or the antibody that binds to this  
XX polypeptide, is useful for treating cancer. The polypeptide is also  
XX useful for identifying compounds that binds to a naturally processed

CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 10 AA;

Query Match 37.1%; Score 49; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.84;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 KDVLEFTTVK 12  
| | | | | | | |  
Db 1 KDVLEFTTVK 10

RESULT 5  
AAM83184  
ID AAM83184 standard; protein; 44 AA.

XX AC AAM83184;

XX DT 07-NOV-2001 (first entry)

XX DE Human immune/haematopoietic antigen SEQ ID NO:10777.

XX KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;  
KW cytostatic; gene therapy; vaccine; metastasis.

XX OS Homo sapiens.

XX PN WO200157182-A2.

XX PD 09-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US001354.

XX PR 31-JAN-2000; 2000US-0179065P.

XX PR 04-FEB-2000; 2000US-0180628P.

XX PR 24-FEB-2000; 2000US-0184564P.

XX PR 02-MAR-2000; 2000US-0186350P.

XX PR 16-MAR-2000; 2000US-0189874P.

XX PR 17-MAR-2000; 2000US-0190076P.

XX PR 18-APR-2000; 2000US-0198123P.

XX PR 19-MAY-2000; 2000US-0205515P.

XX PR 07-JUN-2000; 2000US-0209467P.

XX PR 28-JUN-2000; 2000US-0214886P.

XX PR 30-JUN-2000; 2000US-0215135P.

XX PR 07-JUL-2000; 2000US-0216647P.

XX PR 07-JUL-2000; 2000US-0216800P.

XX PR 11-JUL-2000; 2000US-0217487P.

XX PR 14-JUL-2000; 2000US-0218290P.

XX PR 26-JUL-2000; 2000US-0220963P.

XX PR 26-JUL-2000; 2000US-0220964P.

XX PR 14-AUG-2000; 2000US-0224518P.

XX PR 14-AUG-2000; 2000US-0224519P.

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XX PR 14-AUG-2000; 2000US-0225214P.

XX PR 14-AUG-2000; 2000US-0225266P.

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XX PR 14-AUG-2000; 2000US-0225268P.

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XX PR 14-AUG-2000; 2000US-0225447P.

XX PR 14-AUG-2000; 2000US-0225757P.

XX PR 14-AUG-2000; 2000US-0225758P.

XX PR 14-AUG-2000; 2000US-0225759P.

XX PR 18-AUG-2000; 2000US-0226279P.

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PR	05-SEP-2000;	2000US-02293455P.
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PR	06-SEP-2000;	2000US-02295133P.
PR	06-SEP-2000;	2000US-02304373P.
PR	08-SEP-2000;	2000US-02304388P.
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PR	26-SEP-2000;	2000US-02345844P.
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PR	02-OCT-2000;	2000US-02368022P.
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PR	17-NOV-2000;	2000US-0249207P.
PR	17-NOV-2000;	2000US-0249208P.
PR	17-NOV-2000;	2000US-0249209P.
PR	17-NOV-2000;	2000US-0249210P.
PR	17-NOV-2000;	2000US-0249211P.
PR	17-NOV-2000;	2000US-0249212P.
PR	17-NOV-2000;	2000US-0249213P.
PR	17-NOV-2000;	2000US-0249214P.
PR	17-NOV-2000;	2000US-0249215P.
PR	17-NOV-2000;	2000US-0249216P.
PR	17-NOV-2000;	2000US-0249217P.
PR	17-NOV-2000;	2000US-0249218P.
PR	17-NOV-2000;	2000US-0249244P.
PR	17-NOV-2000;	2000US-0249245P.
PR	17-NOV-2000;	2000US-0249264P.
PR	17-NOV-2000;	2000US-0249265P.
PR	17-NOV-2000;	2000US-0249297P.
PR	17-NOV-2000;	2000US-0249299P.
PR	01-DEC-2000;	2000US-0249300P.
PR	01-DEC-2000;	2000US-0250160P.
PR	01-DEC-2000;	2000US-0250391P.
PR	05-DEC-2000;	2000US-0251030P.
PR	05-DEC-2000;	2000US-0251988P.
PR	05-DEC-2000;	2000US-0256719P.
PR	06-DEC-2000;	2000US-0251479P.
PR	08-DEC-2000;	2000US-0251856P.
PR	08-DEC-2000;	2000US-0251868P.
PR	08-DEC-2000;	2000US-0251869P.
PR	08-DEC-2000;	2000US-0251989P.
PR	08-DEC-2000;	2000US-0251990P.
PR	11-DEC-2000;	2000US-0254097P.
PR	05-JAN-2001;	2001US-0255678P.
XX		
XX	(HUMA-) HUMAN GENOME SCI INC.	
PA		
XX		
PI	Rosen CA, Barash SC, Ruben SM;	
XX		
XX	WPI; 2001-483426/52.	
DR	N-FSDB; AAK5965.	
XX		
XX	Nucleic acids encoding human immune/hematopoietic antigen polypeptides,	
PT	useful for preventing, diagnosing and/or treating cancers and metastasis.	
PT		
XX		
PS	Claim 11; SEQ ID NO 10777; 3071pp + Sequence Listing; English.	
XX		
CC	AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)	
CC	amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic	
CC	activity, and can be used in gene therapy and vaccine production. (I)	
CC	proteins and polynucleotides may be used in the prevention, diagnosis and	
CC	treatment of diseases associated with inappropriate (I) expression. For	
CC	example, they may be used to treat disorders associated with decreased	
CC	expression by rectifying mutations or deletions in a patient's genome	
CC	that affect the activity of (I) by expressing inactive proteins or to	
CC	supplement the patients own production of (I). Additionally, (I)	
CC	polynucleotides may be used to produce the secreted (I), by inserting the	
CC	nucleic acids into a host cell and culturing the cell to express the	
CC	protein. (I) proteins and polynucleotides may be used to prevent,	
CC	diagnose and treat immune/haematopoietic-related diseases, especially	
CC	cancers and cancer metastases of haematopoietic-derived cells. AAK64703	
CC	to AAK87694 represent human immune/haematopoietic antigen genomic	
CC	sequences from the present invention. AAK54942 to AAK54950 and AAM82169	
CC	represent sequences used in the exemplification of the present invention	
XX		
XX	Sequence 44 AA;	



RESULT 6  
AAU20329  
ID AAU20329 standard; protein; 41 AA.  
XX  
XX  
AC AAU20329;  
XX  
XX  
DT 17-DEC-2001 (first entry)  
XX  
XX  
DE Human novel endocrine antigen, SEQ ID NO 386.  
XX  
XX  
KW Human; endocrine antigen; cytostatic; antiinfertility; antidiabetic;  
KW thyroid-active; adrenal-active; androgenic; gastric; gene therapy;  
KW antisense-therapy; antibody; endocrine disorder; hormone imbalance;  
KW reproductive disorder; endocrine cancer; pancreatic disorder;  
KW diabetes mellitus; adrenal gland disorder; hirsutism; thyroid disorder;  
KW hyperthyroidism; hypothalamic disorder; vanishing testes syndrome.  
XX  
OS Homo sapiens.  
XX  
XX  
PN WO200155319-A2.  
XX  
XX  
PD 02-AUG-2001.  
XX  
XX  
PF 17-JAN-2001; 2001WO-US001335.  
XX  
XX  
PR 31-JAN-2000; 2000US-0179065P.  
PR 04-FEB-2000; 2000US-0180628P.  
PR 24-FEB-2000; 2000US-0184664P.  
PR 02-MAR-2000; 2000US-0186350P.  
PR 16-MAR-2000; 2000US-0189874P.  
PR 17-MAR-2000; 2000US-0190076P.  
PR 18-APR-2000; 2000US-0198123P.  
PR 19-MAY-2000; 2000US-0205515P.  
PR 07-JUN-2000; 2000US-0209477P.  
PR 28-JUN-2000; 2000US-0214886P.  
PR 30-JUN-2000; 2000US-0215135P.  
PR 07-JUL-2000; 2000US-0216647P.  
PR 07-JUL-2000; 2000US-0216880P.  
PR 11-JUL-2000; 2000US-0217487P.  
PR 11-JUL-2000; 2000US-0217496P.  
PR 14-JUL-2000; 2000US-0218290P.  
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PR 14-AUG-2000; 2000US-0220964P.  
PR 14-AUG-2000; 2000US-0224518P.  
PR 14-AUG-2000; 2000US-0224519P.  
PR 14-AUG-2000; 2000US-0225213P.  
PR 14-AUG-2000; 2000US-0225214P.  
PR 14-AUG-2000; 2000US-0225266P.  
PR 14-AUG-2000; 2000US-0225267P.  
PR 14-AUG-2000; 2000US-0225268P.  
PR 14-AUG-2000; 2000US-0225270P.  
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PR 14-AUG-2000; 2000US-0225757P.  
PR 14-AUG-2000; 2000US-0225758P.  
PR 14-AUG-2000; 2000US-0225759P.  
PR 18-AUG-2000; 2000US-0226279P.  
PR 22-AUG-2000; 2000US-0226681P.  
PR 22-AUG-2000; 2000US-0226688P.  
PR 22-AUG-2000; 2000US-0227182P.  
PR 23-AUG-2000; 2000US-0227009P.  
PR 30-AUG-2000; 2000US-0228924P.  
PR 01-SEP-2000; 2000US-0229287P.  
PR 01-SEP-2000; 2000US-0229343P.  
PR 01-SEP-2000; 2000US-0229344P.  
PR 01-SEP-2000; 2000US-0229345P.  
PR 05-SEP-2000; 2000US-0229509P.  
PR 05-SEP-2000; 2000US-0229513P.  
PR 06-SEP-2000; 2000US-0230437P.  
PR 06-SEP-2000; 2000US-0230438P.  
PR 08-SEP-2000; 2000US-0231242P.  
PR 08-SEP-2000; 2000US-0231243P.  
PR 08-SEP-2000; 2000US-0231244P.  
PR 08-SEP-2000; 2000US-0231413P.  
PR 08-SEP-2000; 2000US-0231414P.  
PR 08-SEP-2000; 2000US-0231415P.  
PR 08-SEP-2000; 2000US-0232080P.  
PR 12-SEP-2000; 2000US-0232081P.  
PR 14-SEP-2000; 2000US-0231968P.  
PR 14-SEP-2000; 2000US-0232397P.  
PR 14-SEP-2000; 2000US-0232398P.  
PR 14-SEP-2000; 2000US-0232399P.  
PR 14-SEP-2000; 2000US-0232400P.  
PR 14-SEP-2000; 2000US-0232401P.  
PR 14-SEP-2000; 2000US-0233063P.  
PR 14-SEP-2000; 2000US-0233064P.  
PR 14-SEP-2000; 2000US-0233065P.  
PR 21-SEP-2000; 2000US-0234223P.  
PR 21-SEP-2000; 2000US-0234274P.  
PR 25-SEP-2000; 2000US-0234977P.  
PR 25-SEP-2000; 2000US-0234998P.  
PR 26-SEP-2000; 2000US-0235484P.  
PR 27-SEP-2000; 2000US-0235834P.  
PR 27-SEP-2000; 2000US-0235836P.  
PR 29-SEP-2000; 2000US-0236327P.  
PR 29-SEP-2000; 2000US-0236367P.  
PR 29-SEP-2000; 2000US-0236368P.  
PR 29-SEP-2000; 2000US-0236369P.  
PR 29-SEP-2000; 2000US-0236370P.  
PR 02-OCT-2000; 2000US-0236802P.  
PR 02-OCT-2000; 2000US-0237037P.  
PR 02-OCT-2000; 2000US-0237038P.  
PR 02-OCT-2000; 2000US-0237039P.  
PR 13-OCT-2000; 2000US-0237040P.  
PR 13-OCT-2000; 2000US-0239935P.  
PR 13-OCT-2000; 2000US-0239937P.  
PR 20-OCT-2000; 2000US-0240960P.  
PR 20-OCT-2000; 2000US-0241221P.  
PR 20-OCT-2000; 2000US-0241785P.  
PR 20-OCT-2000; 2000US-0241786P.  
PR 20-OCT-2000; 2000US-0241787P.  
PR 20-OCT-2000; 2000US-0241808P.  
PR 20-OCT-2000; 2000US-0241809P.  
PR 20-OCT-2000; 2000US-0241826P.  
PR 01-NOV-2000; 2000US-0244617P.  
PR 08-NOV-2000; 2000US-0246474P.  
PR 08-NOV-2000; 2000US-0246475P.  
PR 08-NOV-2000; 2000US-0246476P.  
PR 08-NOV-2000; 2000US-0246477P.  
PR 08-NOV-2000; 2000US-0246478P.  
PR 08-NOV-2000; 2000US-0246523P.  
PR 08-NOV-2000; 2000US-0246524P.  
PR 08-NOV-2000; 2000US-0246525P.  
PR 08-NOV-2000; 2000US-0246526P.  
PR 08-NOV-2000; 2000US-0246527P.  
PR 08-NOV-2000; 2000US-0246528P.  
PR 08-NOV-2000; 2000US-0246532P.  
PR 08-NOV-2000; 2000US-0246609P.  
PR 08-NOV-2000; 2000US-0246610P.  
PR 08-NOV-2000; 2000US-0246611P.  
PR 08-NOV-2000; 2000US-0246613P.  
PR 17-NOV-2000; 2000US-0249207P.  
PR 17-NOV-2000; 2000US-0249208P.  
PR 17-NOV-2000; 2000US-0249209P.  
PR 17-NOV-2000; 2000US-0249210P.  
PR 17-NOV-2000; 2000US-0249211P.  
PR 17-NOV-2000; 2000US-0249212P.  
PR 17-NOV-2000; 2000US-0249213P.  
PR 17-NOV-2000; 2000US-0249214P.  
PR 17-NOV-2000; 2000US-0249215P.  
PR 17-NOV-2000; 2000US-0249216P.  
PR 17-NOV-2000; 2000US-0249217P.  
PR 17-NOV-2000; 2000US-0249218P.  
PR 17-NOV-2000; 2000US-0249244P.  
PR 17-NOV-2000; 2000US-0249245P.  
PR 17-NOV-2000; 2000US-0249264P.  
PR 17-NOV-2000; 2000US-0249265P.

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PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI
XX WPI; 2001-457726/49.
DR N-PSDB; AAS32432.
DR
XX
XX Isolated polypeptide for treating, preventing and prognosing disorders
PT related to the endocrine system including endocrine disorders,
PT reproductive disorders, and gastrointestinal disorders and also for
PT testing and detection e.g. diagnosis.
XX
XX Claim 11; SEQ ID NO 386; 558pp; English.
XX
XX The invention relates to cDNAs encoding novel human endocrine antigens or
CC a fragment having biological activity, a domain, an epitope, full length
CC protein, variant, allelic variant or a species homologue of the
CC cDNA/antigen. The DNAs and polypeptides are useful for preventing,
CC treating or ameliorating a medical condition when administered (e.g. by
CC gene therapy or antisense-therapy). Identifying mutations in the genes
CC coding for the antigens is useful for diagnosing a pathological condition
CC or a susceptibility to a pathological condition. The DNAs, antigens and
CC antibodies raised against the antigens useful for treating, preventing
CC and/or prognosing disorders related to the endocrine system or hormone
CC imbalance or reproductive disorders, cancers of endocrine tissues,
CC disorders of the pancreas (e.g. diabetes mellitus), the adrenal glands
CC (e.g. hirsutism), ovaries, the thyroid (e.g. hyperthyroidism), the
CC hypothalamus and testes (e.g. vanishing testes syndrome), many examples
CC of diseases and disorders are given in the specification. The present
CC sequence represents an endocrine antigen of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 41 AA;
SQ
Query Match 29.5%; Score 39; DB 4; Length 41;
Best Local Similarity 28.6%; Pred. No. 1.8e+02;
Matches 6; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 PKQVLETFVXSCPDPAIKEV 21
DB 5 PHREIFVFYFTRPAPDVSKHL 25

RESULT 7
ADY51925
ID ADY51925 standard; protein; 46 AA.
XX
AC ADY51925;
XX
DT 19-MAY-2005 (first entry)
XX
DE Phage SPO1 antibacterial protein encoded by gene 54.
XX
XX Phage; metabolism; bacterial infection; antibacterial; infection.
KW

XX OS Bacteriophage SPO1.
XX US2005054571-A1.
XX 10-MAR-2005.
XX
XX 25-MAR-2004; 2004US-00809761.
XX
XX 25-MAR-2003; 2003US-0457287P.
XX (RICV ) UNIV RICE.
XX
XX Stewart CR, Shamoo AY;
XX WPI; 2005-202229/21.
XX
XX New expression vector encoding at least one peptide whose expression is
PT controlled by a tightly regulated inducible promoter, useful for treating
PT patients with bacterial infection.
XX
XX Claim 1; SEQ ID NO 18; 36pp; English.
XX
XX The invention relates to an expression vector encoding at least one
CC peptide comprising any of 22 fully defined sequences appearing as
CC ADY51908-ADY51912, ADY51914-ADY51917 or ADY51919-ADY51931), or a sequence
CC having 95% identity to the amino acid sequences, where expression of the
CC peptide is controlled by a tightly regulated, inducible promoter. The
CC proteins are antibacterial proteins from bacteriophage SPO1, encoded by
CC the host-takeover module genes. Also included are a protein comprising
CC any of ADY51908-ADY51912, ADY51914-ADY51917 or ADY51919-ADY51931 (or a
CC sequence with 95% sequence identity to the amino acid sequences in part,
CC where the protein is anti-bacterial, is purified and made by recombinant
CC technology or by peptide synthesis), treating infection (comprising
CC identifying a bacterial infection, in vivo delivery of anti-bacterial
CC protein to a warm blooded animal having a bacterial infection to treat
CC the bacterial infection), designing an anti-bacterial peptidomimetic
CC (comprising isolating the protein, determining the three dimensional
CC structure of the protein, identifying the functional site of the protein,
CC designing a drug that mimics the structure of the active site of the
CC protein, and testing the drug for anti-bacterial activity), inhibiting
CC bacterial infection (comprising identifying the presence of a bacteria
CC in a mammal, and administering to the mammal the protein or a
CC peptidomimetic small molecule which mimics the activity of the protein)
CC and identifying potential targets for antibiotic action (comprising
CC selecting bacterial mutants resistant to the lethal activity of the
CC protein and their variants, identifying the genes in which such resistant
CC mutations are located, and demonstrating by physical and/or genetic
CC techniques an interaction between each lethal protein and its putative
CC target). The methods and compositions of the present invention are useful
CC for treating patients with bacterial infection through the introduction
CC of proteins, peptide fragments, peptidomimetics or genes encoding them
CC into the bacteria infecting the patient. The present sequence is an
CC antibacterial protein of the invention.
XX
XX Sequence 46 AA;
SQ
Query Match 28.8%; Score 38; DB 9; Length 46;
Best Local Similarity 38.9%; Pred. No. 2.9e+02;
Matches 7; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 5 VLETFVXSCPDPAIKEVF 22
DB 2 VIIRYTKTQTPVKEMF 19

RESULT 8
ABB39440
ID ABB39440 standard; peptide; 33 AA.
XX
XX ABB39440;
XX
XX 04-FEB-2002 (first entry)
DT

```

XX Peptide #6946 encoded by human foetal liver single exon probe.  
DE Human; foetal liver; gene expression; single exon nucleic acid probe.  
KW Homo sapiens.  
OS  
XX WO200157277-A2.  
PN  
XX  
XX 09-AUG-2001.  
XX  
XX 30-JAN-2001; 2001WO-US000669.  
XX  
XX 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
PI  
XX WPI; 2001-483447/52.  
XX  
XX Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human fetal liver.  
XX  
XX Claim 27; SEQ ID NO 32075; 639pp + Sequence Listing; English.  
XX  
XX The invention relates to a single exon nucleic acid probe for measuring  
CC human gene expression in a sample derived from human foetal liver. The  
CC single exon nucleic acid probes may be used for predicting, measuring and  
CC displaying gene expression in samples derived from human fetal liver. The  
CC present sequence is a peptide encoded by a single exon nucleic acid probe  
CC of the invention. Note: The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 33 AA;  
SQ  
Query Match 27.3%; Score 36; DB 4; Length 33;  
Best Local Similarity 36.8%; Pred. No. 4.1e+02;  
Matches 7; Conservative 5; Mismatches 7; Indels 0; Gaps 0;  
XX  
QY 4 DVLETTFTVKSCPDPAIKEVF 22  
Db 3 NMLSTASITMLPFGCLKKEVF 21  
RESULT 9  
ARM32967  
ID RAM32967 standard; protein; 33 AA.  
XX  
XX ARM32967;  
XX  
XX 17-OCT-2001 (first entry)  
XX  
XX Peptide #7004 encoded by probe for measuring placental gene expression.  
DE  
XX  
XX Probe; microarray; human; placenta; antenatal diagnosis;  
KW genetic disorder.  
XX  
XX Homo sapiens.  
OS  
XX WO200157272-A2.  
PN  
XX  
XX 09-AUG-2001.  
XX  
XX 30-JAN-2001; 2001WO-US000663.  
XX

PR 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
PI  
XX WPI; 2001-488897/53.  
XX  
XX Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human placenta.  
XX  
XX Claim 27; SEQ ID NO 33236; 654pp; English.  
XX  
XX The present invention relates to single exon nucleic acid probes (SENP;  
CC see AA131315-AA157546). The present sequence is a peptide encoded by one  
CC such probe. The probes are useful for producing a microarray for  
CC predicting, measuring and displaying gene expression in samples derived  
CC from human placenta. The probes are useful for antenatal diagnosis of  
CC human genetic disorders  
XX  
XX Sequence 33 AA;  
SQ  
Query Match 27.3%; Score 36; DB 4; Length 33;  
Best Local Similarity 36.8%; Pred. No. 4.1e+02;  
Matches 7; Conservative 5; Mismatches 7; Indels 0; Gaps 0;  
XX  
QY 4 DVLETTFTVKSCPDPAIKEVF 22  
Db 3 NMLSTASITMLPFGCLKKEVF 21  
RESULT 10  
AAM72739  
ID AAM72739 standard; protein; 33 AA.  
XX  
XX AAM72739;  
XX  
XX 06-NOV-2001 (first entry)  
XX  
XX Human bone marrow expressed probe encoded protein SEQ ID NO: 33045.  
DE  
XX  
XX Human; bone marrow expressed exon; gene expression analysis; probe;  
KW microarray; cancer; leukaemia; lymphoma; myeloma.  
XX  
XX Homo sapiens.  
OS  
XX WO200157276-A2.  
PN  
XX  
XX 09-AUG-2001.  
XX  
XX 30-JAN-2001; 2001WO-US000668.  
XX  
XX 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
PI  
XX WPI; 2001-488900/53.  
XX  
XX Human genome-derived single exon nucleic acid probes useful for analyzing  
PT

PT gene expression in human bone marrow.

XX Example 4; SEQ ID NO 33045; 659pp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid  
 CC probes which are derived from genomic sequences expressed in the human  
 CC bone marrow. They can be used to measure gene expression in bone marrow  
 CC samples, which may enable the improved diagnosis and treatment of cancers  
 CC such as lymphoma, leukaemia and myeloma. The present sequence is a  
 CC protein encoded by one of the probes of the invention  
 XX  
 XX Sequence 33 AA;

Query Match 27.3%; Score 36; DB 4; Length 33;

Best Local Similarity 36.8%; Pred. No. 4.1e+02;  
 Matches 7; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 4 DVLETFVKSCPDAIKEVF 22

Db 3 NMLSTASITMLPFGLEKEVF 21

RESULT 11

AAM60125

ID AAM60125 standard; protein; 33 AA.

XX AC AAM60125;

XX DT 05-NOV-2001 (first entry)

XX Human brain expressed single exon probe encoded protein SEQ ID NO: 32230.

XX Human; brain expressed exon; gene expression analysis; probe; microarray;  
 KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.

XX OS Homo sapiens.

XX PN WO200157275-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000667.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX DR WPI; 2001-483446/52.

XX Single exon nucleic acid probes for analyzing gene expression in human  
 PT brains.  
 XX Example 4; SEQ ID NO 32230; 650pp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid  
 CC probes which are derived from genomic sequences expressed in the human  
 CC brain. They can be used to measure gene expression in brain cell samples,  
 CC which may enable the diagnosis and improved treatment of nervous system  
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,  
 CC epilepsy and cancers. The present sequence is a protein encoded by one of  
 CC the probes of the invention  
 XX  
 XX Sequence 33 AA;

Query Match 27.3%; Score 36; DB 4; Length 33;

Best Local Similarity 36.8%; Pred. No. 4.1e+02;  
 Matches 7; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 4 DVLETFVKSCPDAIKEVF 22

Db 3 NMLSTASITMLPFGLEKEVF 21

RESULT 12

ABG54437

ID ABG54437 standard; peptide; 33 AA.

XX AC ABG54437;

XX DT 25-FEB-2003 (first entry)

XX Human liver peptide, SEQ ID NO 33085.

XX Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;  
 KW hypercholesterolaemia; coronary heart disease.

XX OS Homo sapiens.

XX PN WO200157273-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000664.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX DR WPI; 2001-488898/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing  
 PT gene expression in human adult liver.

XX PS Claim 27; SEQ ID NO 33085; 658pp; English.

XX The invention relates to a single exon nucleic acid probe (SENP) (I) for  
 CC measuring human gene expression in a sample derived from human adult  
 CC liver, comprising one of 13109 defined nucleotide sequences given in the  
 CC specification (or complements/ fragments). The probe hybridises at high  
 CC stringency to a nucleic acid molecule expressed in the human adult liver.  
 CC (I) may be used for predicting, measuring and displaying gene expression  
 CC in samples derived from human adult liver. The genes identified may be  
 CC involved in genetic liver diseases such as cirrhosis,  
 CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is  
 CC associated with coronary heart disease. ABG47348-ABG59930 represent human  
 CC liver single exon encoded peptides of the invention. Note: The sequence  
 CC information for this patent does not appear in the printed specification  
 CC but was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 33 AA;

Query Match 27.3%; Score 36; DB 4; Length 33;

Best Local Similarity 36.8%; Pred. No. 4.1e+02;  
 Matches 7; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 4 DVLETFVKSCPDAIKEVF 22

Db 3 NMLSTASITMLPFGLEKEVF 21

RESULT 13  
 ABG42563  
 ID ABG42563 standard; peptide; 33 AA.  
 XX  
 AC ABG42563;  
 XX  
 DT 19-AUG-2002 (first entry)  
 XX  
 DE Human peptide encoded by genome-derived single exon probe SEQ ID 32228.  
 XX  
 KW Human; single exon probe; asthma; lung cancer; COPD; ILD;  
 KW chronic obstructive pulmonary disease; interstitial lung disease;  
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;  
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;  
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;  
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;  
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;  
 KW primary ciliary dyskinesia; pulmonary hypertension;  
 KW hyaline membrane disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200186003-A2.  
 XX  
 PD 15-NOV-2001.  
 XX  
 XX 30-JAN-2001; 2001WO-US000665.  
 XX  
 PR 04-FEB-2000; 2000US-0180312P.  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX  
 XX WPI; 2002-114183/15.  
 XX  
 PT Spatially-addressable set of single exon nucleic acid probes, used to  
 PT measure gene expression in human lung samples.  
 XX  
 PS Claim 27; SEQ ID NO 32228; 634pp; English.  
 XX  
 CC The invention relates to a spatially-addressable set of single exon  
 CC nucleic acid probes for measuring gene expression in a sample derived  
 CC from human lung comprising single exon nucleic acid probes having one of  
 CC 12614 nucleic acid sequences mentioned in the specification, or their  
 CC complements or the 12387 open reading frames derived from the 12614  
 CC probes. Also included are a microarray comprising the novel set of probes  
 CC ; the novel set of probes which hybridise at high stringency to a nucleic  
 CC acid expressed in the human lung; measuring gene expression in a sample  
 CC derived from human lung, comprising (a) contacting the array with a  
 CC collection of detectably labeled nucleic acids derived from human lung  
 CC mRNA, and (b) measuring the label detectably bound to each probe of the  
 CC array; identifying exons in a eukaryotic genome, comprising (a)  
 CC algorithmically predicting at least one exon from genomic sequences of  
 CC the eukaryote; and (b) detecting specific hybridisation of detectably  
 CC labeled nucleic acids from eukaryote lung mRNA to a single exon probe,  
 CC having a fragment identical to the predicted exon, the probe is included  
 CC in the above mentioned microarray; assigning exons to a single gene,  
 CC comprising (a) identifying exons from genomic sequence by the method  
 CC above and (b) measuring the expression of each of the exons in several  
 CC tissues and/or cell types using hybridisation to a single exon  
 CC microarrays having a probe with the exon, where a common pattern of  
 CC expression of the exons in the tissues and/or cell types indicates that  
 CC the exons should be assigned to a single gene; a peptide comprising one  
 CC of 12011 sequences, mentioned in the specification, or encoded by the  
 CC probes/open reading frames (ORF). The probes are used for gene expression

CC analysis, and for identifying exons in a gene, particularly using human  
 CC lung derived mRNA and for the study of lung diseases such as asthma, lung  
 CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung  
 CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,  
 CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-  
 CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary  
 CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,  
 CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary  
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The  
 CC present sequence is a peptide/protein encoded by a single exon probe of  
 CC the invention. Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 33 AA;  
 Query Match 27.3%; Score 36; DB 5; Length 33;  
 Best Local Similarity 36.8%; Pred. No. 4.1e+02;  
 Matches 7; Conservative 5; Mismatches 7; Indels 0; Gaps 0;  
 QY 4 DVLETFVKSCPDPAIKEVF 22  
 Db 3 NMLSTASITWLPGLKEVF 21  
 RESULT 14  
 AAY92549  
 ID AAY92549 standard; peptide; 34 AA.  
 XX  
 AC AAY92549;  
 XX  
 DT 10-AUG-2000 (first entry)  
 XX  
 DE Finger 2 subdomain of TGF-beta3.  
 XX  
 KW finger 2 subdomain; BMP; TGF-beta family; protein refolding;  
 KW fusion protein; osteopathic; antibacterial; cytostatic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200020449-A2.  
 XX  
 PD 13-APR-2000.  
 XX  
 PF 07-OCT-1999; 99WO-US023372.  
 XX  
 PR 07-OCT-1998; 98US-0103418P.  
 PR 16-AUG-1999; 99US-00375333.  
 XX  
 PA (STYC ) STRYKER CORP.  
 XX  
 PI Oppermann H, Tai M, McCartney J;  
 XX  
 XX WPI; 2000-303743/26.  
 XX  
 PT A biologically active TGF-beta family member fusion protein competent to  
 PT refold, comprising a C-terminal linked TGF-beta family protein.  
 XX  
 PS Disclosure; Page 131; 160pp; English.  
 XX  
 CC AAY92519-53 are C-terminal residues of the finger 2 subdomain of various  
 CC known members of the BMP and TGF-beta families, starting with the first  
 CC residue following the cysteine doublet. Novel proteins comprise  
 CC biologically active TGF-beta family member fusion proteins competent to  
 CC refold under suitable refolding conditions. The fusion proteins comprise:  
 CC (1) a TGF-beta family protein C-terminal seven cysteine domain,  
 CC comprising finger 1, finger 2 and heel subdomains; and (2) a heterologous  
 CC leader sequence domain operatively linked to the C-terminal domain.  
 CC Truncations, heterodimers and mutants of these fusion proteins and  
 CC methods of purifying the heterodimers are also claimed. The TGF-beta  
 CC family proteins can be used to induce the full cascade of morphogenic  
 CC events which culminate in skeletal tissue formation, including cartilage  
 CC and endochondral bone formation. They are useful in the binding of fibrin

CC and fibronectin to the implanted matrix, chemotaxis of cells.  
 CC proliferation of fibroblasts, differentiation into chondroblasts,  
 CC cartilage formation, vascular invasion, bone formation, remodeling, and  
 CC bone marrow differentiation. The proteins have improved physical  
 CC properties such as solubility and stability, improved biological  
 CC activity, including altered receptor binding and improved targeting  
 CC capabilities

XX SQ Sequence 34 AA;  
 Query Match 27.3%; Score 36; DB 3; Length 34;  
 Best Local Similarity 50.0%; Pred. No. 4.2e+02;  
 Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKQDVLETFVTKSC 14  
 || : | ||||  
 Db 18 PKVEQLSNMVRKSC 31

RESULT 15  
 AAB02778  
 ID AAB02778 standard; protein; 34 AA.

XX AC AAB02778;  
 XX DT 22-AUG-2000 (first entry)

XX DE Human TGF-beta3 finger 2 sub-domain sequence SEQ ID NO:31.

XX KW Tumour growth factor beta; TGF-beta; morphogenic protein; BMP; OP;  
 KW bone morphogenic protein; osteogenic protein; mutant; modified;  
 KW finger 2 sub-domain; finger 1 domain; heel domain; chimeric protein;  
 KW osteogenic; proliferative; antiinflammatory; tissue morphogenesis;  
 KW tissue repair; regeneration; proliferation; differentiation.

XX OS Homo sapiens.  
 XX WO200020591-A2.  
 XX PD 13-APR-2000.

XX PF 07-OCT-1999; 99WO-US023370.  
 XX PR 07-OCT-1998; 98US-0103418P.  
 XX PR 16-AUG-1999; 99US-00374936.

XX PA (STYC ) STRYKER CORP.  
 XX PI Oppermann H, Tai M, Mccartney J;  
 XX DR WPI; 2000-303776/26.

XX Novel TGF-beta superfamily mutant chimeric protein, useful for inducing  
 PT tissue morphogenesis in e.g. bone, comprises a dimer consisting of one  
 PT monomer containing domains from two family members.  
 XX Disclosure; Page 120; 149pp; English.

XX The present invention describes a tumour growth factor beta (TGF-beta)  
 CC superfamily chimeric protein (I) derived from at least 2 different  
 CC members of the superfamily comprising a dimer with one monomer that  
 CC contains a finger 2 domain derived from a first family member and a  
 CC finger 1 domain and heel domain, both derived from a second family  
 CC member. The monomer further comprises a conserved C-terminal cysteine  
 CC skeleton. (I) has osteogenic, proliferative and antiinflammatory  
 CC activities. The TGF-beta superfamily chimeric proteins (I) are useful for  
 CC inducing tissue morphogenesis (i.e. molecules capable of tissue repair  
 CC and regeneration and/or inhibiting inflammation) in bone, non-mineralised  
 CC skeletal tissue, dental tissue, connective tissue, brain, liver and nerve  
 CC and for inducing the proliferation and differentiation of uncommitted  
 CC progenitor cells in a tissue-specific manner to support new tissue  
 CC formation. AAA29887 to AAA29897 and AAB02748 to AAB02824 represent  
 CC sequences used in the exemplification of the present invention

XX SQ

Sequence 34 AA;

Query Match 27.3%; Score 36; DB 3; Length 34;  
 Best Local Similarity 50.0%; Pred. No. 4.2e+02;  
 Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKQDVLETFVTKSC 14  
 || : | ||||  
 Db 18 PKVEQLSNMVRKSC 31

RESULT 16  
 AAW30357  
 ID AAW30357 standard; peptide; 36 AA.

XX AC AAW30357;  
 XX DT 11-FEB-1998 (first entry)

XX DE Fragment #2 of growth factor TGFbeta3.

XX KW Neurturin; human; haematopoietic cell; neuronal cell; stem cell; NT gene;  
 KW neurodegenerative disease; peripheral neuropathy; nervous system tumour;  
 KW amyotrophic lateral sclerosis; Alzheimer's disease; Parkinson's disease;  
 KW Huntington's disease; ischaemic stroke; acute brain injury; basopaenia;  
 KW acute spinal cord injury; multiple sclerosis; eosinopaenia; lymphopaenia;  
 KW monocytopenia; neutropaenia; anaemia; thrombocytopenia; neuroblastoma;  
 KW antibody; obesity; therapy; transforming growth factor beta; TGFbeta3;  
 KW growth factor; hybrid protein.

XX OS Homo sapiens.  
 XX WO9708196-A1.  
 XX PN 06-MAR-1997.

XX PF 27-AUG-1996; 96WO-US014065.  
 XX PR 28-AUG-1995; 95US-00519777.

XX PA (UNIW ) UNIV WASHINGTON.  
 XX PI Johnson EM, Milbrandt JD, Kotzbauer PT, Lampe PA;  
 XX DR WPI; 1997-179176/16.

XX A novel growth factor Neurturin - used to treat neuro-degenerative and  
 PT haematopoietic cell degeneration diseases, e.g. Alzheimer's disease and  
 PT eosinopenia.  
 XX Claim 92; Fig 18; 206pp; English.

XX AAW30355-W30377 represent growth factor fragments that are used in a  
 CC hybrid polypeptide of the invention. These sequences form a hybrid with  
 CC the human neurturin (NT) fragment shown in AAW30354. NT promotes the  
 CC growth and differentiation of haematopoietic and neuronal cells, and  
 CC their stem cells. The NT gene and protein are used to prevent or treat  
 CC neurodegenerative diseases e.g. peripheral neuropathy, amyotrophic  
 CC lateral sclerosis, Alzheimer's disease, Parkinson's disease, Huntingdon's  
 CC disease, ischaemic stroke, acute brain injury, acute spinal cord injury,  
 CC nervous system tumours, multiple sclerosis and infection; and  
 CC haematopoietic cell degenerative diseases, e.g. eosinopenia, basopaenia,  
 CC lymphopaenia, monocytopenia, neutropaenia, anaemia, thrombocytopenia  
 CC and stem cell insufficiencies. The NT protein and gene are also useful to  
 CC treat neuroblastomas. Antibodies against NT and oligonucleotides (used as  
 CC either probes or primers, corresponding to an exon of pre-pro-NT gene or  
 CC flanking a target sequence) can be used for detecting NT in a sample or  
 CC detecting mutations in the NT gene. Antisense sequences of the NT gene  
 CC are used to treat diseases promoted by NT expression e.g. obesity

XX SQ Sequence 36 AA;

Query Match 27.3%; Score 36; DB 2; Length 36;  
Best Local Similarity 50.0%; Pred. No. 4.5e+02;  
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKKDVLETFVVKSC 14  
||| : |||||  
Db 20 PKVEQLSNMVKSC 33

RESULT 17  
AAB09511  
ID AAB09511 standard; peptide; 36 AA.  
XX AAB09511;  
XX  
XX  
XX 11-SEP-2000 (first entry)  
XX  
XX Human TGF-beta 3 finger 2 subdomain.  
XX  
XX TGF-beta superfamily; transforming growth factor-beta;  
KW developmental regulation; finger 2 subdomain; basic region;  
KW protein refolding; stability; solubility; osteogenic protein; OP;  
KW bone morphogenetic protein; BMP; growth/differentiation factor; GDF;  
KW inhibin; tissue morphogenesis; regeneration; bone; dental tissue;  
KW connective tissue; cartilage; vulvular.  
XX  
XX Homo sapiens.  
XX  
XX W0200020607-A2.  
XX  
XX 13-APR-2000.  
XX  
XX 07-OCT-1999; 99WO-US023371.  
XX  
XX 07-OCT-1998; 98US-0103418P.  
XX  
XX 16-AUG-1999; 99US-00374958.  
XX  
XX (STYC ) STRYKER CORP.  
XX  
XX Oppermann H, Tai M, McCartney J;  
XX  
XX WPI; 2000-303787/26.  
XX  
XX  
XX Transforming growth factor-beta superfamily member mutant induces tissue  
PT morphogenesis in e.g. bone, non-mineralized skeletal tissue, dental  
PT tissue and connective tissue and comprises a substitution in a region of  
PT the finger 2 domain.  
XX  
XX Disclosure; Fig 1; 162pp; English.

CC The invention relates to mutant TGF-beta (transforming growth factor-  
CC beta) superfamily members. These mutants comprise one or more amino acid  
CC substitutions in the base region of the finger 2 subdomain, and a C-  
CC terminal residue selected from Arg, Ile, Leu, Ser and Ala. In the finger  
CC 2 subdomain, basic residues (e.g., Arg, Lys), or residues containing an  
CC amide group (e.g., Gln, Asn), are substituted with acidic residues (e.g.,  
CC Glu, Asp) or residues containing a hydroxyl group (e.g., Ser, Thr). TGF-  
CC beta superfamily proteins regulate developmental processes and include  
CC proteins such as the osteogenic proteins (OPs), bone morphogenetic  
CC proteins (BMPs), growth/differentiation factors (GDFs) and inhibitors.  
CC Specific examples of TGF-beta superfamily mutants encompassed by the  
CC invention are the finger 2 subdomain mutants of human osteogenic protein-  
CC 1 (OP-1) (AAB09576-B03615). Mutant TGF-beta proteins are used for  
CC inducing tissue morphogenesis in bone, non-mineralised skeletal tissue,  
CC dental tissue, connective tissue, brain, liver and nerve tissue. The  
CC proteins can be used in conjunction with a biocompatible matrix e.g.,  
CC collagen, hydroxyapatite or carboxymethylcellulose for regenerating bone,  
CC cartilage and/or other mineralised skeletal or connective tissues e.g.,  
CC ligament, tendon, muscle, fibrocartilage, joint capsule and  
CC intervertebral discs. The OP-1 mutants can be used to repair diseased or  
CC damaged mammalian tissue and to prevent or substantially inhibit  
CC immune/inflammatory response-mediated tissue damage and scar tissue  
CC formation following an injury. Compared to the wild-type TGF-beta

CC superfamily members, the mutant proteins have improved in vitro refolding  
CC properties in a pH range of 6-9, increased solubility in aqueous solution  
CC and improved stability and/or activity. Sequences AAB09481-B09516  
CC represent wild-type finger 2 subdomains from a variety of TGF-beta  
CC superfamily proteins referred to in the specification

XX  
SQ Sequence 36 AA;

Query Match 27.3%; Score 36; DB 3; Length 36;  
Best Local Similarity 50.0%; Pred. No. 4.5e+02;  
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKKDVLETFVVKSC 14  
||| : |||||  
Db 20 PKVEQLSNMVKSC 33

RESULT 18  
ADJ81051  
ID ADJ81051 standard; protein; 39 AA.  
XX  
XX ADJ81051;  
XX  
XX 06-MAY-2004 (first entry)  
XX  
XX INSP010 protein sequence exon 29.  
XX  
XX  
XX cytotatic; immunosuppressive; antiinflammatory; cardiant;  
KW neuroprotective; antimicrobial; gene therapy; mucin-like protein;  
KW cystine knot; diagnosis; cell proliferative disorder;  
KW autoimmune disorder; inflammatory disorder; cardiovascular disorder;  
KW neurological disorder; developmental disorder; metabolic disorder.  
XX  
XX Homo sapiens.  
XX  
XX W02003051919-A1.  
XX  
XX 26-JUN-2003.  
XX  
XX 19-DEC-2002; 2002WO-GB005811.  
XX  
XX 19-DEC-2001; 2001GB-00030384.  
XX  
XX (ARES-) ARES TRADING SA.  
XX  
XX Davies MD, Fegan RJ, Phelps CB, Power C;  
XX  
XX WPI; 2003-532999/50.  
XX  
XX N-PSDB; ADJ81050.

CC Novel isolated INSP010 polypeptide which is a secreted protein of the  
CC mucin subfamily of cystine knot containing proteins useful for treating  
CC cell proliferative disorders, autoimmune/inflammatory disorders.  
XX  
XX Example 2; SEQ ID NO 110; 147pp; English.

PS The invention relates to secreted mucin-like protein (INSP009, INSP010  
CC and INSP011), members of a mucin subfamily of cystine knot containing  
CC proteins. The proteins are useful for therapy or diagnosis of a disease  
CC such as cell proliferative disorders, autoimmune/inflammatory disorders,  
CC cardiovascular disorders, neurological disorders, developmental  
CC disorders, metabolic disorders, infections and other pathological  
CC conditions. This sequence corresponds to a protein sequence of the  
CC invention.

XX  
SQ Sequence 39 AA;

Query Match 27.3%; Score 36; DB 7; Length 39;  
Best Local Similarity 41.2%; Pred. No. 5e+02;  
Matches 7; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 7 EFTTVKSCPDAIKEVPD 23  
||| : |||







DT 05-NOV-2001 (first entry)  
XX Human brain expressed single exon probe encoded protein SEQ ID NO: 37477.  
DE Human; brain expressed exon; gene expression analysis; probe; microarray;  
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.  
KW Homo sapiens.  
OS WO200157275-A2.  
XX 09-AUG-2001.  
XX 30-JAN-2001; 2001WO-US000667.  
XX 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
PI WPI; 2001-483446/52.  
XX Single exon nucleic acid probes for analyzing gene expression in human  
PT brains.  
XX Example 4; SEQ ID NO 37477; 650pp + Sequence Listing; English.  
XX The present invention provides a number of single exon nucleic acid  
CC probes which are derived from genomic sequences expressed in the human  
CC brain. They can be used to measure gene expression in brain cell samples,  
CC which may enable the diagnosis and improved treatment of nervous system  
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,  
CC epilepsy and cancers. The present sequence is a protein encoded by one of  
CC the probes of the invention  
XX  
SQ Sequence 41 AA;  
Query Match 26.9%; Score 35.5; DB 4; Length 41;  
Best Local Similarity 42.9%; Pred. No. 6.4e+02;  
Matches 9; Conservative 6; Mismatches 5; Indels 1; Gaps 1;  
QY 1 PKKDVLTF-TVKSCPDIAKE 20  
Db 19 PKEDHLEGFLEVQAKKEAVKD 39  
RESULT 22  
ABG59698  
ID ABG59698 standard; peptide; 41 AA.  
XX ABG59698;  
XX 25-FEB-2003 (first entry)  
XX Human liver peptide, SEQ ID No 38346.  
DE Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;  
KW hypercholesterolaemia; coronary heart disease.  
XX Homo sapiens.  
OS WO200157273-A2.  
XX 09-AUG-2001.  
XX 30-JAN-2001; 2001WO-US000664.  
XX  
XX 05-NOV-2001 (first entry)  
PR Human brain expressed single exon probe encoded protein SEQ ID NO: 37477.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
PI WPI; 2001-488898/53.  
XX Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human adult liver.  
XX Claim 27; SEQ ID NO 38346; 658pp; English.  
XX The invention relates to a single exon nucleic acid probe (SENP) (I) for  
CC measuring human gene expression in a sample derived from human adult  
CC liver, comprising one of 13109 defined nucleotide sequences given in the  
CC specification (or complements/ fragments). The probe hybridizes at high  
CC stringency to a nucleic acid molecule expressed in the human adult liver.  
CC (I) may be used for predicting, measuring and displaying gene expression  
CC in samples derived from human adult liver. The genes identified may be  
CC involved in genetic liver diseases such as cirrhosis,  
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is  
CC associated with coronary heart disease. ABG47348-ABG59930 represent human  
CC liver single exon encoded peptides of the invention. Note: The sequence  
CC information for this patent does not appear in the printed specification  
CC but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 41 AA;  
Query Match 26.9%; Score 35.5; DB 4; Length 41;  
Best Local Similarity 42.9%; Pred. No. 6.4e+02;  
Matches 9; Conservative 6; Mismatches 5; Indels 1; Gaps 1;  
QY 1 PKKDVLTF-TVKSCPDIAKE 20  
Db 19 PKEDHLEGFLEVQAKKEAVKD 39  
RESULT 23  
ADL97737  
ID ADL97737 standard; protein; 42 AA.  
XX ADL97737;  
XX 17-JUN-2004 (first entry)  
XX Protein encoded by human transporter/channel protein INPIONCH10 exon 7.  
XX contraceptive; antiinflammatory; gastrointestinal; cardiac; antiangiinal;  
XX anorectic; antidiabetic; vasotropic; nephrotropic; antiinfertility;  
XX cytostatic; endocrine; gene therapy; vaccine; transporter;  
XX channel protein; diagnosis; contraceptive; colitis; hypertrophy;  
XX fibrosis; heart failure; myocardial infarction; angina; obesity;  
XX hyperinsulinemia; vascular disease; renal disease; fertility disorder;  
XX infertility; testosterone deficiency; testosterone-related disorder;  
XX testicular cancer; sexual dysfunction; exon.  
XX Homo sapiens.  
OS WO2004026905-A2.  
XX 01-APR-2004.  
XX 17-SEP-2003; 2003WO-GB004014.  
XX









```
QY      6 LETFTVKSCPDAIKEVFNK 25
Db      1 LQTTFWLCPYMKRKDSK 20

RESULT 33
ABG52136
ID      ABG52136 standard; peptide; 33 AA.
XX      AC
XX      ABG52136;
DT      25-FEB-2003 (first entry)
XX      DE
XX      Human liver peptide, SEQ ID No 30784.
XX      KW
XX      Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
XX      hypercholesterolaemia; coronary heart disease.
XX      OS
XX      Homo sapiens.
XX      PN
XX      WO200157273-A2.
XX      PD
XX      09-AUG-2001.
XX      PF
XX      30-JAN-2001; 2001WO-US000664.
XX      PR
XX      04-FEB-2000; 2000US-0180312P.
XX      26-MAY-2000; 2000US-0207456P.
XX      30-JUN-2000; 2000US-00608408.
XX      03-AUG-2000; 2000US-00632366.
XX      21-SEP-2000; 2000US-0234687P.
XX      27-SEP-2000; 2000US-0236359P.
XX      04-OCT-2000; 2000GB-00024263.
XX      PA
XX      (MOLE-) MOLECULAR DYNAMICS INC.
XX      PI
XX      Penn SG, Hanzel DK, Chen W, Rank DR;
XX      WPI; 2001-488998/53.
XX      DR
XX      Human genome-derived single exon nucleic acid probes useful for analyzing
XX      gene expression in human adult liver.
XX      PS
XX      Claim 27; SEQ ID NO 30784; 658pp; English.
XX      CC
XX      The invention relates to a single exon nucleic acid probe (SENP) (I) for
XX      measuring human gene expression in a sample derived from human adult
XX      liver, comprising one of 13109 defined nucleotide sequences given in the
XX      specification (or complements/ fragments). The probe hybridises at high
XX      stringency to a nucleic acid molecule expressed in the human adult liver.
XX      (i) may be used for predicting, measuring and displaying gene expression
XX      in samples derived from human adult liver. The genes identified may be
XX      involved in genetic liver diseases such as cirrhosis,
XX      hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
XX      associated with coronary heart disease. ABG47348-ABG59930 represent human
XX      liver single exon encoded peptides of the invention. Note: The sequence
XX      information for this patent does not appear in the printed specification
XX      but was obtained in electronic format directly from WIPO at
XX      ftp.wipo.int/pub/published_pct_sequences
XX      SQ
XX      Sequence 33 AA;

Query Match      26.5%; Score 35; DB 4; Length 33;
Best Local Similarity 40.0%; Pred. No. 5.9e+02;
Matches 8; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY      6 LETFTVKSCPDAIKEVFNK 25
Db      1 LQTTFWLCPYMKRKDSK 20

RESULT 34
ABG52136
ID      ABG52136 standard; peptide; 33 AA.
XX      AC
XX      ABG40088;
DT      19-AUG-2002 (first entry)
XX      DE
XX      Human peptide encoded by genome-derived single exon probe SEQ ID 29753.
XX      PS
XX      Claim 27; SEQ ID NO 14635; 322pp; English.
XX      CC
XX      The present invention relates to novel single exon nucleic acid probes
XX      (see AI100010-AA110067). The present sequence is a peptide encoded by one
XX      such probe. The probes are useful for measuring human gene expression in
XX      a human breast sample, where the probe hybridises at high stringency to a
XX      nucleic acid expressed in the human breast. The probes are useful for
XX      predicting, diagnosing, grading, staging, monitoring and prognosing
XX      diseases of the human breast, particularly those diseases with polygenic
XX      aetiology. The diseases include: breast cancer, disorders of development,
XX      inflammatory diseases of the breast, fibrocystic changes, proliferative
XX      breast disease and non-carcinoma tumours. Note: The sequence data for
XX      this patent did not form part of the printed specification, but was
XX      obtained in electronic format directly from WIPO at
XX      ftp.wipo.int/pub/published_pct_sequences
XX      SQ
XX      Sequence 33 AA;

Query Match      26.5%; Score 35; DB 4; Length 33;
Best Local Similarity 40.0%; Pred. No. 5.9e+02;
Matches 8; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY      6 LETFTVKSCPDAIKEVFNK 25
Db      1 LQTTFWLCPYMKRKDSK 20

RESULT 35
ABG40088
ID      ABG40088 standard; peptide; 33 AA.
XX      AC
XX      ABG40088;
DT      19-AUG-2002 (first entry)
XX      DE
XX      Human peptide encoded by genome-derived single exon probe SEQ ID 29753.
```

XX Human; single exon probe; asthma; lung cancer; COPD; ILD;  
KW chronic obstructive pulmonary disease; interstitial lung disease;  
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;  
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;  
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;  
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;  
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;  
KW primary ciliary dyskinesia; pulmonary hypertension;  
KW hyaline membrane disease.  
XX Homo sapiens.  
XX WO200186003-A2.  
XX 15-NOV-2001.  
XX 30-JAN-2001; 2001WO-US000665.  
XX 04-FEB-2000; 2000US-0180312P.  
XX 26-MAY-2000; 2000US-0207456P.  
XX 30-JUN-2000; 2000US-00608408.  
XX 03-AUG-2000; 2000US-00632366.  
XX 21-SEP-2000; 2000US-0234687P.  
XX 27-SEP-2000; 2000US-0236359P.  
XX 04-OCT-2000; 2000GB-00024263.  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2002-114183/15.  
XX Spatially-addressable set of single exon nucleic acid probes, used to  
XX measure gene expression in human lung samples.  
XX Claim 27; SEQ ID NO 29753; 634pp; English.  
XX The invention relates to a spatially-addressable set of single exon  
XX nucleic acid probes for measuring gene expression in a sample derived  
XX from human lung comprising single exon nucleic acid probes having one of  
XX 1614 nucleic acid sequences mentioned in the specification, or their  
XX complements or the 12387 open reading frames derived from the 12614  
XX probes. Also included are a microarray comprising the novel set of probes  
XX; the novel set of probes which hybridise at high stringency to a nucleic  
XX acid expressed in the human lung; measuring gene expression in a sample  
XX derived from human lung, comprising (a) contacting the array with a  
XX collection of detectably labeled nucleic acids derived from human lung  
XX mRNA, and (b) measuring the label detectably bound to each probe of the  
XX array; identifying exons in a eukaryotic genome, comprising (a)  
XX algorithmically predicting at least one exon from genomic sequences of  
XX the eukaryote; and (b) detecting specific hybridisation of detectably  
XX labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,  
XX having a fragment identical to the predicted exon, the probe is included  
XX in the above mentioned microarray; assigning exons to a single gene,  
XX comprising (a) identifying exons from genomic sequence by the method  
XX above and (b) measuring the expression of each of the exons in several  
XX tissues and/or cell types using hybridisation to a single exon  
XX microarrays having a probe with the exon, where a common pattern of  
XX expression of the exons in the tissues and/or cell types indicates that  
XX the exons should be assigned to a single gene; a peptide comprising one  
XX of 12011 sequences, mentioned in the specification, or encoded by the  
XX probes/open reading frames (ORF). The probes are used for gene expression  
XX analysis, and for identifying exons in a gene, particularly using human  
XX lung derived mRNA and for the study of lung diseases such as asthma, lung  
XX cancer, chronic obstructive pulmonary disease (COPD), interstitial lung  
XX disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,  
XX tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-  
XX Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary  
XX histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,  
XX Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary  
XX dyskinesia, pulmonary hypertension and hyaline membrane disease. The  
XX present sequence is a peptide/protein encoded by a single exon probe of

CC the invention. Note: The sequence data for this patent did not form part  
CC of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX Sequence 33 AA;  
SQ  
Query Match 26.5%; Score 35; DB 5; Length 33;  
Best Local Similarity 40.0%; Pred. No. 5.9e+02;  
Matches 8; Conservative 3; Mismatches 9; Indels 0; Gaps 0;  
QY 6 LETFTVKSCPDALKEVFDNK 25  
DB 1 LQTTTFWLCFYMVKRKRD SK 20  
RESULT 36  
ABB42598  
ID ABB42598 standard; peptide; 38 AA.  
XX AC ABB42598;  
XX 04-FEB-2002 (first entry)  
XX Peptide #10104 encoded by human foetal liver single exon probe.  
XX Human; foetal liver; gene expression; single exon nucleic acid probe.  
XX Homo sapiens.  
XX WO200157277-A2.  
XX 09-AUG-2001.  
XX 30-JAN-2001; 2001WO-US000669.  
XX 04-FEB-2000; 2000US-0180312P.  
XX 26-MAY-2000; 2000US-0207456P.  
XX 30-JUN-2000; 2000US-00608408.  
XX 03-AUG-2000; 2000US-00632366.  
XX 21-SEP-2000; 2000US-0234687P.  
XX 27-SEP-2000; 2000US-0236359P.  
XX 04-OCT-2000; 2000GB-00024263.  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2001-483447/52.  
XX Human genome-derived single exon nucleic acid probes useful for analyzing  
XX gene expression in human fetal liver.  
XX Claim 27; SEQ ID NO 35233; 639pp + Sequence Listing; English.  
XX The invention relates to a single exon nucleic acid probe for measuring  
XX human gene expression in a sample derived from human foetal liver. The  
XX single exon nucleic acid probes may be used for predicting, measuring and  
XX displaying gene expression in samples derived from human fetal liver. The  
XX present sequence is a peptide encoded by a single exon nucleic acid probe  
XX of the invention. Note: The sequence data for this patent did not form  
XX part of the printed specification, but was obtained in electronic format  
XX directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX Sequence 38 AA;  
SQ  
Query Match 26.5%; Score 35; DB 4; Length 38;  
Best Local Similarity 37.5%; Pred. No. 7e+02;  
Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;  
QY 10 TVKSCPDALKEVFDNK 25  
DB 3 TLKGCPSSSNNMFYKK 18





PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
DR WPI; 2001-483446/52.  
XX  
XX Single exon nucleic acid probes for analyzing gene expression in human  
PT brains.  
XX  
XX Example 4; SEQ ID NO 35594; 650pp + Sequence Listing; English.  
XX  
XX The present invention provides a number of single exon nucleic acid  
CC probes which are derived from genomic sequences expressed in the human  
CC brain. They can be used to measure gene expression in brain cell samples,  
CC which may enable the diagnosis and improved treatment of nervous system  
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,  
CC epilepsy and cancers. The present sequence is a protein encoded by one of  
CC the probes of the invention  
XX  
SQ Sequence 38 AA;  
Query Match 26.5%; Score 35; DB 4; Length 38;  
Best Local Similarity 37.5%; Pred. No. 7e+02; 7; Indels 0; Gaps 0;  
Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;  
QY 10 TVKSCPDPAIKEVFDNK 25  
Db 3 TLKGCPSSSSNMVYKK 18  
RESULT 40  
ABG58014  
ID ABG58014 standard; peptide; 38 AA.  
XX  
AC ABG58014;  
XX  
DT 25-FEB-2003 (first entry)  
XX  
DE Human liver peptide, SEQ ID No 36662.  
XX  
XX Human, liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;  
KW hypercholesterolaemia; coronary heart disease.  
XX  
OS Homo sapiens.  
XX  
PN WO200157273-A2.  
XX  
PD 09-AUG-2001.  
XX  
XX 30-JAN-2001; 2001WO-US000664.  
XX  
PR 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
XX WPI; 2001-488898/53.  
XX  
XX Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human adult liver.  
XX  
XX Claim 27; SEQ ID NO 36662; 658pp; English.  
XX  
XX The invention relates to a single exon nucleic acid probe (SENP) (I) for  
CC measuring human gene expression in a sample derived from human adult  
CC liver, comprising one of 13109 defined nucleotide sequences given in the

CC specification (or complements/ fragments). The probe hybridises at high  
CC stringency to a nucleic acid molecule expressed in the human adult liver.  
CC (I) may be used for predicting, measuring and displaying gene expression  
CC in samples derived from human adult liver. The genes identified may be  
CC involved in genetic liver diseases such as cirrhosis,  
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is  
CC associated with coronary heart disease. ABG47348-ABG59930 represent human  
CC liver single exon encoded peptides of the invention. Note: The sequence  
CC information for this patent does not appear in the printed specification  
CC but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 38 AA;

Query Match 26.5%; Score 35; DB 4; Length 38;  
Best Local Similarity 37.5%; Pred. No. 7e+02;  
Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 10 TVKSCPDPAIKEVFDNK 25

Db 3 TLKGCPSSSSNMVYKK 18

Search completed: January 20, 2006, 17:30:41  
Job time : 65.3457 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2006, 17:26:44 ; Search time 17.284 Seconds  
(without alignments)  
119.584 Million cell updates/sec

Title: US-10-619-323-5

Perfect score: 132

Sequence: 1 PKQVLETFVKSCPDPAKEVFNK 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 308952

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 50 summaries

Database : Issued Patents AA:\*

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2: /cgn2\_6/ptodata/1/iaa/6 COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/H COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/RE COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	132	100.0	29	1	US-08-254-493-6
2	132	100.0	29	1	US-08-408-222B-6
3	38	28.8	30	1	US-08-193-977-11
4	36	27.3	28	1	US-08-310-912A-154
5	36	27.3	28	2	US-09-301-085-154
6	36	27.3	28	4	PCT-US95-04589-154
7	36	27.3	31	1	US-08-486-057B-38
8	36	27.3	31	1	US-08-789-588-38
9	36	27.3	32	6	5262319-9
10	36	27.3	34	2	US-09-374-958C-31
11	36	27.3	34	2	US-09-374-936-31
12	36	27.3	42	2	US-09-848-664A-14
13	35	26.5	17	2	US-08-974-549A-100
14	35	26.5	17	2	US-08-912-951-100
15	35	26.5	17	2	US-09-402-181B-100
16	35	26.5	17	2	US-09-721-456-100
17	35	26.5	26	2	US-08-851-843A-140
18	35	26.5	26	2	US-08-974-549A-258
19	35	26.5	26	2	US-08-854-050-140
20	35	26.5	26	2	US-09-430-323-140
21	35	26.5	26	2	US-09-402-181B-258
22	35	26.5	26	2	US-09-721-456-258
23	35	26.5	26	2	US-09-766-253-140
24	35	26.5	26	2	US-10-054-295-140
25	35	26.5	26	2	US-09-438-486A-140
26	35	26.5	27	2	US-08-851-843A-156
27	35	26.5	27	2	US-08-851-843A-162

28	35	26.5	27	2	US-08-974-549A-276	Sequence 276, App
29	35	26.5	27	2	US-08-974-549A-282	Sequence 282, App
30	35	26.5	27	2	US-08-854-050-156	Sequence 156, App
31	35	26.5	27	2	US-08-854-050-162	Sequence 162, App
32	35	26.5	27	2	US-09-430-323-156	Sequence 156, App
33	35	26.5	27	2	US-09-430-323-162	Sequence 162, App
34	35	26.5	27	2	US-09-402-181B-276	Sequence 276, App
35	35	26.5	27	2	US-09-402-181B-282	Sequence 282, App
36	35	26.5	27	2	US-09-721-456-276	Sequence 276, App
37	35	26.5	27	2	US-09-721-456-282	Sequence 282, App
38	35	26.5	27	2	US-09-766-253-156	Sequence 156, App
39	35	26.5	27	2	US-09-766-253-162	Sequence 162, App
40	35	26.5	27	2	US-10-054-295-156	Sequence 156, App
41	35	26.5	27	2	US-10-054-295-162	Sequence 162, App
42	35	26.5	27	2	US-09-438-486A-156	Sequence 156, App
43	35	26.5	27	2	US-09-438-486A-162	Sequence 162, App
44	35	26.5	32	2	US-09-082-358B-57	Sequence 57, Appl
45	35	26.5	34	2	US-08-974-549A-26	Sequence 26, Appl
46	35	26.5	34	2	US-08-974-549A-45	Sequence 45, Appl
47	35	26.5	34	2	US-08-912-951-26	Sequence 26, Appl
48	35	26.5	34	2	US-08-912-951-45	Sequence 45, Appl
49	35	26.5	34	2	US-09-402-181B-25	Sequence 25, Appl
50	35	26.5	34	2	US-09-402-181B-45	Sequence 45, Appl

## ALIGNMENTS

RESULT 1  
US-08-254-493-6  
; Sequence 6, Application US/08254493  
; Patent No. 5439886  
; GENERAL INFORMATION:  
; APPLICANT: IKEYAMA, SHUICHI  
; APPLICANT: KAYAMA, MASARU  
; APPLICANT: MIYAKE, MASAYUKI  
; APPLICANT: SENO, MASAHARU  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND  
; PRODUCTION THEREOF  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
; STREET: 130 WATER STREET  
; CITY: BOSTON  
; STATE: MASSACHUSETTS  
; COUNTRY: US  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/254,493  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/865552  
; FILING DATE: 09-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 079996-1991  
; FILING DATE: 12-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 085396-1991  
; FILING DATE: 17-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 022321-1992  
; FILING DATE: 07-FEB-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: RESNICK, DAVID S.  
; REGISTRATION NUMBER: 34235  
; REFERENCE/DOCKET NUMBER: 41777  
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 523-3400  
TELEFAX: (617) 523-6440  
TELEX: 200291 STRE UR  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-254-493-6

Query Match 100.0%; Score 132; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 5.1e-14;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLETFVTKSCPDPAIKEVFNK 25  
Db 5 PKKDVLETFVTKSCPDPAIKEVFNK 29

RESULT 2  
US-08-408-222B-6  
Sequence 6, Application US/08408222B  
Patent No. 5776727  
GENERAL INFORMATION:  
APPLICANT: Ikeyama, Shuichi  
APPLICANT: Koyama, Masaru  
APPLICANT: Miyake, Masauyuki  
APPLICANT: Senoo, Masaharu  
TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dike, Bronstein, Roberts & Cushman  
STREET: 130 Water Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/408,222B  
FILING DATE: 22-MAR-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/254,493  
FILING DATE: 06-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP-079996-1991  
FILING DATE: 12-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP-085396-1991  
FILING DATE: 14-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP-022321-1992  
FILING DATE: 07-FEB-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Resnick, David S.  
REGISTRATION NUMBER: 34,235  
REFERENCE/DOCKET NUMBER: 41777-DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-08-408-222B-6

Query Match 100.0%; Score 132; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 5.1e-14;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLETFVTKSCPDPAIKEVFNK 25  
Db 5 PKKDVLETFVTKSCPDPAIKEVFNK 29

RESULT 3  
US-08-193-977-11  
Sequence 11, Application US/08193977  
Patent No. 5625031  
GENERAL INFORMATION:  
APPLICANT: WEBSTER, KEVIN R.  
APPLICANT: COLEMAN, KEVIN G.  
TITLE OF INVENTION: PEPTIDE INHIBITORS OF THE P33CDK2 AND  
TITLE OF INVENTION: P34CDK2 CELL CYCLE REGULATORY KINASES AND HUMAN  
TITLE OF INVENTION: PAPILLOMAVIRUS E7 ONCOPROTEIN  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: REED & ROBINS  
STREET: 635 BRYANT STREET  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94301

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/193,977  
FILING DATE: 08-FEB-1994  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: ROBINS, ROBERTA L.  
REGISTRATION NUMBER: 33,208  
REFERENCE/DOCKET NUMBER: 5998-0016  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 617-8999  
TELEFAX: (415) 327-3231  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-193-977-11

Query Match 28.8%; Score 38; DB 1; Length 30;  
Best Local Similarity 50.0%; Pred. No. 4;  
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 9 FTVKSCPDPAIKE 20  
Db 3 FTLVHCPDLMKD 14

RESULT 4  
US-08-310-912A-154  
Sequence 154, Application US/08310912A  
Patent No. 5981730  
GENERAL INFORMATION:  
APPLICANT: Ausubel, Frederick M.  
APPLICANT: Staskawicz, Brian J.  
APPLICANT: Brent, Andrew F.  
APPLICANT: Dahlbeck, Douglas  
APPLICANT: Katagiri, Fumiaki

```
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND DETECTION
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 208
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2904
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/310,912A
; FILING DATE: September 22, 1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/227,360
; FILING DATE: April 13, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lech, Karen F.
; REGISTRATION NUMBER: 35,238
; REFERENCE/DOCKET NUMBER: 00786/254001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 100254
; INFORMATION FOR SEQ ID NO: 154:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-310-912A-154

Query Match      27.3%; Score 36; DB 1; Length 28;
Best Local Similarity 35.0%; Pred. No. 78;
Matches 7; Conservative 4; Mismatches 9; Indels 9; Gaps 0;

QY      1 PKKDVLETFVKSCPDAIKE 20
Db      1 PKLEVLEFDCREIEELISE 20

RESULT 5
US-09-301-085-154
; Sequence 154, Application US/09301085
; Patent No. 6262248
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
; FILE REFERENCE: 00786/254002
; CURRENT APPLICATION NUMBER: US/09/301,085
; CURRENT FILING DATE: 1999-04-28
; EARLIER APPLICATION NUMBER: 08/310,912
; EARLIER FILING DATE: 1994-09-22
; EARLIER APPLICATION NUMBER: 08/227,360
; EARLIER FILING DATE: 1994-04-13
; NUMBER OF SEQ ID NOS: 208
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 154
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; US-09-301-085-154

Query Match      27.3%; Score 36; DB 2; Length 28;
Best Local Similarity 35.0%; Pred. No. 78;
Matches 7; Conservative 4; Mismatches 9; Indels 9; Gaps 0;

QY      1 PKKDVLETFVKSCPDAIKE 20
Db      1 PKLEVLEFDCREIEELISE 20

RESULT 6
PCT-US95-04589-154
; Sequence 154, Application PC/TUS9504589
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE AND USES THEREOF
; NUMBER OF SEQUENCES: 201
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street Suite 3100
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2904
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04589
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,360
; FILING DATE: 13-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/230001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 100254
; INFORMATION FOR SEQ ID NO: 154:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-04589-154

Query Match      27.3%; Score 36; DB 4; Length 28;
Best Local Similarity 35.0%; Pred. No. 78;
Matches 7; Conservative 4; Mismatches 9; Indels 9; Gaps 0;

QY      1 PKKDVLETFVKSCPDAIKE 20
Db      1 PKLEVLEFDCREIEELISE 20
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RESULT 7  
US-08-486-057B-38  
; Sequence 38, Application US/08486057B  
; Patent No. 5650494  
; GENERAL INFORMATION:  
; APPLICANT: Cerletti, Nico  
; APPLICANT: McMaster, Gary K.  
; APPLICANT: Cox, David  
; APPLICANT: Schmitz, Albert  
; APPLICANT: Meyhack, Bernd  
; TITLE OF INVENTION: Process for Refolding Recombinantly  
; Produced TGF-beta-like Proteins  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Henry P. No. 5650494ak  
; STREET: 520 White Plains Road, P.O. Box 2005  
; CITY: Tarrytown  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10591-9005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/08/486,057B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/201,703  
; FILING DATE: 25-FEB-1994  
; PRIOR APPLICATION NUMBER: US 07/960,309  
; FILING DATE: 13-OCT-1992  
; APPLICATION NUMBER: US 07/621,502  
; FILING DATE: 03-DEC-1990  
; APPLICATION NUMBER: GB 8927546.5  
; FILING DATE: 06-DEC-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5650494ak, Henry P.  
; REGISTRATION NUMBER: 33200  
; REFERENCE/DOCKET NUMBER: 4-17861/+ /Cont3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908) 277-5110  
; TELEFAX: (908) 277-4306  
; INFORMATION FOR SEQ ID NO: 38:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 31 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-486-057B-38

Query Match 27.3%; Score 36; DB 1; Length 31;  
Best Local Similarity 50.0%; Pred. No. 88;  
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
QY 1 PKQDVLETFVKSC 14  
|| : | |||  
Db 15 PKVEQLSNMVKSC 28

RESULT 8  
US-08-789-588-38  
; Sequence 38, Application US/08789588  
; Patent No. 5922846  
; GENERAL INFORMATION:  
; APPLICANT: Cerletti, Nico

; APPLICANT: McMaster, Gary K.  
; APPLICANT: Cox, David  
; APPLICANT: Schmitz, Albert  
; APPLICANT: Meyhack, Bernd  
; TITLE OF INVENTION: Process for Refolding Recombinantly  
; Produced TGF-beta-like Proteins  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Henry P. No. 5922846ak  
; STREET: 520 White Plains Road, P.O. Box 2005  
; CITY: Tarrytown  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10591-9005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/08/789,588  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/486,057  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: US 08/201,703  
; FILING DATE: 25-FEB-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/960,309  
; FILING DATE: 13-OCT-1992  
; APPLICATION NUMBER: US 07/621,502  
; FILING DATE: 03-DEC-1990  
; APPLICATION NUMBER: GB 8927546.5  
; FILING DATE: 06-DEC-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5922846ak, Henry P.  
; REGISTRATION NUMBER: 33200  
; REFERENCE/DOCKET NUMBER: 4-17861/+ /Cont3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908) 277-5110  
; TELEFAX: (908) 277-4306  
; INFORMATION FOR SEQ ID NO: 38:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 31 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-789-588-38

Query Match 27.3%; Score 36; DB 1; Length 31;  
Best Local Similarity 50.0%; Pred. No. 88;  
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
QY 1 PKQDVLETFVKSC 14  
|| : | |||  
Db 15 PKVEQLSNMVKSC 28

RESULT 9  
5262319-9  
; Patent No. 5262319  
; APPLICANT: IWATA, KENNETH K.; FOULKES, J. GORDON; DIJKE,  
; PETER T.; HALEY, JOHN D.  
; TITLE OF INVENTION: METHOD FOR OBTAINING BONE MARROW FREE  
; OF TUMOR CELLS USING TRANSFORMING GROWTH FACTOR B3  
; NUMBER OF SEQUENCES: 9  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/543,341  
; FILING DATE: 25-JUN-1990

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 353,410  
; FILING DATE: 17-MAY-1989  
; APPLICATION NUMBER: 183,410  
; FILING DATE: 20-APR-1988  
; APPLICATION NUMBER: 111,022  
; FILING DATE: 20-OCT-1987  
; APPLICATION NUMBER: 922,121  
; FILING DATE: 20-OCT-1986  
; APPLICATION NUMBER: 847,931  
; FILING DATE: 07-APR-1986  
; APPLICATION NUMBER: 725,003  
; FILING DATE: 19-APR-1985  
; SEQ ID NO:9:  
; LENGTH: 32  
5262319-9

Query Match 27.3%; Score 36; DB 6; Length 32;  
Best Local Similarity 50.0%; Pred. No. 91;  
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKQVLETFYVSK 14  
||:|  
DB 19 PKVEQLSNMVKSC 32

RESULT 10  
US-09-374-958C-31  
; Sequence 31, Application US/09374958C  
; Patent No. 6677432  
; GENERAL INFORMATION:  
; APPLICANT: Stryker Corporation  
; TITLE OF INVENTION: Modified Proteins and DNAs of the TGF-beta Superfamily, Including  
; FILE REFERENCE: STK-076  
; CURRENT APPLICATION NUMBER: US/09/374,958C  
; CURRENT FILING DATE: 1999-08-16  
; NUMBER OF SEQ ID NOS: 90  
; SOFTWARE: PatentIn version 2.0  
; SEQ ID NO 31  
; LENGTH: 34  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: TGF-Beta3  
US-09-374-958C-31

Query Match 27.3%; Score 36; DB 2; Length 34;  
Best Local Similarity 50.0%; Pred. No. 98;  
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKQVLETFYVSK 14  
||:|  
DB 18 PKVEQLSNMVKSC 31

RESULT 11  
US-09-374-936-31  
; Sequence 31, Application US/09374936  
; Patent No. 6846906  
; GENERAL INFORMATION:  
; APPLICANT: Oppermann, Hermann  
; APPLICANT: Tai, Mei-Sheng  
; APPLICANT: McCartney, John  
; TITLE OF INVENTION: Modified TGF-beta Superfamily Proteins  
; FILE REFERENCE: STK-077  
; CURRENT APPLICATION NUMBER: US/09/374,936  
; CURRENT FILING DATE: 1999-08-16  
; NUMBER OF SEQ ID NOS: 88  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 31  
; LENGTH: 34  
; TYPE: PRT

; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: TGF-Beta3  
US-09-374-936-31

Query Match 27.3%; Score 36; DB 2; Length 34;  
Best Local Similarity 50.0%; Pred. No. 98;  
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKQVLETFYVSK 14  
||:|  
DB 18 PKVEQLSNMVKSC 31

RESULT 12  
US-09-848-664A-14  
; Sequence 14, Application US/09848664A  
; Patent No. 6723344  
; GENERAL INFORMATION:  
; APPLICANT: Sakiyama-Elbert, Shelly E.  
; APPLICANT: Hubbell, Jeffrey A.  
; TITLE OF INVENTION: Controlled Release of No. 6723344-Heparin Binding Growth  
; FILE REFERENCE: ETH 108  
; CURRENT APPLICATION NUMBER: US/09/848,664A  
; PRIOR FILING DATE: 2001-05-03  
; PRIOR APPLICATION NUMBER: US/09/298,084A  
; PRIOR FILING DATE: 1999-04-22  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 42  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-848-664A-14

Query Match 27.3%; Score 36; DB 2; Length 42;  
Best Local Similarity 50.0%; Pred. No. 1.3e+02;  
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKQVLETFYVSK 14  
||:|  
DB 26 PKVEQLSNMVKSC 39

RESULT 13  
US-08-974-549A-100  
; Sequence 100, Application US/08974549A  
; Patent No. 6166178  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.  
; APPLICANT: Morin, Gregg B.  
; APPLICANT: Harley, Calvin B.  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 727  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/974,549A

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; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..17
; OTHER INFORMATION: /note= "telomerase RT finger motif A
; OTHER INFORMATION: peptide from Saccharomyces
; OTHER INFORMATION: cerevisiae EST2"
US-08-974-549A-100

Query Match 26.5%; Score 35; DB 2; Length 17;
Best Local Similarity 70.0%; Pred. No. 62;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18
Db 8 FDKVSCYDSI 17

RESULT 14
US-08-912-951-100
; Sequence 100, Application US/08912951
; Patent No. 6475789
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.

; FILING DATE: 19-NOV-1997
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; TITLE OF INVENTION: THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..17
; OTHER INFORMATION: /note= "telomerase RT finger motif A
; OTHER INFORMATION: peptide from Saccharomyces
; OTHER INFORMATION: cerevisiae EST2"
US-08-912-951-100

Query Match 26.5%; Score 35; DB 2; Length 17;
Best Local Similarity 70.0%; Pred. No. 62;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18
Db 8 FDKVSCYDSI 17

RESULT 15

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US-09-402-181B-100  
; Sequence 100, Application US/09402181B  
; Patent No. 6610839  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin B.  
; Andrews, William H.  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 633  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/402,181B  
; FILING DATE: 29-Sep-1997  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; APPLICATION NUMBER: US 08/911,312  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: US 08/912,951  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: US 08/915,503  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: WO PCT/US97/17885  
; FILING DATE: 01-OCT-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ausenhus, Scott L.  
; REGISTRATION NUMBER: 42,271  
; REFERENCE/DOCKET NUMBER: 015389-002620US  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 100:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..17  
; OTHER INFORMATION: /note= "telomerase RT finger motif A  
; peptide from Saccharomyces  
; cerevisiae EST2"  
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:  
US-09-402-181B-100

Query Match 26.5%; Score 35; DB 2; Length 17;  
Best Local Similarity 70.0%; Pred. No. 62;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 9 FTVKSCPDAT 18  
Db 8 FDKVSCYDSI 17  
RESULT 16  
US-09-721-456-100  
; Sequence 100, Application US/09721456  
; Patent No. 6617110  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin B.  
; Andrews, William H.  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 727  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/721,456  
; FILING DATE: 22-No. 6617110-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/974,549A  
; FILING DATE: 19-NOV-1997  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; APPLICATION NUMBER: US 08/911,312  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: US 08/912,951  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: US 08/915,503  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: WO PCT/US97/17618  
; FILING DATE: 01-OCT-1997  
; APPLICATION NUMBER: WO PCT/US97/17885  
; FILING DATE: 01-OCT-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph Ted  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002610US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 100:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear

; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..17  
; OTHER INFORMATION: /note= "telomerase RT finger motif A  
; peptide from Saccharomyces  
; cerevisiae EST2"  
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:  
US-09-721-456-100

Query Match 26.5%; Score 35; DB 2; Length 17;  
Best Local Similarity 70.0%; Pred. No. 62;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18  
| | | | | | | |  
Db 8 FDKVSCYDSI 17

RESULT 17  
US-08-851-843A-140  
; Sequence 140, Application US/08851843A  
; Patent No. 6093809  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.  
; APPLICANT: Morin, Gregg B.  
; APPLICANT: Harley, Calvin  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: No. 6093809el Telomerase  
; NUMBER OF SEQUENCES: 225  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/851,843A  
; FILING DATE: 06-MAY-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002930US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 140:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 26 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:

; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..26  
; OTHER INFORMATION: /note= "motif 3(A) peptide from  
; Saccharomyces cerevisiae EST2p"  
US-08-851-843A-140

Query Match 26.5%; Score 35; DB 2; Length 26;  
Best Local Similarity 70.0%; Pred. No. 1e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18  
| | | | | | | |  
Db 7 FDKVSCYDSI 16

RESULT 18  
US-08-974-549A-258  
; Sequence 258, Application US/08974549A  
; Patent No. 6166178  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.  
; APPLICANT: Morin, Gregg B.  
; APPLICANT: Harley, Calvin B.  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 727  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/974,549A  
; FILING DATE: 19-NOV-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/911,312  
; FILING DATE: 14-AUG-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/912,951  
; FILING DATE: 14-AUG-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/915,503  
; FILING DATE: 14-AUG-1997  
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 258:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..26
; OTHER INFORMATION: /note= "motif 3(A) peptide from
; OTHER INFORMATION: Saccharomyces cerevisiae EST2p"
US-08-974-549A-258

Query Match 26.5%; Score 35; DB 2; Length 26;
Best Local Similarity 70.0%; Pred. No. 1e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAl 18
Db 7 FDKVSCYDSI 16

RESULT 19
US-08-854-050-140
; Sequence 140, Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 140:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..26
; OTHER INFORMATION: /note= "motif 3(A) peptide from
; OTHER INFORMATION: Saccharomyces cerevisiae EST2p"
US-08-854-050-140

Query Match 26.5%; Score 35; DB 2; Length 26;
Best Local Similarity 70.0%; Pred. No. 1e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAl 18
Db 7 FDKVSCYDSI 16

RESULT 20
US-09-430-323-140
; Sequence 140, Application US/09430323
; Patent No. 6309867
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6309867el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/430,323
; FILING DATE: 29-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
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APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 140:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..26  
OTHER INFORMATION: /note= "motif 3(A) peptide from  
Saccharomyces cerevisiae EST2p"  
SEQUENCE DESCRIPTION: SEQ ID NO: 140:  
US-09-430-323-140  
  
Query Match 26.5%; Score 35; DB 2; Length 26;  
Best Local Similarity 70.0%; Pred. No. 1e+02;  
Matches 7; Conservative 1; Mismatches 0; Gaps 0;  
  
QY 9 FTVKSCPDAL 18  
DB 7 FDKVSCYDSI 16  
  
RESULT 21  
US-09-402-181B-258  
; Sequence 258, Application US/09402181B  
; Patent No. 6610839  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin B.  
; Andrews, William H.  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 633  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/402,181B  
; FILING DATE: 29-Sep-1997  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ausenius, Scott L.  
REGISTRATION NUMBER: 42,271  
REFERENCE/DOCKET NUMBER: 015389-002620US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 258:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..26  
OTHER INFORMATION: /note= "motif 3(A) peptide from  
Saccharomyces cerevisiae EST2p"  
SEQUENCE DESCRIPTION: SEQ ID NO: 258:  
US-09-402-181B-258  
  
Query Match 26.5%; Score 35; DB 2; Length 26;  
Best Local Similarity 70.0%; Pred. No. 1e+02;  
Matches 7; Conservative 1; Mismatches 0; Gaps 0;  
  
QY 9 FTVKSCPDAL 18  
DB 7 FDKVSCYDSI 16  
  
RESULT 22  
US-09-721-456-258  
; Sequence 258, Application US/09721456  
; Patent No. 6617110  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin B.  
; Andrews, William H.  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 727  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/721,456  
; FILING DATE: 22-No. 6617110-2000

CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,549A  
FILING DATE: 19-NOV-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph Ted  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 258:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..26  
OTHER INFORMATION: /note= "motif 3(A) peptide from  
Saccharomyces cerevisiae EST2p"  
SEQUENCE DESCRIPTION: SEQ ID NO: 258:  
US-09-721-456-258

Query Match 26.5%; Score 35; DB 2; Length 26;  
Best Local Similarity 70.0%; Pred. No. 1e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAl 18  
Db 7 FDKSCYDSI 16

RESULT 23  
US-09-766-253-140  
Sequence 140, Application US/09766253  
Patent No. 6808880  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin  
Andrews, William H.  
TITLE OF INVENTION: No. 6808880el Telomerase  
NUMBER OF SEQUENCES: 171  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco

STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/766,253  
FILING DATE: 19-Jan-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/846,017  
FILING DATE: 1997-04-25  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002920US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 140:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..26  
OTHER INFORMATION: /note= "motif 3(A) peptide from  
Saccharomyces cerevisiae EST2p"  
SEQUENCE DESCRIPTION: SEQ ID NO: 140:  
US-09-766-253-140

Query Match 26.5%; Score 35; DB 2; Length 26;  
Best Local Similarity 70.0%; Pred. No. 1e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAl 18  
Db 7 FDKSCYDSI 16

RESULT 24  
US-10-054-295-140  
Sequence 140, Application US/10054295  
Patent No. 6921664  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin  
Andrews, William H.  
TITLE OF INVENTION: No. 6921664el Telomerase  
NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

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/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/054,295
/ FILING DATE: 18-Jan-2002
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/854,050
/ FILING DATE: <Unknown>
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph T.
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002930US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 140:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 26 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ MOLECULE TYPE: linear
/ FEATURE:
/ NAME/KEY: Peptide
/ LOCATION: 1..26
/ OTHER INFORMATION: /note= "motif 3(A) peptide from
/ Saccharomyces cerevisiae EST2p"
/ SEQUENCE DESCRIPTION: SEQ ID NO: 140:
US-10-054-295-140

Query Match 26.5%; Score 35; DB 2; Length 26;
Best Local Similarity 70.0%; Pred. No. 1e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18
| | | | | | |
Db 7 FDKVSCYDSI 16

RESULT 25
US-09-438-486A-140
/ Sequence 140, Application US/09438486A
/ Patent No. 6927285
/ GENERAL INFORMATION:
/ APPLICANT: CECCH, THOMAS R.
/ APPLICANT: LINGNER, JOACHIM
/ APPLICANT: NAKAMURA, TORU
/ APPLICANT: CHAPMAN, KAREN B.
/ APPLICANT: MORIN, GREGG B.
/ APPLICANT: HARLEY, CALVIN
/ APPLICANT: ANDREWS, WILLIAM H.
/ TITLE OF INVENTION: GENE FOR HUMAN TELOMERASE REVERSE TRANSCRIPTASE AND
/ TELEMERASE VARIANTS
/ FILE REFERENCE: 018/062
/ CURRENT APPLICATION NUMBER: US/09/438,486A
/ CURRENT FILING DATE: 1999-11-12
/ PRIOR APPLICATION NUMBER: 08/851,843
/ PRIOR FILING DATE: 1997-05-06
/ PRIOR APPLICATION NUMBER: 08/846,017
/ PRIOR FILING DATE: 1997-04-25
/ PRIOR APPLICATION NUMBER: 08/844,419
/ PRIOR FILING DATE: 1997-04-18
/ PRIOR APPLICATION NUMBER: 08/724,643
/ PRIOR FILING DATE: 1996-10-01
/ NUMBER OF SEQ ID NOS: 223
/ SOFTWARE: PatentIn Ver. 3.2
/ SEQ ID NO 140
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/ LENGTH: 26
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Recombinant
US-09-438-486A-140

Query Match 26.5%; Score 35; DB 2; Length 26;
Best Local Similarity 70.0%; Pred. No. 1e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18
| | | | | | |
Db 7 FDKVSCYDSI 16

RESULT 26
US-08-851-843A-156
/ Sequence 156, Application US/08851843A
/ Patent No. 6093809
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/ APPLICANT: Lingner, Joachim
/ APPLICANT: Nakamura, Toru
/ APPLICANT: Chapman, Karen B.
/ APPLICANT: Morin, Gregg B.
/ APPLICANT: Harley, Calvin
/ APPLICANT: Andrews, William H.
/ TITLE OF INVENTION: No. 6093809el Telomerase
/ NUMBER OF SEQUENCES: 225
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, 8th Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: United States of America
/ ZIP: 94111
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/851,843A
/ FILING DATE: 06-MAY-1997
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph T.
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002930US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 156:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 27 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
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;
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..27
; OTHER INFORMATION:
; OTHER INFORMATION: /note= "motif A peptide from
US-08-851-843A-156 Schizosaccharomyces pombe tez1"

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Query Match 26.5%; Score 35; DB 2; Length 27;  
Best Local Similarity 36.8%; Pred. No. 1.1e+02;  
Matches 7; Conservative 3; Mismatches 9; Indels

Qy 2 KKDVLFTFKSCPDAlKE 20  
:|:|:|:|:|:  
Db 1 RKKYFVRIDIKSCYDRIKO 19

RESULT 27  
US-08-851-843A-162  
; Sequence 162, Application US/08851843A  
: Patent No. 6093809

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? GENERAL INFORMATION:
?
? APPLICANT: Cech, Thomas R.
? APPLICANT: Lingner, Joachim
? APPLICANT: Nakamura, Toru
? APPLICANT: Chapman, Karen B.
? APPLICANT: Morin, Gregg B.
? APPLICANT: Harley, Calvin
? APPLICANT: Andrews, William H.
?
? TITLE OF INVENTION: No. 6093809el Telomerase
?
? NUMBER OF SEQUENCES: 225
?

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CONFORMANCE ADDRESS:  
ADDRESS: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0851,943A
FILING DATE: 06-MAY-1997

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CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996

CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36, 429  
REFERENCE/DOCKET NUMBER: 015389-0029300US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEO ID NO: 162:

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;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
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; NAME/KEY: Peptide
; LOCATION: 1..27
; OTHER INFORMATION: /note= "motif A peptide from
; OTHER INFORMATION: Saccharomyces cerevisiae EST2"
US-08-851-843A-162

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Query Match 26.5%; Score 35; DB 2; Length 27;  
Best Local Similarity 70.0%; Pred. NO. 1.1e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels

Qy	9	F	T	V	K	S	C	P	D	A	I	18
									:			
Db	8	F	D	V	K	S	C	Y	D	S	I	17

RESULT 28  
US-08-974-549A-276  
; Sequence 276, Application US/08974549A  
; Patent No. 6166178

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? GENERAL INFORMATION:
?
? APPLICANT: Cech, Thomas R.
? APPLICANT: Lingner, Joachim
? APPLICANT: Nakamura, Toru
? APPLICANT: Chapman, Karen B.
? APPLICANT: Morin, Gregg B.
? APPLICANT: Harley, Calvin B.
? APPLICANT: Andrews, William H.
?
? TITLE OF INVENTION: Human Telomerase Catalytic Subunit
?
? NUMBER OF SEQUENCES: 727
?
? CORRESPONDENCE ADDRESS:
?
?

```

ADDRESS: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,549A  
FILING DATE: 19-NOV-1997

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1 PRIOR APPLICATION DATA: US 08/724,643
2 APPLICATION NUMBER: US 08/724,643
3 FILING DATE: 01-OCT-1996
4 PRIOR APPLICATION DATA:
5 APPLICATION NUMBER: US 08/844,419
6 FILING DATE: 18-APR-1997
7 PRIOR APPLICATION DATA:
8 APPLICATION NUMBER: US 08/846,017
9 FILING DATE: 25-APR-1997
10 PRIOR APPLICATION DATA:
11 APPLICATION NUMBER: US 08/851,843
12 FILING DATE: 06-MAY-1997
13 PRIOR APPLICATION DATA:
14 APPLICATION NUMBER: US 08/854,050
15 FILING DATE: 09-MAY-1997
16 PRIOR APPLICATION DATA:
17 APPLICATION NUMBER: US 08/911,312
18 FILING DATE: 14-AUG-1997
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: US 08/912,951
21 FILING DATE: 14-AUG-1997
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: US 08/915,503
24 FILING DATE: 14-AUG-1997
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: WO PCT/US97/1
27 FILING DATE: 01-OCT-1997
28 PRIOR APPLICATION DATA:

```

APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph Ted  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 276:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..27  
OTHER INFORMATION: /note= "motif A peptide from  
OTHER INFORMATION: Schizosaccharomyces pombe tezi"  
US-08-974-549A-276

Query Match 26.5%; Score 35; DB 2; Length 27;  
Best Local Similarity 36.8%; Pred. No. 1.1e+02;  
Matches 7; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 2 KKDVLFTFTVKSCPDAIKE 20  
Db 1 RKKYFVRIDIKSCYDRIKQ 19

RESULT 29  
US-08-974-549A-282  
Sequence 282, Application US/08974549A  
Patent No. 6166178  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
APPLICANT: Lingner, Joachim  
APPLICANT: Nakamura, Toru  
APPLICANT: Chapman, Karen B.  
APPLICANT: Morin, Gregg B.  
APPLICANT: Harley, Calvin B.  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: Human telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 727  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,549A  
FILING DATE: 19-NOV-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph Ted  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 282:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..27  
OTHER INFORMATION: /note= "motif A peptide from  
OTHER INFORMATION: Saccharomyces cerevisiae EST2"  
US-08-974-549A-282

Query Match 26.5%; Score 35; DB 2; Length 27;  
Best Local Similarity 70.0%; Pred. No. 1.1e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18  
Db 8 FDKSCYDSI 17

RESULT 30  
US-08-854-050-156  
Sequence 156, Application US/08854050  
Patent No. 6261836  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
APPLICANT: Lingner, Joachim  
APPLICANT: Nakamura, Toru  
APPLICANT: Chapman, Karen B.  
APPLICANT: Morin, Gregg B.  
APPLICANT: Harley, Calvin  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: No. 6261836el Telomerase  
NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible



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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 156:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..27
; OTHER INFORMATION: /note= "motif A peptide from
; Schizosaccharomyces pombe te21"
; US-08-854-050-156

Query Match 26.5%; Score 35; DB 2; Length 27;
Best Local Similarity 36.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 2 KDVLETFTVKSCPDALKE 20
Db 1 RKKYFVRIDIKSCVDRIKQ 19

RESULT 31
US-08-854-050-162
; Sequence 162, Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 162:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..27
; OTHER INFORMATION: /note= "motif A peptide from
; Saccharomyces cerevisiae EST2"
; US-08-854-050-162

Query Match 26.5%; Score 35; DB 2; Length 27;
Best Local Similarity 70.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18
Db 8 FDKSCYDSI 17

RESULT 32
US-09-430-323-156
; Sequence 156, Application US/09430323
; Patent No. 6309867
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6309867el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco

```

STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/430,323  
FILING DATE: 29-Oct-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 156:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..27  
OTHER INFORMATION: /note= "motif A peptide from Schizosaccharomyces pombe tel1"  
SEQUENCE DESCRIPTION: SEQ ID NO: 156:  
US-09-430-323-156  
Query Match 26.5%; Score 35; DB 2; Length 27;  
Best Local Similarity 36.8%; Pred. No. 1.1e+02;  
Matches 7; Conservative 3; Mismatches 9; Indels 0; Gaps 0;  
QY 2 KKVLETFVTKSCPDAIKE 20  
DB 1 RKXYFVRIDIKSCYDIKQ 19  
RESULT 33  
US-09-430-323-162  
Sequence 162, Application US/09430323  
Patent No. 6309867  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin  
Andrews, William H.  
TITLE OF INVENTION: No. 6309867el Telomerase  
NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California

COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/430,323  
FILING DATE: 29-Oct-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 162:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..27  
OTHER INFORMATION: /note= "motif A peptide from Saccharomyces cerevisiae EST2"  
SEQUENCE DESCRIPTION: SEQ ID NO: 162:  
US-09-430-323-162  
Query Match 26.5%; Score 35; DB 2; Length 27;  
Best Local Similarity 70.0%; Pred. No. 1.1e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 9 FTVKSCPDAI 18  
DB 8 FDKSCYDSI 17  
RESULT 34  
US-09-402-181B-276  
Sequence 276, Application US/09402181B  
Patent No. 6610839  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin B.  
Andrews, William H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 633  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA

ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/402,181B  
FILING DATE: 29-Sep-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ausenhus, Scott L.  
REGISTRATION NUMBER: 42,271  
REFERENCE/DOCKET NUMBER: 015389-002620US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 276:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..27  
OTHER INFORMATION: /note= "motif A peptide from Schizosaccharomyces pombe tezi"  
SEQUENCE DESCRIPTION: SEQ ID NO: 276:  
US-09-402-181B-276  
Query Match 26.5%; Score 35; DB 2; Length 27;  
Best Local Similarity 36.8%; Pred. No. 1.1e+02;  
Matches 7; Conservative 3; Mismatches 9; Indels 0; Gaps 0;  
QY 2 KQDVLETFVKSCPDALKE 20  
Db 1 RKXVFVRIDIKSCVDRIKQ 19  
RESULT 35  
US-09-402-181B-282  
Sequence 282, Application US/09402181B  
Patent No. 6610839  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin B.  
Andrews, William H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 633  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/402,181B  
FILING DATE: 29-Sep-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ausenhus, Scott L.  
REGISTRATION NUMBER: 42,271  
REFERENCE/DOCKET NUMBER: 015389-002620US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 282:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..27  
OTHER INFORMATION: /note= "motif A peptide from Saccharomyces cerevisiae EST2"  
SEQUENCE DESCRIPTION: SEQ ID NO: 282:  
US-09-402-181B-282  
Query Match 26.5%; Score 35; DB 2; Length 27;  
Best Local Similarity 70.0%; Pred. No. 1.1e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 9 FTVKSCPDAL 18  
Db 8 FDKVSCYDSI 17  
RESULT 36  
US-09-721-456-276  
Sequence 276, Application US/09721456  
Patent No. 6617110  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.

Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin B.  
Andrews, William H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 727  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/721,456  
FILING DATE: 22-NOV-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,549A  
FILING DATE: 19-NOV-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph Ted  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 276:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..27  
OTHER INFORMATION: /note="motif A peptide from Schizosaccharomyces pombe tez1"  
SEQUENCE DESCRIPTION: SEQ ID NO: 276:  
US-09-721-456-276

Query Match 26.5%; Score 35; DB 2; Length 27;  
Best Local Similarity 36.8%; Pred. No. 1.1e+02;  
Matches 7; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 2 KKDVLFTVTKSCPDRAIKE 20  
Db 1 RKKYFVRIDIKSCYDRIKQ 19  
RESULT 37  
US-09-721-456-282  
; Sequence 282, Application US/09721456  
; Patent No. 6617110  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin B.  
; Andrews, William H.  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 727  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/721,456  
; FILING DATE: 22-NOV-1997  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/974,549A  
; FILING DATE: 19-NOV-1997  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; APPLICATION NUMBER: US 08/911,312  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: US 08/912,951  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: US 08/915,503  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: WO PCT/US97/17618  
; FILING DATE: 01-OCT-1997  
; APPLICATION NUMBER: WO PCT/US97/17885  
; FILING DATE: 01-OCT-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph Ted  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002610US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 282:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 27 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:

NAME/KEY: Peptide  
LOCATION: 1..27  
OTHER INFORMATION: /note= "motif A peptide from  
Saccharomyces cerevisiae EST2"  
SEQUENCE DESCRIPTION: SEQ ID NO: 282:  
US-09-721-456-282

Query Match 26.5%; Score 35; DB 2; Length 27;  
Best Local Similarity 70.0%; Pred. No. 1.1e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18  
| | | | | | | | | |  
Db 8 FDVKSCYDSI 17

RESULT 38  
US-09-766-253-156  
; Sequence 156, Application US/09766253  
; Patent No. 6808880  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin  
; Andrews, William H.

TITLE OF INVENTION: No. 6808880el Telomerase  
NUMBER OF SEQUENCES: 171  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/766,253  
FILING DATE: 19-Jan-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/846,017  
FILING DATE: 1997-04-25  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002920US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 156:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 amino acids  
TYPE: amino acid  
STRANDEDNESS: <unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..27  
OTHER INFORMATION: /note= "motif A peptide from  
Schizosaccharomyces pombe tez1"  
SEQUENCE DESCRIPTION: SEQ ID NO: 156:  
US-09-766-253-156

Query Match 26.5%; Score 35; DB 2; Length 27;  
Best Local Similarity 36.8%; Pred. No. 1.1e+02;  
Matches 7; Conservative 3; Mismatches 9; Indels 0; Gaps 0;  
QY 2 KQDVLETFVVKSCPDALKE 20  
| | | | | | | | | |  
Db 1 RKKYFVRIDIKSCYDRIKQ 19

RESULT 39  
US-09-766-253-162  
; Sequence 162, Application US/09766253  
; Patent No. 6808880  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin  
; Andrews, William H.

TITLE OF INVENTION: No. 6808880el Telomerase  
NUMBER OF SEQUENCES: 171  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/766,253  
FILING DATE: 19-Jan-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/846,017  
FILING DATE: 1997-04-25  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002920US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 162:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 amino acids  
TYPE: amino acid  
STRANDEDNESS: <unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..27  
OTHER INFORMATION: /note= "motif A peptide from  
Saccharomyces cerevisiae EST2"  
SEQUENCE DESCRIPTION: SEQ ID NO: 162:  
US-09-766-253-162

Query Match 26.5%; Score 35; DB 2; Length 27;  
Best Local Similarity 70.0%; Pred. No. 1.1e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18  
| | | | | | | | | |  
Db 8 FDVKSCYDSI 17



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2006, 17:27:09 ; Search time 47.8395 Seconds  
(without alignments)  
218.350 Million cell updates/sec

Title: US-10-619-323-5  
Perfect score: 132  
Sequence: 1 PKKDVLFTTVKSCPDAlKEVFDNK 25

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 549595

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 50 summaries

Database : Published Applications AA Main:  
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2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
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4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
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6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	132	100.0	25	4	US-10-619-323-5
2	95	72.0	18	4	US-10-619-323-6
3	61	46.2	30	5	US-10-473-127-1717
4	49	37.1	10	5	US-10-473-127-165
5	39.5	29.9	50	4	US-10-425-115-244355
6	39	29.5	41	4	US-10-074-024-386
7	39	29.5	49	4	US-10-424-599-278211
8	39	29.5	50	4	US-10-424-599-165124
9	38.5	29.2	40	4	US-10-424-599-162982
10	38.5	29.2	50	4	US-10-437-963-136536
11	38	28.8	43	4	US-10-425-115-193153
12	38	28.8	46	5	US-10-809-761-18
13	37	28.0	46	4	US-10-437-963-170639
14	36	27.3	28	3	US-09-867-852-154
15	36	27.3	28	4	US-10-613-472-154
16	36	27.3	28	3	US-10-613-765-154
17	36	27.3	33	3	US-09-864-761-43932
18	36	27.3	42	3	US-09-848-664-14
19	36	27.3	46	4	US-10-724-972A-5875
20	35.5	26.9	41	3	US-09-864-761-46252
21	35.5	26.9	42	4	US-10-425-115-209264
22	35.5	26.9	43	6	US-11-097-143-27786
23	35	26.5	17	4	US-10-044-692-100
24	35	26.5	17	4	US-10-044-539-100
25	35	26.5	17	4	US-10-325-810-100
26	35	26.5	17	5	US-10-877-124-100
27	35	26.5	17	5	US-10-877-022-100

ALIGNMENTS

RESULT 1

US-10-619-323-5  
; Sequence 5, Application US/10619323  
; Publication No. US20040136985A1  
; GENERAL INFORMATION:  
; APPLICANT: Jennings, Lisa K.  
; APPLICANT: Longhurst, Celia M.  
; APPLICANT: Cook, George A.  
; APPLICANT: Bao, Jianxiong  
; APPLICANT: Zhang, Chunxiang  
; APPLICANT: White, Melanie M.  
; APPLICANT: Crossno, Jr., Joseph T.  
; APPLICANT: Lu, Yi  
; TITLE OF INVENTION: METHODS OF MODIFYING BEHAVIOR OF CD9-EXPRESSING CELLS  
; FILE REFERENCE: 20609/241  
; CURRENT APPLICATION NUMBER: US/10/619,323  
; CURRENT FILING DATE: 2003-07-14  
; PRIOR APPLICATION NUMBER: 60/395,864  
; PRIOR FILING DATE: 2002-07-12  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: CD9 peptide

Query Match 100.0%; Score 132; DB 4; Length 25;  
Best Local Similarity 100.0%; Pred. No. 8.4e-13;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLFTTVKSCPDAlKEVFDNK 25

Db 1 PKKDVLFTTVKSCPDAlKEVFDNK 25

RESULT 2

US-10-619-323-6  
; Sequence 6, Application US/10619323  
; Publication No. US20040136985A1  
; GENERAL INFORMATION:  
; APPLICANT: Jennings, Lisa K.  
; APPLICANT: Longhurst, Celia M.

```
; APPLICANT: Cook, George A.
; APPLICANT: Bao, Jianxiong
; APPLICANT: Zhang, Chunxiang
; APPLICANT: White, Melanie M.
; APPLICANT: Croseno, Jr., Joseph T.
; APPLICANT: Lu, Yi
; TITLE OF INVENTION: METHODS OF MODIFYING BEHAVIOR OF CD9-EXPRESSING CELLS
; FILE REFERENCE: 20609/241
; CURRENT APPLICATION NUMBER: US/10/619,323
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: 60/395,864
; PRIOR FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CD9 peptide
US-10-619-323-6

Query Match 72.0%; Score 95; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLFTFTVKSQDAI 18
Db 1 PKKDVLFTFTVKSQDAI 18
|||||

RESULT 3
US-10-473-127-1717
; Sequence 1717, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026WO1
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1717
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1717

Query Match 46.2%; Score 61; DB 5; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLFTFTVK 12
Db 19 PKKDVLFTFTVK 30
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RESULT 4
US-10-473-127-165
; Sequence 165, Application US/10473127
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; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026WO1
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 165
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-165

Query Match 37.1%; Score 49; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KDVLFTFTVK 12
Db 1 KDVLFTFTVK 10
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RESULT 5
US-10-425-115-244355
; Sequence 244355, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 244355
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRF4577_154437C.1.pep
US-10-425-115-244355

Query Match 29.9%; Score 39.5; DB 4; Length 50;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 9; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 8 TFTVKS-CPDAIKVFDN 24
Db 26 TFLRLTDLDPAMKEAFIN 43
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RESULT 6
US-10-074-024-386
; Sequence 386, Application US/10074024
; Publication No. US20030232975A1
; GENERAL INFORMATION:
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; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PC001C1  
; CURRENT APPLICATION NUMBER: US/10/074,024  
; CURRENT FILING DATE: 2002-02-14  
; Prior Application removed - See file Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 879  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 386  
; LENGTH: 41  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-074-024-386

Query Match 29.5%; Score 39; DB 4; Length 41;  
Best Local Similarity 28.6%; Pred. No. 2e+02;  
Matches 6; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 PKDVLTFVTKSCPDPAKEV 21  
| : : | : : | : :  
Db 5 PHREIFYFFTLRPAPDVSKHL 25

RESULT 7  
US-10-424-599-278211  
; Sequence 278211, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 278211  
; LENGTH: 49  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(49)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_93248C.1.pep  
US-10-424-599-278211

Query Match 29.5%; Score 39; DB 4; Length 49;  
Best Local Similarity 63.6%; Pred. No. 2.5e+02;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 EFTFVKSCPDPA 17  
| : : | : : | : :  
Db 9 EFTFVKSCPDPA 19

RESULT 8  
US-10-424-599-165124  
; Sequence 165124, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 165124  
; LENGTH: 50  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_120122C.1.pep  
US-10-424-599-165124

Query Match 29.5%; Score 39; DB 4; Length 50;  
Best Local Similarity 58.3%; Pred. No. 2.5e+02;  
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 LETFTVKSCPDPA 17  
| : : | : : | : :  
Db 36 LESKTLKTCPSA 47

RESULT 9  
US-10-424-599-162982  
; Sequence 162982, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 162982  
; LENGTH: 40  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_118190C.1.pep  
US-10-424-599-162982

Query Match 29.2%; Score 38.5; DB 4; Length 40;  
Best Local Similarity 56.2%; Pred. No. 2.3e+02;  
Matches 9; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 6 LETFTVKSC-PDAIKE 20  
| : : | : : | : :  
Db 15 LASLAVKSCPPQALKE 30

RESULT 10  
US-10-437-963-136536  
; Sequence 136536, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 136536  
; LENGTH: 50  
; TYPE: PRT  
; ORGANISM: Oryza sativa

; FEATURE:		Db		2		VLIKYTTKTQTPVKEMP 19	
; OTHER INFORMATION: Clone ID: PAT_MRT4530_38105C.1.pep							
US-10-437-963-136536							
Query Match							
Best Local Similarity							
Matches							
9; Conservative							
1; Mismatches							
8; Indels							
1; Gaps							
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1; Gaps							
1; Gaps							
1; Gaps							

```
Matches 7; Conservative 4; Mismatches 9; Indels 9; Gaps 0;
QY 1 PKQVLETFVTKSPDAIKE 20
||:|:|:|:|:|
Db 1 PKLEVIEFDCREIEELISE 20

RESULT 15
US-10-613-472-154
; Sequence 154, Application US/10613472
; Publication No. US20040088756A1
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
; FILE REFERENCE: 00786/254004
; CURRENT APPLICATION NUMBER: US/10/613,472
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: US 09/867,852
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 09/301,085
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: US 08/310,912
; PRIOR FILING DATE: 1994-09-22
; PRIOR APPLICATION NUMBER: US 08/227,360
; PRIOR FILING DATE: 1994-04-13
; NUMBER OF SEQ ID NOS: 214
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 154
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-613-472-154

Query Match 27.3%; Score 36; DB 4; Length 28;
Best Local Similarity 35.0%; Pred. No. 3.7e+02;
Matches 7; Conservative 4; Mismatches 9; Indels 9; Gaps 0;

QY 1 PKQVLETFVTKSPDAIKE 20
||:|:|:|:|:|
Db 1 PKLEVIEFDCREIEELISE 20

RESULT 16
US-10-613-765-154
; Sequence 154, Application US/10613765
; Publication No. US20040172673A1
; GENERAL INFORMATION:
; APPLICANT: AUSUBEL, FREDERICK M.
; APPLICANT: STASKAWICZ, BRIAN J.
; APPLICANT: KATAGIRI, FUMIAKI
; APPLICANT: KUNKEL, BARBARA N.
; APPLICANT: MINDRINOS, MICHAEL N.
; APPLICANT: YU, GUO-LIANG
; APPLICANT: BAKER, BARBARA
; APPLICANT: ELLIS, JEFFREY
; APPLICANT: SALMERON, JOHN
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
; FILE REFERENCE: 00786/254005
; CURRENT APPLICATION NUMBER: US/10/613,765
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: US 09/867,852
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 09/301,085
; PRIOR FILING DATE: 1999-04-28
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; PRIOR APPLICATION NUMBER: US 08/310,912
; PRIOR FILING DATE: 1994-09-22
; PRIOR APPLICATION NUMBER: US 08/227,360
; PRIOR FILING DATE: 1994-04-13
; NUMBER OF SEQ ID NOS: 214
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 154
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-613-765-154

Query Match 27.3%; Score 36; DB 4; Length 28;
Best Local Similarity 35.0%; Pred. No. 3.7e+02;
Matches 7; Conservative 4; Mismatches 9; Indels 9; Gaps 0;

QY 1 PKQVLETFVTKSPDAIKE 20
||:|:|:|:|:|
Db 1 PKLEVIEFDCREIEELISE 20

RESULT 17
US-09-864-761-43932
; Sequence 43932, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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; SEQ ID NO 43932
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005586.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.85
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.68
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.83
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.86
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.91
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.81
US-09-864-761-43932

Query Match          27.3%; Score 36; DB 3; Length 33;
Best Local Similarity 36.8%; Pred. No. 4.4e+02;
Matches 7; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 4 DVLETFVKSCPDAIKEVP 22
DB 3 NMLSTASITWLPGLKEVP 21

RESULT 18
US-09-848-664-14
; Sequence 14, Application US/09848664
; Patent No. US20020146414A1
; GENERAL INFORMATION:
; APPLICANT: Sakiyama-Elbert, Shelly E.
; APPLICANT: Hubbell, Jeffrey A.
; TITLE OF INVENTION: Controlled Release of No. US20020146414A1-Heparin Binding Growth
; TITLE OF INVENTION: Factors from Heparin Containing Matrices
; FILE REFERENCE: ETH 108
; CURRENT APPLICATION NUMBER: US/09/848,664
; CURRENT FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 09/298,084
; PRIOR FILING DATE: 1999-04-22
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 14
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-848-664-14

Query Match          27.3%; Score 36; DB 3; Length 42;
Best Local Similarity 50.0%; Pred. No. 5.9e+02;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKDVLETFVKSC 14
DB 26 PKVEQLSNMVKSC 39

RESULT 19
US-10-724-972A-5875
; Sequence 5875, Application US/10724972A
; Publication No. US20040147734A1
; GENERAL INFORMATION:
; APPLICANT: Doucette-Staum, Lynn
; APPLICANT: Bush, David
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PATH03-16
; CURRENT APPLICATION NUMBER: US/10/724,972A
; CURRENT FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: 09/450,969
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/134,001
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: 60/055,779
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; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 7544
; SEQ ID NO 5875
; LENGTH: 46
; TYPE: PRT
; ORGANISM: S.epidermidis
US-10-724-972A-5875

Query Match          27.3%; Score 36; DB 4; Length 46;
Best Local Similarity 35.3%; Pred. No. 6.5e+02;
Matches 6; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 2 KQDVLETFVKSCPDAL 18
DB 4 KEDMNTYRLKECDIL 20

RESULT 20
US-09-864-761-46252
; Sequence 46252, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 46252
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Homo sapiens
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;  
; FEATURE:  
; OTHER INFORMATION: MAP TO AC023154.3  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 62  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5  
; OTHER INFORMATION: EST HUMAN HIT: T56807.1, EVALUATE 4.80e-01  
; OTHER INFORMATION: SWISSPROT HIT: P17980, EVALUATE 1.90e-01  
US-09-864-761-46252

Query Match 26.9%; Score 35.5; DB 3; Length 41;  
Best Local Similarity 42.9%; Pred. No. 6.8e+02;  
Matches 9; Conservative 6; Mismatches 5; Indels 1; Gaps 1;

QY 1 PKQDVLETP-TVKSCPDPAIKE 20  
||:|||||:|:|:|:  
Db 19 PKEDHLEGFLEVOAKKEAVKD 39

RESULT 21  
US-10-425-115-209264  
; Sequence 209264, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 209264  
; LENGTH: 42  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_122443C.1.pep  
US-10-425-115-209264

Query Match 26.9%; Score 35.5; DB 4; Length 42;  
Best Local Similarity 50.0%; Pred. No. 7e+02;  
Matches 9; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 6 LETFTVKSCPDPAIKEVPD 23  
|||:|:|:|:|:|:  
Db 17 LETWLYYCKEA-KEKFD 33

RESULT 22  
US-11-097-143-27786  
; Sequence 27786, Application US/11097143  
; Publication No. US20050208558A1  
; GENERAL INFORMATION:  
; APPLICANT: et al.  
; APPLICANT: Venter, J. Craig  
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID  
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE  
; TITLE OF INVENTION: DROSOPHILA GENES.  
; FILE REFERENCE: CL000728  
; CURRENT APPLICATION NUMBER: US/11/097,143  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: 60/157,832  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: 60/160,191  
; PRIOR FILING DATE: 1999-10-19  
; PRIOR APPLICATION NUMBER: 60/161,932  
; PRIOR FILING DATE: 1999-10-28  
; PRIOR APPLICATION NUMBER: 60/164,769  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: 60/173,383  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: 60/175,693

;  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: 60/184,831  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/191,637  
; PRIOR FILING DATE: 2000-03-23  
; NUMBER OF SEQ ID NOS: 43008  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 27786  
; LENGTH: 43  
; TYPE: PRT  
; ORGANISM: DROSOPHILA  
US-11-097-143-27786

Query Match 26.9%; Score 35.5; DB 6; Length 43;  
Best Local Similarity 43.8%; Pred. No. 7.2e+02;  
Matches 7; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 11 VKSCPDPAIK-EVPDNK 25  
:|||||:|:|:  
Db 7 LKSCPDVWKWETMSNE 22

RESULT 23  
US-10-044-692-100  
; Sequence 100, Application US/10044692  
; Publication No. US20030096344A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.  
; APPLICANT: Morin, Gregg B.  
; APPLICANT: Harley, Calvin  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND  
; THERAPEUTIC METHODS  
; NUMBER OF SEQUENCES: 335  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/044,692  
; FILING DATE: 11-Jan-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/912,951  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002600US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300

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; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 17 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: <Unknown>
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   FEATURE:
;     NAME/KEY: Peptide
;     LOCATION: 1..17
;     OTHER INFORMATION: /note= "telomerase RT finger motif A
;     peptide from Saccharomyces
;     cerevisiae EST2"
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-044-692-100

Query Match      26.5%; Score 35; DB 4; Length 17;
Best Local Similarity 70.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      9 FTVKSCPDAl 18
Db      8 FDKVSCYDSI 17

RESULT 24
US-10-044-539-100
; Sequence 100, Application US/10044539
; Publication No. US20030100093A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
;   Lingner, Joachim
;   Nakamura, Toru
;   Chapman, Karen B.
;   Morin, Gregg B.
;   Harley, Calvin
;   Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
;   THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
;   STREET: Two Embarcadero and Townsend and Crew LLP
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: United States of America
;   ZIP: 94111
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/044,539
;   FILING DATE: 11-Jan-2002
;   CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/912,951
;   FILING DATE: <Unknown>
;   APPLICATION NUMBER: US 08/854,050
;   FILING DATE: 09-MAY-1997
;   APPLICATION NUMBER: US 08/851,843
;   FILING DATE: 06-MAY-1997
;   APPLICATION NUMBER: US 08/846,017
;   FILING DATE: 25-APR-1997
;   APPLICATION NUMBER: US 08/844,419
;   FILING DATE: 18-APR-1997
;   APPLICATION NUMBER: US 08/724,643
;   FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
;   NAME: Apple, Randolph T.
;   REGISTRATION NUMBER: 36,429
;   REFERENCE/DOCKET NUMBER: 015389-002600US
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 17 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: <Unknown>
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   FEATURE:
;     NAME/KEY: Peptide
;     LOCATION: 1..17
;     OTHER INFORMATION: /note= "telomerase RT finger motif A
;     peptide from Saccharomyces
;     cerevisiae EST2"
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-044-539-100

Query Match      26.5%; Score 35; DB 4; Length 17;
Best Local Similarity 70.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      9 FTVKSCPDAl 18
Db      8 FDKVSCYDSI 17

RESULT 25
US-10-325-810-100
; Sequence 100, Application US/10325810
; Publication No. US20030204069A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
;   Lingner, Joachim
;   Nakamura, Toru
;   Chapman, Karen B.
;   Morin, Gregg B.
;   Harley, Calvin B.
;   Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
;   STREET: Townsend and Townsend and Crew LLP
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94111-3834
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/325,810
;   FILING DATE: 20-Dec-2002
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/09/402,181
;   FILING DATE: 29-Sep-1997
;   APPLICATION NUMBER: US 08/724,643
;   FILING DATE: 01-OCT-1996
;   APPLICATION NUMBER: US 08/844,419
;   FILING DATE: 18-APR-1997
;   APPLICATION NUMBER: US 08/846,017
;   FILING DATE: 25-APR-1997
;   APPLICATION NUMBER: US 08/851,843
;   FILING DATE: 06-MAY-1997
;   APPLICATION NUMBER: US 08/854,050
;   FILING DATE: 09-MAY-1997
;   APPLICATION NUMBER: US 08/911,312
;   FILING DATE: 14-AUG-1997
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APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..17
OTHER INFORMATION: /note= "telomerase RT finger motif A
peptide from Saccharomyces
cerevisiae EST2"
SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-877-124-100
Query Match 26.5%; Score 35; DB 5; Length 17;
Best Local Similarity 70.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 9 FTVKSCPDAI 18
DB 8 FDVKSICYDSI 17
RESULT 27
US-10-877-022-100
; Sequence 100, Application US/10877022
; Publication No. US20040247613A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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## RESULT 29

US-09-843-676-140  
; Sequence 140, Application US/09843676  
; Patent No. US20020164786A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin  
; Andrews, William H.  
; TITLE OF INVENTION: No. US20020164786A1el Telomerase  
; NUMBER OF SEQUENCES: 225  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/843,676  
; FILING DATE: 26-Apr-2001  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/854,050  
; FILING DATE: 09-MAY-1997  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002930US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 140:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 26 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..26  
; OTHER INFORMATION: /note= "motif 3(A) peptide from  
; Saccharomyces cerevisiae EST2p"  
; SEQUENCE DESCRIPTION: SEQ ID NO: 140:  
US-09-843-676-140

Query Match 26.5%; Score 35; DB 3; Length 26;  
Best Local Similarity 70.0%; Pred. No. 4.8e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAl 18

Db 7 FDVKSCYDSI 16

## RESULT 30

US-09-766-253-140

; Sequence 140, Application US/09766253  
; Publication No. US20020187471A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin  
; Andrews, William H.  
; TITLE OF INVENTION: No. US20020187471A1el Telomerase  
; NUMBER OF SEQUENCES: 171  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/766,253  
; FILING DATE: 19-Jan-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/846,017  
; FILING DATE: 1997-04-25  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002920US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 140:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 26 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..26  
; OTHER INFORMATION: /note= "motif 3(A) peptide from  
; Saccharomyces cerevisiae EST2p"  
; SEQUENCE DESCRIPTION: SEQ ID NO: 140:  
US-09-766-253-140

Query Match 26.5%; Score 35; DB 3; Length 26;  
Best Local Similarity 70.0%; Pred. No. 4.8e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAl 18

Db 7 FDVKSCYDSI 16

## RESULT 31

US-09-438-486-140  
; Sequence 140, Application US/09438486  
; Publication No. US20030009019A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.

APPLICANT: Morin, Gregg B.  
APPLICANT: Harley, Calvin  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: No. US20030009019A1el Telomerase  
NUMBER OF SEQUENCES: 223  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/438,486  
FILING DATE: 12-NOV-1999  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002931US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 140:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..26  
OTHER INFORMATION: /note= "motif 3(A) peptide from  
Saccharomyces cerevisiae EST2p"

US-09-438-486-140  
Query Match 26.5%; Score 35; DB 3; Length 26;  
Best Local Similarity 70.0%; Pred. No. 4.8e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAl 18  
Db 7 FDVKSCYDSI 16

RESULT 32  
US-10-053-758-140  
Sequence 140, Application US/10053758  
Publication No. US20030032075A1  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.

Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin  
Andrews, William H.  
TITLE OF INVENTION: No. US20030032075A1el Telomerase  
NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/053,758  
FILING DATE: 18-Jan-2002  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 140:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..26  
OTHER INFORMATION: /note= "motif 3(A) peptide from  
Saccharomyces cerevisiae EST2p"

US-10-053-758-140  
Query Match 26.5%; Score 35; DB 4; Length 26;  
Best Local Similarity 70.0%; Pred. No. 4.8e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAl 18  
Db 7 FDVKSCYDSI 16

RESULT 33  
US-10-054-295-140  
Sequence 140, Application US/10054295  
Publication No. US2003004953A1  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim

;/ Nakamura, Toru  
;/ Chapman, Karen B.  
;/ Morin, Gregg B.  
;/ Harley, Calvin  
;/ Andrews, William H.  
;/ TITLE OF INVENTION: No. US20030044953A1el Telomerase  
;/ NUMBER OF SEQUENCES: 225  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: Townsend and Townsend and Crew LLP  
;/ STREET: Two Embarcadero Center, 8th Floor  
;/ CITY: San Francisco  
;/ STATE: California  
;/ COUNTRY: United States of America  
;/ ZIP: 94111  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/10/054,295  
;/ FILING DATE: 18-Jan-2002  
;/ CLASSIFICATION: 536  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: 08/854,050  
;/ FILING DATE: <Unknown>  
;/ APPLICATION NUMBER: US 08/846,017  
;/ FILING DATE: 25-APR-1997  
;/ APPLICATION NUMBER: US 08/844,419  
;/ FILING DATE: 18-APR-1997  
;/ APPLICATION NUMBER: US 08/724,643  
;/ FILING DATE: 01-OCT-1996  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Apple, Randolph T.  
;/ REGISTRATION NUMBER: 36,429  
;/ REFERENCE/DOCKET NUMBER: 015389-002930US  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (415) 576-0200  
;/ TELEFAX: (415) 576-0300  
;/ INFORMATION FOR SEQ ID NO: 140:  
;/ LENGTH: 26 amino acids  
;/ TYPE: amino acid  
;/ STRANDEDNESS: <Unknown>  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: peptide  
;/ FEATURE:  
;/ NAME/KEY: Peptide  
;/ LOCATION: 1..26  
;/ OTHER INFORMATION: /note= "motif 3(A) peptide from  
;/ Saccharomyces cerevisiae EST2p"  
;/ SEQUENCE DESCRIPTION: SEQ ID NO: 140:  
;/ US-10-054-295-140

Query Match 26.5%; Score 35; DB 4; Length 26;  
Best Local Similarity 70.0%; Pred. No. 4.8e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAl 18  
Db 7 FDVKSICYDSI 16

## RESULT 34

US-10-054-611-140  
;/ Sequence 140, Application US/10054611  
;/ Publication No. US20030059787A1  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Cech, Thomas R.  
;/ Lingner, Joachim  
;/ Nakamura, Toru  
;/ Chapman, Karen B.  
;/ Morin, Gregg B.

;/ Harley, Calvin  
;/ Andrews, William H.  
;/ TITLE OF INVENTION: No. US20030059787A1el Telomerase  
;/ NUMBER OF SEQUENCES: 225  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: Townsend and Townsend and Crew LLP  
;/ STREET: Two Embarcadero Center, 8th Floor  
;/ CITY: San Francisco  
;/ STATE: California  
;/ COUNTRY: United States of America  
;/ ZIP: 94111  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/10/054,611  
;/ FILING DATE: 18-Jan-2002  
;/ CLASSIFICATION: 536  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: 08/854,050  
;/ FILING DATE: <Unknown>  
;/ APPLICATION NUMBER: US 08/846,017  
;/ FILING DATE: 25-APR-1997  
;/ APPLICATION NUMBER: US 08/844,419  
;/ FILING DATE: 18-APR-1997  
;/ APPLICATION NUMBER: US 08/724,643  
;/ FILING DATE: 01-OCT-1996  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Apple, Randolph T.  
;/ REGISTRATION NUMBER: 36,429  
;/ REFERENCE/DOCKET NUMBER: 015389-002930US  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (415) 576-0200  
;/ TELEFAX: (415) 576-0300  
;/ INFORMATION FOR SEQ ID NO: 140:  
;/ LENGTH: 26 amino acids  
;/ TYPE: amino acid  
;/ STRANDEDNESS: <Unknown>  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: peptide  
;/ FEATURE:  
;/ NAME/KEY: Peptide  
;/ LOCATION: 1..26  
;/ OTHER INFORMATION: /note= "motif 3(A) peptide from  
;/ Saccharomyces cerevisiae EST2p"  
;/ SEQUENCE DESCRIPTION: SEQ ID NO: 140:  
;/ US-10-054-611-140

Query Match 26.5%; Score 35; DB 4; Length 26;  
Best Local Similarity 70.0%; Pred. No. 4.8e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAl 18  
Db 7 FDVKSICYDSI 16

## RESULT 35

US-10-325-810-258  
;/ Sequence 258, Application US/10325810  
;/ Publication No. US20030204069A1  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Cech, Thomas R.  
;/ Lingner, Joachim  
;/ Nakamura, Toru  
;/ Chapman, Karen B.  
;/ Morin, Gregg B.  
;/ Harley, Calvin B.  
;/ Andrews, William H.  
;/ TITLE OF INVENTION: Human Telomerase Catalytic Subunit

;/ NUMBER OF SEQUENCES: 633  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: Townsend and Townsend and Crew LLP  
;/ STREET: Two Embarcadero Center, Eighth Floor  
;/ CITY: San Francisco  
;/ STATE: California  
;/ COUNTRY: USA  
;/ ZIP: 94111-3834  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/10/325,810  
;/ FILING DATE: 20-Dec-2002  
;/ CLASSIFICATION: <Unknown>  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: US/09/402,181  
;/ FILING DATE: 29-Sep-1997  
;/ APPLICATION NUMBER: US 08/724,643  
;/ FILING DATE: 01-OCT-1996  
;/ APPLICATION NUMBER: US 08/844,419  
;/ FILING DATE: 18-APR-1997  
;/ APPLICATION NUMBER: US 08/846,017  
;/ FILING DATE: 25-APR-1997  
;/ APPLICATION NUMBER: US 08/851,843  
;/ FILING DATE: 06-MAY-1997  
;/ APPLICATION NUMBER: US 08/854,050  
;/ FILING DATE: 09-MAY-1997  
;/ APPLICATION NUMBER: US 08/911,312  
;/ FILING DATE: 14-AUG-1997  
;/ APPLICATION NUMBER: US 08/912,951  
;/ FILING DATE: 14-AUG-1997  
;/ APPLICATION NUMBER: US 08/915,503  
;/ FILING DATE: 01-OCT-1997  
;/ APPLICATION NUMBER: WO PCT/US97/17885  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Ausehus, Scott L.  
;/ REGISTRATION NUMBER: 42,271  
;/ REFERENCE/DOCKET NUMBER: 015389-002620US  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (415) 576-0200  
;/ TELEFAX: (415) 576-0300  
;/ INFORMATION FOR SEQ ID NO: 258:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 26 amino acids  
;/ TYPE: amino acid  
;/ STRANDEDNESS: <Unknown>  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: peptide  
;/ FEATURE:  
;/ NAME/KEY: Peptide  
;/ LOCATION: 1..26  
;/ OTHER INFORMATION: /note= "motif 3(A) peptide from  
;/ Saccharomyces cerevisiae EST2p"  
;/ SEQUENCE DESCRIPTION: SEQ ID NO: 258:  
US-10-325-810-258

Query Match 26.5%; Score 35; DB 4; Length 26;  
Best Local Similarity 70.0%; Pred. No. 4.8e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAI 18

Db 7 FDKVSCYDSI 16

RESULT 36

US-10-877-124-258

; Sequence 258, Application US/10877124

; Publication No. US20040242529A1

;/ GENERAL INFORMATION:  
;/ APPLICANT: Cech, Thomas R.  
;/ Lingner, Joachim  
;/ Nakamura, Toru  
;/ Chapman, Karen B.  
;/ Morin, Gregg B.  
;/ Harley, Calvin B.  
;/ Andrews, William H.  
;/ TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
;/ NUMBER OF SEQUENCES: 727  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: Townsend and Townsend and Crew LLP  
;/ STREET: Two Embarcadero Center, Eighth Floor  
;/ CITY: San Francisco  
;/ STATE: California  
;/ COUNTRY: USA  
;/ ZIP: 94111-3834  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/10/877,124  
;/ FILING DATE: 24-Jun-2004  
;/ CLASSIFICATION: <Unknown>  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: US/09/432,503  
;/ FILING DATE: 02-Nov-1999  
;/ APPLICATION NUMBER: 08/974,549  
;/ FILING DATE: <Unknown>  
;/ APPLICATION NUMBER: US 08/844,419  
;/ FILING DATE: 18-APR-1997  
;/ APPLICATION NUMBER: US 08/846,017  
;/ FILING DATE: 25-APR-1997  
;/ APPLICATION NUMBER: US 08/851,843  
;/ FILING DATE: 06-MAY-1997  
;/ APPLICATION NUMBER: US 08/854,050  
;/ FILING DATE: 09-MAY-1997  
;/ APPLICATION NUMBER: US 08/911,312  
;/ FILING DATE: 14-AUG-1997  
;/ APPLICATION NUMBER: US 08/912,951  
;/ FILING DATE: 14-AUG-1997  
;/ APPLICATION NUMBER: US 08/915,503  
;/ FILING DATE: 14-AUG-1997  
;/ APPLICATION NUMBER: WO PCT/US97/17618  
;/ APPLICATION NUMBER: WO PCT/US97/17885  
;/ FILING DATE: 01-OCT-1997  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Apple, Randolph Ted  
;/ REGISTRATION NUMBER: 36,429  
;/ REFERENCE/DOCKET NUMBER: 015389-002610US  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (415) 576-0200  
;/ TELEFAX: (415) 576-0300  
;/ INFORMATION FOR SEQ ID NO: 258:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 26 amino acids  
;/ TYPE: amino acid  
;/ STRANDEDNESS: <Unknown>  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: peptide  
;/ FEATURE:  
;/ NAME/KEY: Peptide  
;/ LOCATION: 1..26  
;/ OTHER INFORMATION: /note= "motif 3(A) peptide from  
;/ Saccharomyces cerevisiae EST2p"  
;/ SEQUENCE DESCRIPTION: SEQ ID NO: 258:  
US-10-877-124-258

Query Match 26.5%; Score 35; DB 5; Length 26;  
Best Local Similarity 70.0%; Pred. No. 4.8e+02;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 9 FTVKSCPDAl 18  
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Db 7 FDVKSVCYDSI 16

RESULT 37  
US-10-877-022-258  
; Sequence 258, Application US/10877022  
; Publication No. US20040247613A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin B.  
; Andrews, William H.  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 727  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/877,022  
; FILING DATE: 24-Jun-2004  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/432,503  
; FILING DATE: 02-Nov-1999  
; APPLICATION NUMBER: 08/974,549  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; APPLICATION NUMBER: US 08/911,312  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: US 08/912,951  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: US 08/915,503  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: WO PCT/US97/17618  
; FILING DATE: 01-OCT-1997  
; APPLICATION NUMBER: WO PCT/US97/17885  
; FILING DATE: 01-OCT-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph Ted  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002610US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 258:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 26 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear

MOLECULE TYPE: peptide  
FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..26  
; OTHER INFORMATION: /note= "motif 3(A) peptide from  
; Saccharomyces cerevisiae EST2p"  
; SEQUENCE DESCRIPTION: SEQ ID NO: 258:  
US-10-877-022-258

Query Match 26.5%; Score 35; DB 5; Length 26;  
Best Local Similarity 70.0%; Pred. NO. 4.8e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 9 FTVKSCPDAl 18  
| | | | | | | |  
Db 7 FDVKSVCYDSI 16

RESULT 38  
US-10-877-146-258  
; Sequence 258, Application US/10877146  
; Publication No. US20050013825A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin B.  
; Andrews, William H.  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 727  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/877,146  
; FILING DATE: 24-Jun-2004  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/432,503  
; FILING DATE: 02-Nov-1999  
; APPLICATION NUMBER: 08/974,549  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; APPLICATION NUMBER: US 08/911,312  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: US 08/912,951  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: US 08/915,503  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: WO PCT/US97/17618  
; FILING DATE: 01-OCT-1997  
; APPLICATION NUMBER: WO PCT/US97/17885  
; FILING DATE: 01-OCT-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph Ted

/ / REGISTRATION NUMBER: 36,429  
/ / REFERENCE/DOCKET NUMBER: 015389-002610US  
/ / TELECOMMUNICATION INFORMATION:  
/ / TELEPHONE: (415) 576-0200  
/ / TELEFAX: (415) 576-0300  
/ / INFORMATION FOR SEQ ID NO: 258:  
/ / SEQUENCE CHARACTERISTICS:  
/ / LENGTH: 26 amino acids  
/ / TYPE: amino acid  
/ / STRANDEDNESS: <Unknown>  
/ / MOLECULE TYPE: peptide  
/ / TOPOLOGY: linear  
/ / NAME/KEY: Peptide  
/ / LOCATION: 1..26  
/ / OTHER INFORMATION: /note= "motif 3(A) peptide from  
/ / Saccharomyces cerevisiae EST2p"  
/ / SEQUENCE DESCRIPTION: SEQ ID NO: 258:  
US-10-877-146-258

Query Match 26.5%; Score 35; DB 5; Length 26;  
Best Local Similarity 70.0%; Pred. No. 4.8e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAI 18  
Db 7 FDKSCYDSI 16

RESULT 39  
US-09-843-676-156  
/ Sequence 156, Application US/09843676  
/ Patent No. US20020164786A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Cech, Thomas R.  
/ Lingner, Joachim  
/ Nakamura, Toru  
/ Chapman, Karen B.  
/ Morin, Gregg B.  
/ Harley, Calvin  
/ Andrews, William H.  
/ TITLE OF INVENTION: No. US20020164786A1el Telomerase  
/ NUMBER OF SEQUENCES: 225  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Townsend and Townsend and Crew LLP  
/ STREET: Two Embarcadero Center, 8th Floor  
/ CITY: San Francisco  
/ STATE: California  
/ COUNTRY: United States of America  
/ ZIP: 94111

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/843,676  
FILING DATE: 26-Apr-2001  
CLASSIFICATION: 536

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300

/ / TELEPHONE: (415) 576-0200  
/ / TELEFAX: (415) 576-0300  
/ / INFORMATION FOR SEQ ID NO: 156:  
/ / SEQUENCE CHARACTERISTICS:  
/ / LENGTH: 27 amino acids  
/ / TYPE: amino acid  
/ / STRANDEDNESS: <Unknown>  
/ / TOPOLOGY: linear  
/ / MOLECULE TYPE: peptide  
/ / FEATURE:  
/ / NAME/KEY: Peptide  
/ / LOCATION: 1..27  
/ / OTHER INFORMATION: /note= "motif A peptide from  
/ / Schizosaccharomyces pombe tez1"  
/ / SEQUENCE DESCRIPTION: SEQ ID NO: 156:  
US-09-843-676-156

Query Match 26.5%; Score 35; DB 3; Length 27;  
Best Local Similarity 36.8%; Pred. No. 5e+02;  
Matches 7; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 2 KQVLETFVKSCPDAIXE 20  
Db 1 RKKYFVRIDIKSCYDRIKQ 19

RESULT 40  
US-09-843-676-162  
/ Sequence 162, Application US/09843676  
/ Patent No. US20020164786A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Cech, Thomas R.  
/ Lingner, Joachim  
/ Nakamura, Toru  
/ Chapman, Karen B.  
/ Morin, Gregg B.  
/ Harley, Calvin  
/ Andrews, William H.  
/ TITLE OF INVENTION: No. US20020164786A1el Telomerase  
/ NUMBER OF SEQUENCES: 225  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Townsend and Townsend and Crew LLP  
/ STREET: Two Embarcadero Center, 8th Floor  
/ CITY: San Francisco  
/ STATE: California  
/ COUNTRY: United States of America  
/ ZIP: 94111

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/843,676  
FILING DATE: 26-Apr-2001  
CLASSIFICATION: 536

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 162:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..27
; OTHER INFORMATION: /note= "motif A peptide from
; Saccharomyces cerevisiae EST2"
; SEQUENCE DESCRIPTION: SEQ ID NO: 162:
US-09-843-676-162

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Query Match      26.5%; Score 35; DB 3; Length 27;
Best Local Similarity 70.0%; Pred. No. 5e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy      9 FTVKSCPDAl 18
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Db      8 FDVKSCYDSI 17

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Search completed: January 20, 2006, 17:38:19  
Job time : 48.8395 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:30:50 ; Search time 4.32099 Seconds  
(without alignments)  
58.632 Million cell updates/sec

Title: US-10-619-323-5

Perfect score: 132

Sequence: 1 PKQVLETFVTKSPDAKEVPDNK 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 70606 seqs, 10133881 residues

Total number of hits satisfying chosen parameters: 41278

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

#### Database :

Published Applications AA New:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	36	27.3	34	6	US-10-816-768-31
2	34	25.8	34	6	US-10-816-768-30
3	34	25.8	37	6	US-10-957-351-6
4	33	25.0	43	6	US-10-952-535A-39
5	32	24.2	32	6	US-10-957-351-196
6	32	24.2	34	6	US-10-816-768-29
7	32	24.2	35	6	US-10-957-351-195
8	32	24.2	35	6	US-10-957-351-194
9	31	23.5	35	6	US-10-957-351-112
10	31	23.5	38	6	US-10-957-351-32
11	31	23.5	38	7	US-11-093-118-6
12	31	23.5	44	6	US-10-986-501-356
13	30	22.7	30	6	US-10-467-657-6336
14	30	22.7	33	6	US-10-957-351-183
15	29.5	22.3	33	6	US-10-504-879-63
16	29.5	22.3	33	7	US-11-121-301-50
17	29.5	22.3	48	6	US-10-504-879-62
18	29	22.0	38	6	US-10-957-351-155
19	29	22.0	47	7	US-11-123-896-453
20	28	21.2	19	6	US-10-503-575-243
21	28	21.2	20	7	US-11-022-562-157
22	28	21.2	20	7	US-11-022-562-158
23	28	21.2	24	7	US-11-006-119-30
24	28	21.2	24	7	US-11-033-116-4
25	28	21.2	34	7	US-11-033-116-6

26	28	21.2	35	6	US-10-957-351-329	Sequence 329, App
27	28	21.2	44	6	US-10-467-657-1118	Sequence 1118, App
28	28	21.2	44	6	US-10-957-887B-278	Sequence 278, App
29	28	21.2	46	6	US-10-957-887B-258	Sequence 258, App
30	27	20.5	9	6	US-10-859-643-2	Sequence 2, Appli
31	27	20.5	9	6	US-10-859-643-254	Sequence 254, App
32	27	20.5	9	6	US-10-859-643-690	Sequence 690, App
33	27	20.5	9	7	US-11-097-864-2	Sequence 2, Appli
34	27	20.5	9	7	US-11-097-864-254	Sequence 254, App
35	27	20.5	9	7	US-11-097-864-690	Sequence 690, App
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37	27	20.5	9	7	US-11-097-912-254	Sequence 254, App
38	27	20.5	9	7	US-11-097-912-690	Sequence 690, App
39	27	20.5	10	6	US-10-859-643-350	Sequence 350, App
40	27	20.5	10	7	US-11-097-864-350	Sequence 350, App
41	27	20.5	10	7	US-11-097-912-350	Sequence 350, App
42	27	20.5	15	7	US-11-019-894A-28	Sequence 10, Appl
43	27	20.5	16	7	US-11-060-646-10	Sequence 72, Appl
44	27	20.5	17	6	US-10-723-207-72	Sequence 192, App
45	27	20.5	19	6	US-10-503-575-192	Sequence 3848, Ap
46	27	20.5	21	6	US-10-467-657-3848	Sequence 5752, Ap
47	27	20.5	30	6	US-10-467-657-5752	Sequence 995, App
48	27	20.5	33	6	US-10-821-234-995	Sequence 7362, Ap
49	27	20.5	35	6	US-10-467-657-7362	Sequence 8218, Ap
50	27	20.5	35	6	US-10-467-657-8218	

#### ALIGNMENTS

RESULT 1  
US-10-816-768-31  
; Sequence 31, Application US/10816768  
; Publication No. US20050250936A1  
; GENERAL INFORMATION:  
; APPLICANT: Oppermann, Hermann  
; APPLICANT: Tai, Mei-Sheng  
; APPLICANT: McCartney, John  
; TITLE OF INVENTION: Modified TGF-beta Superfamily Proteins  
; FILE REFERENCE: STK-075  
; CURRENT APPLICATION NUMBER: US/10/816,768  
; CURRENT FILING DATE: 2004-04-02  
; NUMBER OF SEQ ID NOS: 124  
; SOFTWARE: PatentIn version 2.0  
; SEQ ID NO 31  
; LENGTH: 34  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: TGF-Beta3  
US-10-816-768-31

Query Match 27.3%; Score 36; DB 6; Length 34;  
Best Local Similarity 50.0%; Pred. No. 15;  
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
QY 1 PKQVLETFVTKSC 14  
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Db 18 PKVEQLSNMVKSC 31

RESULT 2  
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; Sequence 30, Application US/10816768  
; Publication No. US20050250936A1  
; GENERAL INFORMATION:  
; APPLICANT: Oppermann, Hermann  
; APPLICANT: Tai, Mei-Sheng  
; APPLICANT: McCartney, John  
; TITLE OF INVENTION: Modified TGF-beta Superfamily Proteins  
; FILE REFERENCE: STK-075  
; CURRENT APPLICATION NUMBER: US/10/816,768  
; CURRENT FILING DATE: 2004-04-02

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; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 30
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: TGF-Beta2
US-10-816-768-30

Query Match      25.8%; Score 34; DB 6; Length 34;
Best Local Similarity 50.0%; Pred. No. 30;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKQDVLETFVKSVC 14
   ||:|:|
Db 18 PKIEQLSNMIVKSC 31

RESULT 3
US-10-957-351-6
; Sequence 6, Application US/10957351
; Publication No. US20060008844A1
; GENERAL INFORMATION:
; APPLICANT: Stemmer, Willem P. C.
; APPLICANT: Perliroth, D. Victor
; APPLICANT: Satyal, Sanjeev
; APPLICANT: Avidia Research Institute
; TITLE OF INVENTION: c-Met Kinase Binding Proteins
; FILE REFERENCE: 022013-001400US
; CURRENT APPLICATION NUMBER: US/10/957,351
; CURRENT FILING DATE: 2004-09-30
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 471
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human LDL-receptor class A domain
US-10-957-351-6

Query Match      25.8%; Score 34; DB 6; Length 37;
Best Local Similarity 66.7%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 12 KSCPDPAIKE 20
   |||||
Db 26 KSCPDGADE 34

RESULT 4
US-10-952-535A-39
; Sequence 39, Application US/10952535A
; Publication No. US20050255113A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Messer, Anne
; APPLICANT: Lecerf, Jean-Michel
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING POLYPEPTIDE
; TITLE OF INVENTION: ACCUMULATION ASSOCIATED WITH NEUROLOGICAL DISORDERS
; FILE REFERENCE: INR-004CP
; CURRENT APPLICATION NUMBER: US/10/952,535A
; CURRENT FILING DATE: 2004-09-27
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 43
; TYPE: PRT

; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 30
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: TGF-Beta2
US-10-816-768-30

Query Match      25.8%; Score 34; DB 6; Length 34;
Best Local Similarity 50.0%; Pred. No. 30;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKQDVLETFVKSVC 14
   ||:|:|
Db 18 PKIEQLSNMIVKSC 31

RESULT 3
US-10-957-351-6
; Sequence 6, Application US/10957351
; Publication No. US20060008844A1
; GENERAL INFORMATION:
; APPLICANT: Stemmer, Willem P. C.
; APPLICANT: Perliroth, D. Victor
; APPLICANT: Satyal, Sanjeev
; APPLICANT: Avidia Research Institute
; TITLE OF INVENTION: c-Met Kinase Binding Proteins
; FILE REFERENCE: 022013-001400US
; CURRENT APPLICATION NUMBER: US/10/957,351
; CURRENT FILING DATE: 2004-09-30
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 471
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human LDL-receptor class A domain
US-10-957-351-6

Query Match      25.8%; Score 34; DB 6; Length 37;
Best Local Similarity 66.7%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 12 KSCPDPAIKE 20
   |||||
Db 26 KSCPDGADE 34

RESULT 4
US-10-952-535A-39
; Sequence 39, Application US/10952535A
; Publication No. US20050255113A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Messer, Anne
; APPLICANT: Lecerf, Jean-Michel
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING POLYPEPTIDE
; TITLE OF INVENTION: ACCUMULATION ASSOCIATED WITH NEUROLOGICAL DISORDERS
; FILE REFERENCE: INR-004CP
; CURRENT APPLICATION NUMBER: US/10/952,535A
; CURRENT FILING DATE: 2004-09-27
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 43
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-952-535A-39

Query Match      25.0%; Score 33; DB 6; Length 43;
Best Local Similarity 33.3%; Pred. No. 56;
Matches 7; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 2 KQDVLETFVKSVCDAIKEVF 22
   ||:|:|
Db 1 KKEYVELYTQWRIVDRVQEQF 21

RESULT 5
US-10-957-351-196
; Sequence 196, Application US/10957351
; Publication No. US20060008844A1
; GENERAL INFORMATION:
; APPLICANT: Stemmer, Willem P. C.
; APPLICANT: Perliroth, D. Victor
; APPLICANT: Satyal, Sanjeev
; APPLICANT: Avidia Research Institute
; TITLE OF INVENTION: c-Met Kinase Binding Proteins
; FILE REFERENCE: 022013-001400US
; CURRENT APPLICATION NUMBER: US/10/957,351
; CURRENT FILING DATE: 2004-09-30
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 471
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 196
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human LDL-receptor class A domain
US-10-957-351-196

Query Match      24.2%; Score 32; DB 6; Length 32;
Best Local Similarity 50.0%; Pred. No. 57;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 11 VKSCPDPAIKE 20
   |||||
Db 20 VKDCPGLDE 29

RESULT 6
US-10-816-768-29
; Sequence 29, Application US/10816768
; Publication No. US20050250936A1
; GENERAL INFORMATION:
; APPLICANT: Oppermann, Hermann
; APPLICANT: Tai, Mei-Sheng
; APPLICANT: McCartney, John
; TITLE OF INVENTION: Modified TGF-beta Superfamily Proteins
; FILE REFERENCE: STK-075
; CURRENT APPLICATION NUMBER: US/10/816,768
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 29
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: TGF-Betal
US-10-816-768-29

Query Match      24.2%; Score 32; DB 6; Length 34;
Best Local Similarity 42.9%; Pred. No. 61;
```

Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 PKDVLFTFTVKSC 14  
|| : |||  
Db 18 PKVEQLSNMIVRSC 31

RESULT 7  
US-10-957-351-34  
; Sequence 34, Application US/10957351  
; Publication No. US20060008844A1  
; GENERAL INFORMATION:  
; APPLICANT: Stemmer, Willem P. C.  
; APPLICANT: Perliroth, D. Victor  
; APPLICANT: Satyal, Sanjeev  
; APPLICANT: Avidia Research Institute  
; TITLE OF INVENTION: c-Met Kinase Binding Proteins  
; FILE REFERENCE: 022013-001400US  
; CURRENT APPLICATION NUMBER: US/10/957,351  
; CURRENT FILING DATE: 2004-09-30  
; PRIOR APPLICATION NUMBER: US 10/871,602  
; PRIOR FILING DATE: 2004-06-17  
; NUMBER OF SEQ ID NOS: 471  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 34  
; LENGTH: 35  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: human LDL-receptor class A domain  
US-10-957-351-34

Query Match 24.2%; Score 32; DB 6; Length 35;  
Best Local Similarity 46.7%; Pred. No. 63;  
Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 6 LETFTVKSCPDATKE 20  
|| : |||  
Db 18 LECDDTPNCPDASDE 32

RESULT 8  
US-10-957-351-195  
; Sequence 195, Application US/10957351  
; Publication No. US20060008844A1  
; GENERAL INFORMATION:  
; APPLICANT: Stemmer, Willem P. C.  
; APPLICANT: Perliroth, D. Victor  
; APPLICANT: Satyal, Sanjeev  
; APPLICANT: Avidia Research Institute  
; TITLE OF INVENTION: c-Met Kinase Binding Proteins  
; FILE REFERENCE: 022013-001400US  
; CURRENT APPLICATION NUMBER: US/10/957,351  
; CURRENT FILING DATE: 2004-09-30  
; PRIOR APPLICATION NUMBER: US 10/871,602  
; PRIOR FILING DATE: 2004-06-17  
; NUMBER OF SEQ ID NOS: 471  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 195  
; LENGTH: 35  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: human LDL-receptor class A domain  
US-10-957-351-195

Query Match 24.2%; Score 32; DB 6; Length 35;  
Best Local Similarity 50.0%; Pred. No. 63;  
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 11 VKSCPDATKEVF 22  
|| : |||  
Db 23 VQCCPDGSDDF 34

RESULT 9  
US-10-957-351-112  
; Sequence 112, Application US/10957351  
; Publication No. US20060008844A1  
; GENERAL INFORMATION:  
; APPLICANT: Stemmer, Willem P. C.  
; APPLICANT: Perliroth, D. Victor  
; APPLICANT: Satyal, Sanjeev  
; APPLICANT: Avidia Research Institute  
; TITLE OF INVENTION: c-Met Kinase Binding Proteins  
; FILE REFERENCE: 022013-001400US  
; CURRENT APPLICATION NUMBER: US/10/957,351  
; CURRENT FILING DATE: 2004-09-30  
; PRIOR APPLICATION NUMBER: US 10/871,602  
; PRIOR FILING DATE: 2004-06-17  
; NUMBER OF SEQ ID NOS: 471  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 112  
; LENGTH: 35  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: human LDL-receptor class A domain  
US-10-957-351-112

Query Match 23.5%; Score 31; DB 6; Length 35;  
Best Local Similarity 50.0%; Pred. No. 90;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 11 VKSCPDATKE 20  
|| : |||  
Db 23 VRDCPDGAD 32

RESULT 10  
US-10-957-351-32  
; Sequence 32, Application US/10957351  
; Publication No. US20060008844A1  
; GENERAL INFORMATION:  
; APPLICANT: Stemmer, Willem P. C.  
; APPLICANT: Perliroth, D. Victor  
; APPLICANT: Satyal, Sanjeev  
; APPLICANT: Avidia Research Institute  
; TITLE OF INVENTION: c-Met Kinase Binding Proteins  
; FILE REFERENCE: 022013-001400US  
; CURRENT APPLICATION NUMBER: US/10/957,351  
; CURRENT FILING DATE: 2004-09-30  
; PRIOR APPLICATION NUMBER: US 10/871,602  
; PRIOR FILING DATE: 2004-06-17  
; NUMBER OF SEQ ID NOS: 471  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 32  
; LENGTH: 38  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: human LDL-receptor class A domain  
US-10-957-351-32

Query Match 23.5%; Score 31; DB 6; Length 38;  
Best Local Similarity 53.8%; Pred. No. 98;  
Matches 7; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

Qy 13 SCPDAIKEVFNK 25  
|| : |||  
Db 26 NCPDGSDE--DNK 36

RESULT 11  
US-11-093-118-6  
; Sequence 6, Application US/11093118

```

; Publication No. US2006000820A1
;
; GENERAL INFORMATION:
; APPLICANT: Theodore M. Klein
; APPLICANT: zude weng
; APPLICANT: Rebecca E. Cahoon
; APPLICANT: Karlene H. Butler
; TITLE OF INVENTION: Cell Cycle Genes In Plants
;
; FILE REFERENCE: BM1345
; CURRENT APPLICATION NUMBER: US/11/093,118
; CURRENT FILING DATE: 2003-03-29
; PRIOR APPLICATION NUMBER: US/09/958,110
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/128,192
; PRIOR FILING DATE: 1999-04-07
;
; NUMBER OF SEQ ID NOS: 39
;
; SOFTWARE: Microsoft Office 97
;
; SEQ ID NO 6
;
; LENGTH: 38
;
; TYPE: PRT
;
; ORGANISM: Glycine max
;
; US-11-093-118-6

```

Query Match 23.5%; Score 31; DB 7; Length 38;  
Best Local Similarity 35.0%; Pred. NO. 98;  
Matches 7; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

```
Qy      2 KKDVLFTFTVKSCPDAIKEV 21
         :||:| | | :|:|
db      6 EKDIQRFQDKYNYDIVKDV 25
```

```

RESULT 12
US-10-986-501-356
; Sequence 356, Application US/10986501
; Publication No. US20050244945A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: PZ013P2C1
; CURRENT APPLICATION NUMBER: US/10/986,501
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US/10/621,363
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/969,730
; PRIOR FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: 09/774,639
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/238,291
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: PCT/US98/16235
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/056,371
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,732
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,366
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,364
; PRIOR FILING DATE: 1997-08-19
; Remaining Prior Application data removed - See
; NUMBER OF SEQ ID NOS: 373
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 356
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-986-501-356

```

Query Match 23.5%; Score 31; DB 6; Length 44;  
Best Local Similarity 35.7%; Pred. No. 1.2e+02;  
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy	6	LETFTVKSCPD	19
	:	:	:
Db	28	IOTRTAVSCVD	41

```

RESULT 13
US-10-467-657-6336
US-10-467-657-6336, Application US/10467657
; Sequence 6336,
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 6336
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6336

```

Query Match	22.7%;	Score 30;	DB 6;	Length 30;
Best Local Similarity	42.9%;	Pred. No. 1.le+02;		
Matches 6; Conservative	2;	Mismatches 6;	Indcls 0;	Gaps 0;

Qy 9 FTVKSCPDAlKEVF 22  
: : | | | |  
pb 17 YSVLKLpDTTKVVF 30

```

RESULT 14
US-10-957-351-183
; Sequence 183, Application US/10957351
; Publication No. US2006008844A1
; GENERAL INFORMATION:
; APPLICANT: Stemmer, Willem P. C.
; APPLICANT: Perlroth, D. Victor
; APPLICANT: Sacyal, Sanjeev
; APPLICANT: Avidia Research Institute
; TITLE OF INVENTION: c-Met Kinase Binding Proteins
; FILE REFERENCE: 022013-001400US
; CURRENT APPLICATION NUMBER: US/10/957,351
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: US 10/871,602
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 471
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 183
; LENGTH: 38
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human LDL-receptor class A domain
US-10-957-351-183

```

Query Match 22.7%; Score 30; DB 6; Length 38;  
Best Local Similarity 50.0%; Pred. No. 1.4e+02;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy	11	VKSCPD	AIKE	20
		:		
Db	24	VRQCPD	GSDE	33

```
RESULT 15
US-10-504-879-63
; Sequence 63, Application US/10504879
; Publication No. US20060008801A1
; GENERAL INFORMATION:
; APPLICANT: MATSUSHIMA, Kouji et al.
; TITLE OF INVENTION: MOLECULE ASSOCIATING WITH INTRACELLULAR C-TERMINAL DOMAIN OF RECH
; FILE REFERENCE: 1752-0167PUS1
; CURRENT APPLICATION NUMBER: US/10/504,879
; CURRENT FILING DATE: 2004-08-17
; PRIOR APPLICATION NUMBER: PCT/JP03/01699
; PRIOR FILING DATE: 2003-02-18
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-504-879-63
Query Match      22.3%; Score 29.5; DB 6; Length 33;
Best Local Similarity 31.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 4; Mismatches 10; Indels 1; Gaps 1;

QY      2 KKVLETFVTKSCPDAlKEVFD 23
Db      13 RKHITKRF-CKQCPVFYRETVD 33

RESULT 16
US-11-121-301-50
; Sequence 50, Application US/11121301
; Publication No. US2005027176A1
; GENERAL INFORMATION:
; APPLICANT: MCCRAY, JR., PAUL B.
; APPLICANT: SCHUTTE, BRIAN C.
; APPLICANT: JIA, HONG PENG
; APPLICANT: CASAVANT, THOMAS L.
; TITLE OF INVENTION: HUMAN AND MOUSE b-DEFENSINS, ANTIMICROBIAL PEPTIDES
; FILE REFERENCE: IOWA:041USD1
; CURRENT APPLICATION NUMBER: US/11/121,301
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/323,991
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 10/252,734
; PRIOR FILING DATE: 2002-09-23
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-121-301-50
Query Match      22.3%; Score 29.5; DB 7; Length 33;
Best Local Similarity 63.6%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY      7 ETTVTKSCPD 17
Db      18 ETF-MHLCPD 27

RESULT 17
US-10-504-879-62
; Sequence 62, Application US/10504879
; Publication No. US20060008801A1
; GENERAL INFORMATION:
; APPLICANT: MATSUSHIMA, Kouji et al.
; TITLE OF INVENTION: MOLECULE ASSOCIATING WITH INTRACELLULAR C-TERMINAL DOMAIN OF RECH
; FILE REFERENCE: 1752-0167PUS1
; CURRENT APPLICATION NUMBER: US/10/504,879
; CURRENT FILING DATE: 2004-08-17
```

```
; PRIOR APPLICATION NUMBER: PCT/JP03/01699
; PRIOR FILING DATE: 2003-02-18
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-504-879-62
Query Match      22.3%; Score 29.5; DB 6; Length 48;
Best Local Similarity 31.8%; Pred. No. 2.2e+02;
Matches 7; Conservative 4; Mismatches 10; Indels 1; Gaps 1;

QY      2 KKVLETFVTKSCPDAlKEVFD 23
Db      13 RKHITKRF-CKQCPVFYRETVD 33

RESULT 18
US-10-957-351-155
; Sequence 155, Application US/10957351
; Publication No. US20060008844A1
; GENERAL INFORMATION:
; APPLICANT: Stemmer, Willem P. C.
; APPLICANT: Perlroth, D. Victor
; APPLICANT: Satyal, Sanjeev
; APPLICANT: Avidia Research Institute
; TITLE OF INVENTION: c-Met Kinase Binding Proteins
; FILE REFERENCE: 022013-001400US
; CURRENT APPLICATION NUMBER: US/10/957,351
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: US 10/871,602
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 471
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 155
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human LDL-receptor class A domain
US-10-957-351-155
Query Match      22.0%; Score 29; DB 6; Length 38;
Best Local Similarity 55.8%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      12 KSCPDAIKE 20
Db      26 KQCPDGSDE 34

RESULT 19
US-11-123-896-453
; Sequence 453, Application US/11123896
; Publication No. US20050273881A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Harvell, Leslie
; APPLICANT: Cahoon, Rebecca
; APPLICANT: McOutchen, Billy Fred
; APPLICANT: Lu, Albert
; APPLICANT: Herrmann, Rafael
; APPLICANT: Wong, James
; TITLE OF INVENTION: Defensin Polynucleotides and Methods of
; FILE REFERENCE: 35718/246703
; CURRENT APPLICATION NUMBER: US/11/123,896
; CURRENT FILING DATE: 2005-05-06
; PRIOR APPLICATION NUMBER: 60/300,152
; PRIOR FILING DATE: 2001-06-22
```

```
; PRIOR APPLICATION NUMBER: 60/300,241
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 459
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 453
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Arachis hypogaea
US-11-123-896-453

Query Match      22.0%; Score 29; DB 7; Length 47;
Best Local Similarity 54.5%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 9 FTVKSCPDIAK 19
Db 15 FTTGSCDDHCK 25

RESULT 20
US-10-503-575-243
; Sequence 243, Application US/10503575
; Publication No. US20050244823A1
; GENERAL INFORMATION:
; APPLICANT: Drijfhout, Jan Wouter
; APPLICANT: van Veelen, Petrus Antonius
; APPLICANT: Koning, Frits
; TITLE OF INVENTION: NOVEL EPITOPES FOR CELIAC DISEASE AND AUTOIMMUNE DISEASES, METHOD
; TITLE OF INVENTION: DETECTING THOSE AND NOVEL NON-ANTIGENIC FOOD COMPOUNDS
; FILE REFERENCE: 2799/72843-PC7-US
; CURRENT APPLICATION NUMBER: US/10/503,575
; CURRENT FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: PCT/NL03/00077
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: EP 02075456.0
; PRIOR FILING DATE: 2002-02-04
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 243
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-503-575-243

Query Match      21.2%; Score 28; DB 6; Length 19;
Best Local Similarity 35.3%; Pred. No. 1.3e+02;
Matches 6; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 7 EFTTVKSCPDIAKEVFD 23
Db 2 EFTTLKSLQDPWKLVLE 18

RESULT 21
US-11-022-562-157
; Sequence 157, Application US/11022562
; Publication No. US20050249742A1
; GENERAL INFORMATION:
; APPLICANT: Ruprecht, Ruth M.
; APPLICANT: Shisong, Jiang
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
; TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
; FILE REFERENCE: DFN-043CN
; CURRENT APPLICATION NUMBER: US/11/022,562
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: PCT/US03/20322
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/392718
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 157
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Simian Immunodeficiency Virus
US-11-022-562-158
; Sequence 158, Application US/11022562
; Publication No. US20050249742A1
; GENERAL INFORMATION:
; APPLICANT: Ruprecht, Ruth M.
; APPLICANT: Shisong, Jiang
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
; TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
; FILE REFERENCE: DFN-043CN
; CURRENT APPLICATION NUMBER: US/11/022,562
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: PCT/US03/20322
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/392718
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 158
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Simian Immunodeficiency Virus
US-11-022-562-158

Query Match      21.2%; Score 28; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 DAIKEV 21
Db 2 DAIKEV 7

RESULT 23
US-11-006-119-30
; Sequence 30, Application US/11006119
; Publication No. US20050260691A1
; GENERAL INFORMATION:
; APPLICANT: Ndao, Momar
; APPLICANT: Ward, Brian
; APPLICANT: Caffrey, Rebecca
; APPLICANT: Spithill, Terry
; APPLICANT: Li, Hongshan
; APPLICANT: Podust, Vladimir
; APPLICANT: Perichon, Regis
; APPLICANT: CIPHERGEN Biosystems, Inc.
; TITLE OF INVENTION: Serum Biomarkers for Chagas Disease
; FILE REFERENCE: 016866-012130US
; CURRENT APPLICATION NUMBER: US/11/006,119
; CURRENT FILING DATE: 2004-12-06
; PRIOR APPLICATION NUMBER: US 60/527,153
; PRIOR FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: US 60/565,093
; PRIOR FILING DATE: 2004-04-22
; PRIOR APPLICATION NUMBER: US 60/625,519
; PRIOR FILING DATE: 2004-11-06
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 24
```

```
; TYPE: PRT
; ORGANISM: Simian Immunodeficiency Virus
US-11-022-562-157

Query Match      21.2%; Score 28; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 DAIKEV 21
Db 12 DAIKEV 17

RESULT 22
US-11-022-562-158
; Sequence 158, Application US/11022562
; Publication No. US20050249742A1
; GENERAL INFORMATION:
; APPLICANT: Ruprecht, Ruth M.
; APPLICANT: Shisong, Jiang
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
; TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
; FILE REFERENCE: DFN-043CN
; CURRENT APPLICATION NUMBER: US/11/022,562
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: PCT/US03/20322
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/392718
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 158
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Simian Immunodeficiency Virus
US-11-022-562-158

Query Match      21.2%; Score 28; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 DAIKEV 21
Db 2 DAIKEV 7

RESULT 23
US-11-006-119-30
; Sequence 30, Application US/11006119
; Publication No. US20050260691A1
; GENERAL INFORMATION:
; APPLICANT: Ndao, Momar
; APPLICANT: Ward, Brian
; APPLICANT: Caffrey, Rebecca
; APPLICANT: Spithill, Terry
; APPLICANT: Li, Hongshan
; APPLICANT: Podust, Vladimir
; APPLICANT: Perichon, Regis
; APPLICANT: CIPHERGEN Biosystems, Inc.
; TITLE OF INVENTION: Serum Biomarkers for Chagas Disease
; FILE REFERENCE: 016866-012130US
; CURRENT APPLICATION NUMBER: US/11/006,119
; CURRENT FILING DATE: 2004-12-06
; PRIOR APPLICATION NUMBER: US 60/527,153
; PRIOR FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: US 60/565,093
; PRIOR FILING DATE: 2004-04-22
; PRIOR APPLICATION NUMBER: US 60/625,519
; PRIOR FILING DATE: 2004-11-06
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 24
```

```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:N-terminal 28.7
; OTHER INFORMATION: kDa fragment of fibronectin Chagas disease
; OTHER INFORMATION: biomarker tryptic digest fragment peptide
US-11-006-119-30

Query Match      21.2%; Score 28; DB 7; Length 24;
Best Local Similarity 40.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY  9 FTVKSCPDAIKEYVD 23
    | : | : | : |
Db   2 FNCESKPEABETCFD 16

RESULT 24
US-11-033-116-4
; Sequence 4, Application US/11033116
; Publication No. US20050288224A1
; GENERAL INFORMATION:
; APPLICANT: TAKAKURA, Yoshimitsu et al.
; TITLE OF INVENTION: A NOVEL PROTEIN, A GENE CODING THEREFOR AND A METHOD OF USING THE
; FILE REFERENCE: 0230-0157P
; CURRENT APPLICATION NUMBER: US/11/033,116
; CURRENT FILING DATE: 2005-01-12
; PRIOR APPLICATION NUMBER: US/05/856,327
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Lyophyllum shimeji
US-11-033-116-4

Query Match      21.2%; Score 28; DB 7; Length 24;
Best Local Similarity 27.8%; Pred. No. 1.7e+02;
Matches 5; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY  3 KDVLETFVTKSCPDAIKEY 20
    : : | : | : | :
Db   4 ESIRHTLVLRSLQDAYKD 21

RESULT 25
US-11-033-116-6
; Sequence 6, Application US/11033116
; Publication No. US20050288224A1
; GENERAL INFORMATION:
; APPLICANT: TAKAKURA, Yoshimitsu et al.
; TITLE OF INVENTION: A NOVEL PROTEIN, A GENE CODING THEREFOR AND A METHOD OF USING THE
; FILE REFERENCE: 0230-0157P
; CURRENT APPLICATION NUMBER: US/11/033,116
; CURRENT FILING DATE: 2005-01-12
; PRIOR APPLICATION NUMBER: US/05/856,327
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 6
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Lyophyllum shimeji
US-11-033-116-6

Query Match      21.2%; Score 28; DB 7; Length 34;
Best Local Similarity 27.8%; Pred. No. 2.5e+02;
Matches 5; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY  3 KDVLETFVTKSCPDAIKEY 20
    : : | : | : | :
Db   14 ESIRHTLVLRSLQDAYKD 31
```

```
RESULT 26
US-10-957-351-329
; Sequence 329, Application US/10957351
; Publication No. US20060008844A1
; GENERAL INFORMATION:
; APPLICANT: Stemmer, Willem P. C.
; APPLICANT: Perlroth, D. Victor
; APPLICANT: Satval, Sanjeev
; APPLICANT: Avidia Research Institute
; TITLE OF INVENTION: c-Met Kinase Binding Proteins
; FILE REFERENCE: 022013-001400US
; CURRENT APPLICATION NUMBER: US/10/957,351
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: US 10/871,602
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 471
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 329
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DH3/2 selected clone 2
US-10-957-351-329

Query Match      21.2%; Score 28; DB 6; Length 35;
Best Local Similarity 54.5%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY  11 VKSCPDIAKEY 21
    | | | | |
Db   23 VGDCPDSDDEV 33

RESULT 27
US-10-467-657-1118
; Sequence 1118, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1118
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1118

Query Match      21.2%; Score 28; DB 6; Length 44;
Best Local Similarity 38.9%; Pred. No. 3.4e+02;
Matches 7; Conservative 2; Mismatches 7; Indels 2; Gaps 1;

QY  1 PKQVLETFVTKS--CPD 16
    | : | : | : |
Db   25 PRLAVLSVLAAASPCPD 42

RESULT 28
US-10-957-887B-278
; Sequence 278, Application US/10957887B
; Publication No. US20050272677A1
```

```
/ GENERAL INFORMATION:
/ APPLICANT: Friesen, Robert H. E.
/ APPLICANT: Leenhouts, Cornelius J.
/ APPLICANT: Hektor, Harm
/ APPLICANT: van Esch, Johannes H.
/ APPLICANT: Heeres, Andre
/ TITLE OF INVENTION: DELIVERY OF A SUBSTANCE TO A PRE-DETERMINED SITE
/ FILE REFERENCE: 2183-6668US
/ CURRENT APPLICATION NUMBER: US/10/957,887B
/ PRIOR FILING DATE: 2004-10-04
/ PRIOR APPLICATION NUMBER: PCT/NL/00256
/ NUMBER OF SEQ ID NOS: 309
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 278
/ LENGTH: 44
/ TYPE: PRT
/ ORGANISM: Sinorhizobium meliloti
US-10-957-887B-278

Query Match      21.2%; Score 28; DB 6; Length 44;
Best Local Similarity 38.5%; Pred. No. 3.4e+02;
Matches 5; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY      1 PKQVLETFVK 13
Db      19 PEKEILKANGLKS 31

RESULT 29
US-10-957-887B-258
/ Sequence 258, Application US/10957887B
/ Publication No. US2005027267A1
/ GENERAL INFORMATION:
/ APPLICANT: Friesen, Robert H. E.
/ APPLICANT: Leenhouts, Cornelius J.
/ APPLICANT: Hektor, Harm
/ APPLICANT: van Esch, Johannes H.
/ APPLICANT: Heeres, Andre
/ TITLE OF INVENTION: DELIVERY OF A SUBSTANCE TO A PRE-DETERMINED SITE
/ FILE REFERENCE: 2183-6668US
/ CURRENT APPLICATION NUMBER: US/10/957,887B
/ CURRENT FILING DATE: 2004-10-04
/ PRIOR APPLICATION NUMBER: PCT/NL/00256
/ PRIOR FILING DATE: 2003-04-04
/ NUMBER OF SEQ ID NOS: 309
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 258
/ LENGTH: 46
/ TYPE: PRT
/ ORGANISM: Oryza sativa
US-10-957-887B-258

Query Match      21.2%; Score 28; DB 6; Length 46;
Best Local Similarity 41.2%; Pred. No. 3.6e+02;
Matches 7; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY      3 KDVLETFVKSCPDIAK 19
Db      22 KDILDLNPRVANPDFIK 38

RESULT 30
US-10-859-643-2
/ Sequence 2, Application US/10859643
/ Publication No. US20060002993A1
/ GENERAL INFORMATION:
/ APPLICANT: Challita-Eid, Pia M.
/ APPLICANT: Raitano, Arthur B.
/ APPLICANT: Paris, Mary
/ APPLICANT: Hubert, Rene S.
/ APPLICANT: Morrison, Karen Jane Meyrick
/ APPLICANT: Jakobovits, Aya
/ TITLE OF INVENTION: Nucleic Acid and Corresponding Protein

/ GENERAL INFORMATION:
/ APPLICANT: Challita-Eid, Pia M.
/ APPLICANT: Raitano, Arthur B.
/ APPLICANT: Paris, Mary
/ APPLICANT: Hubert, Rene S.
/ APPLICANT: Morrison, Karen Jane Meyrick
/ APPLICANT: Jakobovits, Aya
/ TITLE OF INVENTION: Nucleic Acid and Corresponding Protein

/ TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
/ TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
/ FILE REFERENCE: 511582006203
/ CURRENT APPLICATION NUMBER: US/10/859,643
/ CURRENT FILING DATE: 2004-06-02
/ PRIOR APPLICATION NUMBER: US 10/005,480
/ PRIOR FILING DATE: 2001-11-07
/ NUMBER OF SEQ ID NOS: 765
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-859-643-2

Query Match      20.5%; Score 27; DB 6; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      11 VKSCPD 16
Db      2 VESCP 7

RESULT 31
US-10-859-643-254
/ Sequence 254, Application US/10859643
/ Publication No. US20060002993A1
/ GENERAL INFORMATION:
/ APPLICANT: Challita-Eid, Pia M.
/ APPLICANT: Raitano, Arthur B.
/ APPLICANT: Paris, Mary
/ APPLICANT: Hubert, Rene S.
/ APPLICANT: Morrison, Karen Jane Meyrick
/ APPLICANT: Jakobovits, Aya
/ TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
/ TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
/ FILE REFERENCE: 511582006203
/ CURRENT APPLICATION NUMBER: US/10/859,643
/ CURRENT FILING DATE: 2004-06-02
/ PRIOR APPLICATION NUMBER: US 10/005,480
/ PRIOR FILING DATE: 2001-11-07
/ NUMBER OF SEQ ID NOS: 765
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 254
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-859-643-254

Query Match      20.5%; Score 27; DB 6; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      11 VKSCPD 16
Db      2 VESCP 7

RESULT 32
US-10-859-643-690
/ Sequence 690, Application US/10859643
/ Publication No. US20060002993A1
/ GENERAL INFORMATION:
/ APPLICANT: Challita-Eid, Pia M.
/ APPLICANT: Raitano, Arthur B.
/ APPLICANT: Paris, Mary
/ APPLICANT: Hubert, Rene S.
/ APPLICANT: Morrison, Karen Jane Meyrick
/ APPLICANT: Jakobovits, Aya
/ TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
```



; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of  
; FILE OF INVENTION: Cancer  
; FILE REFERENCE: 511582006203  
; CURRENT APPLICATION NUMBER: US/10/859,643  
; CURRENT FILING DATE: 2004-06-02  
; PRIOR APPLICATION NUMBER: US 10/005,480  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 765  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 690  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-859-643-690

Query Match 20.5%; Score 27; DB 6; Length 9;  
Best Local Similarity 66.7%; Pred. No. 5.5e+04;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKSCPD 16  
|:|:|:  
Db 2 VESCP 7

## RESULT 33

US-11-097-864-2  
; Sequence 2, Application US/11097864  
; Publication No. US20050265924A1  
; GENERAL INFORMATION:  
; APPLICANT: Challita-Eid, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B  
; FILE REFERENCE: 511582006205  
; CURRENT APPLICATION NUMBER: US/11/097,864  
; CURRENT FILING DATE: 2005-04-01  
; PRIOR APPLICATION NUMBER: US 10/062,109  
; PRIOR FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: US 10/005,480  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 765  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-11-097-864-2

Query Match 20.5%; Score 27; DB 7; Length 9;  
Best Local Similarity 66.7%; Pred. No. 5.5e+04;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKSCPD 16  
|:|:|:  
Db 2 VESCP 7

## RESULT 34

US-11-097-864-254  
; Sequence 254, Application US/11097864  
; Publication No. US20050265924A1  
; GENERAL INFORMATION:  
; APPLICANT: Challita-Eid, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B

; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 511582006205  
; CURRENT APPLICATION NUMBER: US/11/097,864  
; CURRENT FILING DATE: 2005-04-01  
; PRIOR APPLICATION NUMBER: US 10/062,109  
; PRIOR FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: US 10/005,480  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 765  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 254  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-11-097-864-254

Query Match 20.5%; Score 27; DB 7; Length 9;  
Best Local Similarity 66.7%; Pred. No. 5.5e+04;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKSCPD 16  
|:|:|:  
Db 2 VESCP 7

## RESULT 35

US-11-097-864-690  
; Sequence 690, Application US/11097864  
; Publication No. US20050265924A1  
; GENERAL INFORMATION:  
; APPLICANT: Challita-Eid, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B  
; FILE REFERENCE: 511582006205  
; CURRENT APPLICATION NUMBER: US/11/097,864  
; CURRENT FILING DATE: 2005-04-01  
; PRIOR APPLICATION NUMBER: US 10/062,109  
; PRIOR FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: US 10/005,480  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 765  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 690  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-11-097-864-690

Query Match 20.5%; Score 27; DB 7; Length 9;  
Best Local Similarity 66.7%; Pred. No. 5.5e+04;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKSCPD 16  
|:|:|:  
Db 2 VESCP 7

## RESULT 36

US-11-097-912-2  
; Sequence 2, Application US/11097912  
; Publication No. US20050265921A1  
; GENERAL INFORMATION:  
; APPLICANT: Challita-Eid, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Jakobovits, Aya

```
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 511582006204
; CURRENT APPLICATION NUMBER: US/11/097,912
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-912-2
```

```
Query Match 20.5%; Score 27; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 11 VKSCPD 16
|:|:|:
Db 2 VESCE 7
```

```
RESULT 37
US-11-097-912-254
; Sequence 254, Application US/11097912
; Publication No. US20050265921A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 511582006204
; CURRENT APPLICATION NUMBER: US/11/097,912
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 254
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-912-254
```

```
Query Match 20.5%; Score 27; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 11 VKSCPD 16
|:|:|:
Db 2 VESCE 7
```

```
RESULT 38
US-11-097-912-690
; Sequence 690, Application US/11097912
; Publication No. US20050265921A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
```

```
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 511582006204
; CURRENT APPLICATION NUMBER: US/11/097,912
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 690
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-912-690
```

```
Query Match 20.5%; Score 27; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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```
QY 11 VKSCPD 16
|:|:|:
Db 2 VESCP 7
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```
RESULT 39
US-10-859-643-350
; Sequence 350, Application US/10859643
; Publication No. US20060002993A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 511582006203
; CURRENT APPLICATION NUMBER: US/10/859,643
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 350
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-859-643-350
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Query Match 20.5%; Score 27; DB 6; Length 10;
Best Local Similarity 66.7%; Pred. No. 87;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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```
QY 11 VKSCPD 16
|:|:|:
Db 3 VESCP 8
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RESULT 40
US-11-097-864-350
; Sequence 350, Application US/11097864
; Publication No. US20050265924A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
```

; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B  
; FILE REFERENCE: 511582006205  
; CURRENT APPLICATION NUMBER: US/11/097,864  
; PRIOR FILING DATE: 2005-04-01  
; PRIOR APPLICATION NUMBER: US 10/062,109  
; PRIOR FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: US 10/005,480  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 765  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 350  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-11-097-864-350

Query Match 20.5%; Score 27; DB 7; Length 10;  
Best Local Similarity 66.7%; Pred. No. 87;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VKSCPD 16  
|:|:|:  
Db 3 VESCP 8

Search completed: January 20, 2006, 17:38:43  
Job time : 4.32099 secs

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Db 7 DAVKEAFQN 15

||:|||||

RESULT 3

S03353

plastocyanin - Microcystis aeruginosa (fragment)

C:Species: Microcystis aeruginosa

C>Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 09-Jul-2004

C:Accession: S03353

R;Tan, S.; Ho, K.K.

Biochim. Biophys. Acta 973, 111-117, 1989

A:Title: Purification of an acidic plastocyanin from Microcystis aeruginosa.

A:Reference number: S03353; MUID:89134784; PMID:2537099

A:Accession: S03353

A:Molecule type: protein

A:Residues: 1-15 <TAN>

A:Cross-references: UNIPROT:P10625; UNIPARC:UPI0000131BAF

Query Match 25.8%; Score 34; DB 2; Length 15;

Best Local Similarity 72.7%; Pred. No. 1.4e+02;

Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 ETEFTVKSCPPDA 17

|||||||

Db 1 ETEFTVKMGDDA 11

RESULT 4

B84144

hypothetical protein BH3954 [imported] - Bacillus halodurans (strain C-125)

C:Species: Bacillus halodurans

C>Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004

C:Accession: B84144

R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hara

Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A:Reference number: A83650; MUID:20512582; PMID:11058132

A:Accession: B84144

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-29 <STO>

A:Cross-references: UNIPROT:Q9K5V2; UNIPARC:UPI00000C435A; GB:AP001520; GB:BA000004; NID

A:Experimental source: strain C-125

C:Genetics:

A:Gene: BH3954

Query Match 25.0%; Score 33; DB 2; Length 29;

Best Local Similarity 42.9%; Pred. No. 3.7e+02;

Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 9 FTVKSCPDAIKEYF 22

|||||

Db 3 FVLKGPDPYFEKVF 16

RESULT 5

S55462

mer5 protein homolog - human (fragment)

N:Alternate names: humer

C:Species: Homo sapiens (man)

C>Date: 01-Aug-1995 #sequence\_revision 01-Sep-1995 #text\_change 09-Jul-2004

C:Accession: S55462

R;Oberbaumer, I.

submitted to the EMBL Data Library, March 1995

A:Description: A new member of the highly conserved multigene family of thiol-specific a

As by their 3' untranslated regions.

A:Reference number: S55462

A:Accession: S55462

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-30 <ORE>

A:Cross-references: UNIPROT:Q14579; UNIPARC:UPI000006D89A; EMBL:X85129; NID:g854125; PID

C:Genetics:

A:Gene: mers

C:Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 pro

Query Match 25.0%; Score 33; DB 2; Length 30;

Best Local Similarity 53.8%; Pred. No. 3.8e+02;

Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 10 TVKSCPDAIKEYF 22

|||||

Db 13 TIKPSPAAKSEYF 25

RESULT 6

G72312

hypothetical protein - Thermotoga maritima (strain MSB8)

C:Species: Thermotoga maritima

C>Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004

C:Accession: G72312

R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey

Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.

C.M.

Nature 399, 323-329, 1999

A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se

A:Reference number: A72200; MUID:99287316; PMID:10360571

A:Accession: G72312

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-41 <ARN>

A:Cross-references: UNIPROT:Q9X065; UNIPARC:UPI00000C1340; GB:AE001759; GB:AE0000512; NI

A:Experimental source: strain MSB8

C:Genetics:

A:Gene: TW0970

Query Match 25.0%; Score 33; DB 2; Length 41;

Best Local Similarity 54.5%; Pred. No. 5.2e+02;

Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 DVLETFTVKSC 14

|||||

Db 23 EVLETHTSQTC 33

RESULT 7

AD1753

Lactococcus lactis prophage pi2 protein 41 homolog lin2569 [imported] - Listeria innocua

C:Species: Listeria innocua

C>Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004

C:Accession: AD1753

R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker

; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A:Authors: Kref, J.; Kuhn, M.; Kunet, P.; Kurapk, G.; Madueno, E.; Maitournam, A.; Ma

ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,

A:Title: Comparative genomics of Listeria species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AD1753

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-44 <GLA>

A:Cross-references: UNIPROT:Q928G6; UNIPARC:UPI00000CC8BF; GB:AL592022; PIDN:CAC97796.1.1;

A:Experimental source: strain Clp11262

C:Genetics:

A:Gene: lin2569

Query Match 25.0%; Score 33; DB 2; Length 44;

Best Local Similarity 47.1%; Pred. No. 5.5e+02;

Matches 8; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 4 DVLETFTVKSCPDAIKE 20

|||||

Db 4 DDLEMTTGSCLDYFAE 20

RESULT 8  
JQ1600  
N;protein - Clostridium butyricum plasmid pCB101  
N;Alternate names: hypothetical 5.6K protein; hypothetical protein C'  
C;Species: Clostridium butyricum  
C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004  
C;Accession: JQ1600; S18113  
R;Brehm, J.K.; Pennock, A.; Bullman, H.M.S.; Young, M.; Oultram, J.D.; Minton, N.P.  
Plasmid 28, 1-13, 1992  
A;Title: Physical characterization of the replication origin of the cryptic plasmid pCB1  
A;Reference number: PQ0372; MUID:92390513; PMID:1518909  
A;Accession: JQ1600  
A;Molecule type: DNA  
A;Residues: 1-49 <BRE>  
A;Cross-references: UNIPROT:Q45960; UNIPARC:UPI00000B3E35; EMBL:X62684; NID:g40399; PIDN  
A;Experimental source: strain NCIB7423  
C;Genetics:  
A;Genome: plasmid

Query Match 25.0%; Score 33; DB 2; Length 49;  
Best Local Similarity 41.7%; Pred. No. 6.1e+02;  
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 13 SCPDAIKEVPDN 24  
|||:|:|:  
Db 6 SIPDEVKQFPED 17

RESULT 9  
H70224  
hypothetical protein BBR05 - Lyme disease spirochete plasmid E/1p25  
C;Species: Borrelia burgdorferi (Lyme disease spirochete)  
C;Date: 13-Feb-1998 #sequence\_revision 13-Feb-1998 #text\_change 09-Jul-2004  
C;Accession: H70224  
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White  
son, D.; Peterson, J.; Kervilave, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,  
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.  
Nature 390, 580-586, 1997  
A;Authors: Smith, H.O.; Venter, J.C.  
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.  
A;Reference number: A70100; MUID:98065943; PMID:9403685  
A;Accession: H70224  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-50 <KLE>  
A;Cross-references: UNIPROT:O50701; UNIPARC:UPI0000056836; GB:AE000785; NID:g2689951; PI  
A;Experimental source: strain B31  
C;Genetics:  
A;Genome: plasmid

Query Match 24.6%; Score 32.5; DB 2; Length 50;  
Best Local Similarity 47.6%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

QY 3 KDVLFTFKSCPDAIKEVPD 23  
|||:|:|:|:|:|:|:  
Db 17 KGVEEKYKVKSPDLISEVLN 36

RESULT 10  
S72793  
cysteine synthase (EC 4.2.99.8) B - Mycobacterium leprae  
N;Alternate names: B1549 C3 238 protein; O-Acetylserine sulphydrolase B  
C;Species: Mycobacterium leprae  
C;Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
C;Accession: S72793  
R;Smith, D.R.; Robison, K.  
submitted to the EMBL Data Library, November 1993  
A;Description: Mycobacterium leprae cosmid B1549.  
A;Reference number: S72582  
A;Accession: S72793

A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-49 <SMI>  
A;Cross-references: UNIPROT:Q59529; UNIPARC:UPI00000B1374; EMBL:U00014; NID:g466903; PI  
C;Genetics:  
C;Keywords: carbon-oxygen lyase

Query Match 24.2%; Score 32; DB 2; Length 49;  
Best Local Similarity 33.3%; Pred. No. 8.6e+02;  
Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 3 KDVLFTFKSC 14  
|||:|:|:  
Db 38 KDLFPSTVTRTC 49

RESULT 11  
E97894  
orf47 [imported] - Streptococcus pneumoniae (strain R6)  
C;Species: Streptococcus pneumoniae  
C;Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 09-Jul-2004  
C;Accession: E97894  
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.;  
e, R.; Leblanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.;  
Y, P.; Sun, P.M.; Winkler, M.E.  
J. Bacteriol. 183, 5709-5717, 2001  
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.  
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.  
A;Reference number: A97872; MUID:21429245; PMID:11544234  
A;Accession: E97894  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-47 <KUR>  
A;Cross-references: UNIPROT:Q8DR08; UNIPARC:UPI00000E33D7; GB:AE007317; PIDN:AAK989895.1  
C;Genetics:  
A;Gene: orf47

Query Match 23.9%; Score 31.5; DB 2; Length 47;  
Best Local Similarity 46.7%; Pred. No. 9.8e+02;  
Matches 7; Conservative 4; Mismatches 3; Indels 1; Gaps 1;

QY 6 LETFTVKSCPDAIKE 20  
:|:|:|:|:|:|:  
Db 24 IETP-VLCKCKSLKQ 37

RESULT 12  
B33600  
glutamate-ammonia ligase (EC 6.3.1.2) - Bradyrhizobium japonicum (fragment)  
C;Species: Bradyrhizobium japonicum  
C;Date: 27-Feb-1990 #sequence\_revision 27-Feb-1990 #text\_change 09-Jul-2004  
C;Accession: B33600  
R;Martin, G.B.; Thomasow, M.F.; Chelms, B.K.  
J. Bacteriol. 171, 5638-5645, 1989  
A;Title: Bradyrhizobium japonicum glnB, a putative nitrogen-regulatory gene, is regulat  
A;Reference number: A33600; MUID:9000805; PMID:2793830  
A;Accession: B33600  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-21 <MAR>  
A;Cross-references: UNIPROT:P05457; UNIPARC:UPI000016E706; GB:M26753; NID:g152093; PIDN  
C;Keywords: ligase

Query Match 23.5%; Score 31; DB 2; Length 21;  
Best Local Similarity 35.7%; Pred. No. 5.3e+02;  
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 11 VKSCPDAIKEVPDN 24  
:|:|:|:|:|:|:  
Db 1 MKTAKDVLKSIKDN 14

```
RESULT 13
S12409
ribosomal protein S12 - wheat chloroplast (fragment)
C:Species: chloroplast Triticum aestivum (common wheat)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: S12409
R:Gray, J.C.; Hird, S.M.; Dyer, T.A.
Plant Mol. Biol. 15, 947-950, 1990
A:title: Nucleotide sequence of a wheat chloroplast gene encoding the proteolytic subunit
A:Reference number: S12407; MUID:91355920; PMID:2103485
A:Accession: S12409
A:Molecule type: DNA
A:Residues: 1-38 <GRA>
A:Cross-references: UNIPROT:P24066; UNIPARC:UPI000016D3FB; EMBL:X54484; NID:g12334; PIDN
C:Genetics:
A:Gene: rps12
A:Genome: chloroplast
C:Superfamily: ribosomal protein S12
C:Keywords: chloroplast; protein biosynthesis; ribosome

Query Match      23.5%; Score 31; DB 2; Length 38;
Best Local Similarity 33.3%; Pred. No. 9.4e+02;
Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKDVLFTFTVKSCP 15
| : : : : : : : : : :
Db 14 PIRNARKTAALKGCP 28

RESULT 14
AB0925
hypothetical protein STY3659 [imported] - Salmonella enterica subsp. enterica serovar Ty
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A>Note: this species has also been called Salmonella typhi
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AB0925
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AB0925
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-50 <PAR>
A:Cross-references: UNIPARC:UPI000005A5A3; GB:AL513382; PIDN:CAD09420.1; PID:g16504537;
C:Genetics:
A:Gene: STY3659

Query Match      23.5%; Score 31; DB 2; Length 50;
Best Local Similarity 75.0%; Pred. No. 1.2e+03;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PKDVLFT 8
| : : : : : : :
Db 33 PKKSVLKT 40

RESULT 15
A38882
GTP-binding protein Cdc42 - mouse (fragment)
N:Alternate names: rab protein Cdc42
C:Species: Mus musculus (house mouse)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: A38882; JH0651
R:Chavrier, P.; Simons, K.; Zerial, M.
submitted to GenBank, June 1992
A:Reference number: A38879
A:Accession: A38882
A:Molecule type: mRNA
A:Residues: 1-48 <CHA>
```

```
A:Cross-references: UNIPROT:Q99JI7; UNIPARC:UPI00000E67CE; GB:M79301
R:Chavrier, P.; Simons, K.; Zerial, M.
Gene 112, 261-264, 1992
A:title: The complexity of the Rab and Rho GTP-binding protein subfamilies revealed by
A:Reference number: JH0639; MUID:92210010; PMID:1555775
A:Accession: JH0651
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-41,'W',43-48 <CH2>
A:Cross-references: UNIPARC:UPI00000176444
A:Experimental source: kidney
C:Genetics:
A:Gene: Cdc42
A:Superfamily: ras transforming protein; translation elongation factor Tu homology
C:Keywords: GTP binding

Query Match      23.1%; Score 30.5; DB 2; Length 48;
Best Local Similarity 33.3%; Pred. No. 1.4e+03;
Matches 8; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

QY 2 KKDVLFTFTVKSCP-DAIKEVFVN 24
| : : : : : : : : : :
Db 2 KSCLLISVTNNKFPSEYVPTVFN 25

RESULT 16
B60507
pepsin Iia (EC 3.4.23.-) - Atlantic cod (fragment)
C:Species: Gadus morhua (Atlantic cod)
C>Date: 19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change 16-Aug-2004
C:Accession: B60507
R:Gildberg, A.; Olsen, R.L.; Bjarnason, J.B.
Comp. Biochem. Physiol. B 96, 323-330, 1990
A:title: Catalytic properties and chemical composition of pepsins from Atlantic cod (Ga
A:Reference number: A60507; MUID:90298622; PMID:2113846
A:Accession: B60507
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-31 <GIL>
A:Cross-references: UNIPROT:Q7LZP3; UNIPARC:UPI0000175D39
C:Superfamily: Pepsin
C:Keywords: aspartic proteinase; hydrolase; protein digestion

Query Match      22.7%; Score 30; DB 2; Length 31;
Best Local Similarity 27.8%; Pred. No. 1.1e+03;
Matches 5; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 6 LETFTVKSCPDAIKEVED 23
| : : : : : : : : : :
Db 14 LGVISIGTPPESFKVIFD 31

RESULT 17
T15602
hypothetical protein C25E10.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T15602
R:Bradshaw, H.
submitted to the EMBL Data Library, February 1996
A:Description: The sequence of C. elegans cosmid C25E10.
A:Reference number: Z18376
A:Accession: T15602
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-35 <BRA>
A:Cross-references: UNIPARC:UPI000007DDA7; EMBL:U50311; NID:g1226295; PID:g1226296; PIDN
C:Genetics:
A:Gene: CESP:C25E10.6
A:Introns: 31/3

Query Match      22.7%; Score 30; DB 2; Length 35;
```



[illegible]

QY	9	FTVKSCP 15	
Db	6	FTMQGP 12	
RESULT 23			
S30361			
1,2-alpha-D-mannosidase - Penicillium citrinum			
C;Species: Penicillium citrinum			
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004			
C;Accession: S30361			
R;Yoshida, T.; Inoue, T.; Ichishima, E.			
Biochem. J. 290, 349-354, 1993			
A;Title: 1,2-alpha-D-mannosidase from Penicillium citrinum: molecular and enzymic properties			
A;Reference number: S30361; MUID:93199503; PMID:8452520			
A;Accession: S30361			
A;Status: preliminary			
A;Molecule type: protein			
A;Residues: 1-25 <YOS>			
A;Cross-references: UNIPROT:Q7M527; UNIPARC:UPI000017B3EA			
Query Match			
Best Local Similarity			
Matches			
QY			
Db			
RESULT 24			
A60698			
trichocyst protein 12 - Paramesium tetraurelia (fragment)			
C;Species: Paramesium tetraurelia			
C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 07-Dec-1999			
A;Accession: A60698			
R;Tindall, S.H.; Devito, L.D.; Nelson, D.L.			
J. Cell Sci. 92, 441-447, 1989			
A;Title: Biochemical characterization of the proteins of Paramesium secretory granules.			
A;Reference number: A60698; MUID:90078398; PMID:2592449			
A;Accession: A60698			
A;Molecule type: protein			
A;Residues: 1-28 <TIN>			
A;Cross-references: UNIPARC:UPI000017B66F			
C;Comment: This protein was purified from the extruded matrix (contents) of trichocysts			
C;Genetics:			
A;Genetic code: SGCS			
C;Keywords: extracellular protein			
Query Match			
Best Local Similarity			
Matches			
QY			
Db			
RESULT 25			
S11610			
ribosomal protein S4_eR [validated] - Halobacterium salinarum (fragment)			
N;Alternate names: ribosomal protein HS5			
C;Species: Halobacterium salinarum			
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 05-Oct-2004			
A;Accession: S11610			
R;Yaguchi, M.; Visentin, L.P.; Zuker, M.; Matheson, A.T.; Roy, C.; Strom, A.R.			
Zbl. Bakt. Hyg. I. Abt. Orig. C 3, 200-208, 1982			
A;Title: Amino-terminal sequences of ribosomal proteins from the 30S subunit of archaea			
A;Reference number: S11609			
A;Accession: S11610			
A;Molecule type: protein			
A;Residues: 1-32 <YAG>			
A;Cross-references: UNIPROT:Q7M553; UNIPARC:UPI000017725F			

A;Note: the protein is designated as ribosomal protein HS5			
A;Note: the source is designated as Halobacterium cutirubrum			
C;Superfamily: ribosomal protein S4			
C;Keywords: protein biosynthesis; ribosome			
Query Match			
Best Local Similarity			
Matches			
QY			
Db			
RESULT 26			
S42051			
GTP-binding protein (clone pSH-RHO2) - penaeid shrimp (Penaeus monodon) (fragment)			
C;Species: Penaeus monodon			
C;Date: 27-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004			
A;Accession: S42051			
R;Gendreau, S.; Lee, R.; Mialhe, E.			
submitted to the EMBL Data Library, February 1994			
A;Reference number: S42050			
A;Accession: S42051			
A;Molecule type: DNA			
A;Residues: 1-34 <GEN>			
A;Cross-references: UNIPROT:Q26078; UNIPARC:UPI000007D998; EMBL:Z30081; NID:G454998; PIR			
C;Superfamily: ras transforming protein; translation elongation factor Tu homology			
C;Keywords: GTP binding; transforming protein			
Query Match			
Best Local Similarity			
Matches			
QY			
Db			
RESULT 27			
E49754			
hypothetical protein L4 - Bacillus licheniformis (fragment)			
C;Species: Bacillus licheniformis			
C;Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 09-Jul-2004			
A;Accession: E49754			
R;Lee, J.W.K.; Edwards, C.W.; Hulett, F.M.			
J. Gen. Microbiol. 137, 667-677, 1991			
A;Title: Identification of four unique clones encoding 10 kDa proteins from Bacillus tha			
A;Reference number: A49754; MUID:91237328; PMID:2033382			
A;Accession: E49754			
A;Status: preliminary			
A;Molecule type: DNA			
A;Residues: 1-34 <LEE>			
A;Cross-references: UNIPROT:Q7M148; UNIPARC:UPI0000178E1B; GB:M37167			
C;Superfamily: hypothetical protein b1540			
Query Match			
Best Local Similarity			
Matches			
QY			
Db			
RESULT 28			
F95187			
hypothetical protein SP1611 [imported] - Streptococcus pneumoniae (strain TIGR4)			
C;Species: Streptococcus pneumoniae			
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004			
A;Accession: F95187			
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Hei-			
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,			

nsen, T.; Hickey, E.K.; Holt, I.E.  
Science 293, 498-506, 2001  
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,  
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.  
A;Reference number: A95000; MUID:21357209; PMID:11463916  
A;Accession: F95187  
A;Status: preliminary  
A;Molecule type: DNA  
A;Cross-references: UNIPROT:Q97PJ8; UNIPARC:UPI00000518FB; GB:AE005672; PIDN:AAK75695.1;  
C;Genetics:  
A;Gene: SPI611

Query Match 22.0%; Score 29; DB 2; Length 34;  
Best Local Similarity 35.7%; Pred. No. 1.7e+03;  
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 PKQVLETFVKSC 14  
|:|:|:|:|  
Db 12 FEEDIIVTGLPKYC 25

RESULT 29  
A23691  
apolipoprotein C-I - rabbit (fragment)  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 04-Oct-1991 #sequence\_revision 04-Oct-1991 #text\_change 09-Jul-2004  
C;Accession: A23691  
R;Weisgraber, K.H.; Mahley, R.W.; Kowal, R.C.; Herz, J.; Goldstein, J.L.; Brown, M.S.  
J. Biol. Chem. 285, 22453-22459, 1990  
A;Title: Apolipoprotein C-I modulates the interaction of apolipoprotein E with beta-mig-  
ceptor-related protein.  
A;Reference number: A23691; MUID:91093092; PMID:2266137  
A;Accession: A23691  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-28 <WEI>  
A;Cross-references: UNIPROT:P33047; UNIPARC:UPI0000125C1C  
C;Superfamily: apolipoprotein A-I  
C;Keywords: lipid binding; lipoprotein

Query Match 21.6%; Score 28.5; DB 2; Length 28;  
Best Local Similarity 46.7%; Pred. No. 1.6e+03;  
Matches 7; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY 10 TVKSCPDAIKEVDN 24  
|:|:|:|:|  
Db 6 TLELIPDKLKE-FGN 19

RESULT 30  
WISMAA  
alpha-amylase inhibitor AI-3688 - Streptomyces aureofaciens  
C;Species: Streptomyces aureofaciens  
C;Date: 17-Mar-1987 #sequence\_revision 17-Mar-1987 #text\_change 09-Jul-2004  
C;Accession: A01331  
R;Vertesy, L.; Tripiet, D.  
FEBS Lett. 185, 187-190, 1985  
A;Title: Isolation and structure elucidation of an alpha-amylase inhibitor, AI-3688, fro  
A;Reference number: A01331; MUID:85204394; PMID:2581812  
A;Accession: A01331  
A;Molecule type: protein  
A;Residues: 1-36 <VER>  
A;Cross-references: UNIPROT:P04082; UNIPARC:UPI000012D0A7  
A;Experimental source: FHL656, strain DSM 2790  
C;Comment: This protein is an effective inhibitor of pancreatic alpha-amylase, forming a  
does not inhibit the B. subtilis enzyme. Inhibition is pH-independent but does require  
C;Superfamily: alpha-amylase inhibitor, Streptomyces type  
C;Keywords: alpha-amylase inhibitor  
F;14-18/Region: inhibitory #status predicted  
F;9-25/Disulfide bonds: #status experimental

Query Match 21.6%; Score 28.5; DB 1; Length 36;  
Best Local Similarity 28.6%; Pred. No. 2.1e+03;  
Matches 8; Conservative 3; Mismatches 10; Indels 7; Gaps 1;

QY 1 PKQVLETF-----TVKSCPDAIKEV 21  
|:|:|:|:|  
Db 5 PAPDCVESFQSWRYTDVRNGCSDAVTV 32

RESULT 31  
S32316  
3,5-dichlorocatechol 1,2-dioxygenase (EC 1.13.11.1) - Pseudomonas cepacia (fragment)  
C;Species: Pseudomonas cepacia  
C;Date: 19-Mar-1997 #sequence\_revision 24-Jul-1998 #text\_change 09-Jul-2004  
C;Accession: S32316  
R;Bhat, M.A.; Ishida, T.; Horike, K.; Vaidyanathan, C.S.; Nozaki, M.  
Arch. Biochem. Biophys. 300, 738-746, 1993  
A;Title: Purification of 3,5-dichlorocatechol 1,2-dioxygenase, a nonheme iron dioxygenase  
as cepacia CSV90.  
A;Reference number: S32316; MUID:93167864; PMID:7679568  
A;Accession: S32316  
A;Molecule type: protein  
A;Residues: 1-44 <BHA>  
A;Cross-references: UNIPROT:Q9RSD3; UNIPARC:UPI0000088F82  
A;Experimental source: strain CSV90  
C;Function:  
A;Description: catalyzes intradiol cleavage of different catechol derivatives  
A;Note: Involved in degradation of the herbicide 2,4-dichlorophenoxyacetic acid  
A;Note: a nonheme ferric dioxygenase  
C;Superfamily: protocatechuate 3,4-dioxygenase beta chain  
C;Keywords: homodimer; oxidoreductase

Query Match 21.6%; Score 28.5; DB 2; Length 44;  
Best Local Similarity 30.4%; Pred. No. 2.5e+03;  
Matches 7; Conservative 4; Mismatches 7; Indels 5; Gaps 1;

QY 3 KDVLTFVTKSCPDAIKEVFDNK 25  
|:|:|:|:|  
Db 6 KDVDVAIVA-----AVQVLDQK 23

RESULT 32  
E85938  
hypothetical protein Z4177 [imported] - Escherichia coli (strain O157:H7, substrain EDL  
C;Species: Escherichia coli  
C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
C;Accession: E85938  
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe  
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca  
Nature 409, 529-533, 2001  
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A;Reference number: A85480; MUID:21074935; PMID:11206551  
A;Accession: E85938  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-44 <STO>  
A;Cross-references: UNIPROT:O8X3M1; UNIPARC:UPI00000D0EF2; GB:AE005174; MID:gl2517352;  
A;Experimental source: strain O157:H7, substrain EDL933  
C;Genetics:  
A;Gene: Z4177

Query Match 21.6%; Score 28.5; DB 2; Length 44;  
Best Local Similarity 31.6%; Pred. No. 2.5e+03;  
Matches 6; Conservative 2; Mismatches 8; Indels 3; Gaps 1;

QY 7 EFTTVKSCPDAIKEVFDNK 25  
|:|:|:|:|  
Db 29 ELFIATKEC---VSHIFSTK 44

RESULT 33  
S09607  
phenylalanine-tRNA ligase (EC 6.1.1.20) beta chain - Salmonella typhimurium (fragment)

C:Species: Salmonella typhimurium  
C:Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 09-Jul-2004  
C:Accession: S09607  
R;Li, Z.J.; Hillyard, D.; Higgins, P.  
Nucleic Acids Res. 17, 8880, 1989  
A:Title: Nucleotide sequence of the Salmonella typhimurium himA gene.  
A:Reference number: S09607; MUID:90067874; PMID:2685752  
A:Accession: S09607  
A:Molecule type: DNA  
A:Residues: 1-17 <LIZ>  
A:Cross-references: UNIPROT:P15434; UNIPARC:UPI000017035D; EMBL:X16739; NID:g47703; PIDN  
C:Genetics: phet  
C:Function:  
A:Description: catalyzes transfer of activated phenylalanine to phenylalanyl-tRNA  
C:Superfamily: phenylalanine-tRNA ligase beta chain  
C:Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 21.2%; Score 28; DB 2; Length 17;  
Best Local Similarity 55.8%; Pred. No. 1.2e+03;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 14 CPDAIKVF 22  
| : : | : |  
Db 3 CVEALKRF 11

RESULT 34  
A27375  
Photosystem I iron-sulfur protein - barley chloroplast (fragment)  
N:Alternate names: photosystem I 9K protein  
C:Species: chloroplast Hordeum vulgare (barley)  
C:Date: 30-Jun-1988 #sequence\_revision 30-Jun-1988 #text\_change 12-Jul-2004  
C:Accession: A27375  
R;Hoj, P.B.; Svendsen, I.; Scheller, H.V.; Moller, B.L.  
J. Biol. Chem. 262, 12676-12684, 1987  
A:Title: Identification of a chloroplast-encoded 9-kDa polypeptide as a 2[4Fe-4S] protein  
A:Reference number: A27375; MUID:87308302; PMID:3105312  
A:Accession: A27375  
A:Molecule type: DNA  
A:Residues: 1-30 <HOJ>  
A:Cross-references: UNIPROT:P10794; UNIPARC:UPI0000174DD7  
C:Genetics: chloroplast  
A:Genome: chloroplast  
C:Keywords: 4Fe-4S; chloroplast; electron transfer; iron-sulfur protein; membrane-associ

Query Match 21.2%; Score 28; DB 2; Length 30;  
Best Local Similarity 35.7%; Pred. No. 2.1e+03;  
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 8 TFTVKSCPDAIKVF 21  
| : : | : |  
Db 14 TQCVRACTDVLEM 27

RESULT 35  
A60507  
pepsin I (EC 3.4.23.-) - Atlantic cod (fragment)  
C:Species: Gadus morhua (Atlantic cod)  
C:Date: 19-Mar-1993 #sequence\_revision 19-Mar-1993 #text\_change 16-Aug-2004  
C:Accession: A60507  
R;Glibberg, A.; Olsen, R.L.; Bjarnason, J.B.  
Comp. Biochem. Physiol. B 96, 323-330, 1990  
A:Title: Catalytic properties and chemical composition of pepsins from Atlantic cod (Gad  
A:Reference number: A60507; MUID:90298622; PMID:2113846  
A:Accession: A60507  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-33 <GL>  
A:Cross-references: UNIPROT:Q7LZP5; UNIPARC:UPI0000175D37  
C:Superfamily: Pepsin  
C:Keywords: aspartic proteinase; hydrolase; protein digestion

Query Match 21.2%; Score 28; DB 2; Length 33;  
Best Local Similarity 44.4%; Pred. No. 2.3e+03;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 15 PDAIKVF 23  
| : : | : |  
Db 25 PESFKVIFD 33

RESULT 36  
A60601  
keratin, 55k, nuclear matrix - rat (fragments)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004  
C:Accession: A60601  
R;Alique, R.; Bastos, R.; Serratos, J.; Enrich, C.; James, P.; Pujades, C.; Bachs, O.  
Exp. Cell Res. 186, 346-353, 1990  
A:Title: Increase in a 55-kDa keratin-like protein in the nuclear matrix of rat liver c  
A:Reference number: A60601; MUID:90127112; PMID:1688805  
A:Accession: A60601  
A:Molecule type: protein  
A:Residues: 1-33 <ALI>  
A:Cross-references: UNIPROT:Q7MOB6; UNIPARC:UPI00001774C5  
C:Superfamily: cytoskeletal keratin  
C:Keywords: nuclear matrix; nucleus

Query Match 21.2%; Score 28; DB 2; Length 33;  
Best Local Similarity 54.5%; Pred. No. 2.3e+03;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 KQDVLETFVK 12  
| : : | : |  
Db 8 KQDVDEAYXK 18

RESULT 37  
S42050  
GTP-binding protein (clone pSH-RH01) - penaeid shrimp (Penaeus monodon) (fragment)  
C:Species: Penaeus monodon  
C:Date: 27-Jan-1995 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: S42050  
R;Gendreau, S.; Lee, R.; Mialhe, E.  
submitted to the EMBL Data Library, February 1994  
A:Reference number: S42050  
A:Accession: S42050  
A:Molecule type: DNA  
A:Residues: 1-34 <GEN>  
A:Cross-references: UNIPROT:Q26077; UNIPARC:UPI0000075244; EMBL:Z30080; NID:g454996; PII  
C:Superfamily: ras transforming protein; translation elongation factor Tu homology  
C:Keywords: GTP binding; transforming protein

Query Match 21.2%; Score 28; DB 2; Length 34;  
Best Local Similarity 36.4%; Pred. No. 2.3e+03;  
Matches 8; Conservative 6; Mismatches 6; Indels 2; Gaps 2;

QY 1 PKQDV-LFTFTVKSCPDAIKVF 21  
| : : | : |  
Db 9 PDTDVILMCFSDS-PDSLENI 29

RESULT 38  
G95151  
hypothetical protein SPI305 [imported] - Streptococcus pneumoniae (strain TIGR4)  
C:Species: Streptococcus pneumoniae  
C:Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 09-Jul-2004  
C:Accession: G95151  
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Hei  
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,  
non, T.D.; Hickey, E.K.; Holt, I.E.  
Science 293, 498-506, 2001  
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,  
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.  
A:Reference number: A95000; MUID:21357209; PMID:11463916

Qy	4	DVLETF	TKSCPD	16
		::	:	:
Db	9	ELLEDT	VRRIPN	21

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2006, 17:22:44 ; Search time 54.321 Seconds  
(without alignments)  
324.703 Million cell updates/sec

Title: US-10-619-323-5  
Perfect score: 132  
Sequence: 1 PKXVLETFVKSCPDIAKEVFDNK 25

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 90886

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 50 summaries

Database : UniProt 05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	34.1	25	Q7M3G0_BOVIN	Q7m3g0 bos taurus
2	43.5	33.0	48	Q4RC18_TETNG	Q4rc18 tetraodon n
3	41	31.1	44	Q8U2Q3_PYPFU	Q8u2q3 pyrococcus
4	40	30.3	45	Q5UZA6_HALWA	Q5uza6 haloarcula
5	39	29.5	47	Q8F5I4_LEPIN	Q8f5i4 leptospira
6	38.5	29.2	35	Q8E9Z3_SHEON	Q8e9z3 shewanella
7	38.5	29.2	43	Q8F6T4_LEPIN	Q8f6t4 leptospira
8	38	28.8	39	Q4RAQ9_TETNG	Q4raq9 tetraodon n
9	38	28.8	46	GP54_BFSP1	Q48408 bacterioph
10	37	28.0	45	Q65H21_BACLD	Q65h21 bacillus li
11	36	27.3	41	Q91G73_IRV6	Q91g73 chilo iride
12	36	27.3	43	Q87JQ4_VIBPA	Q87jq4 vibrio para
13	36	27.3	37	Q570A7_ARATH	Q570a7 arabidopsis
14	35	26.5	45	Q86B24_9CAEN	Q86b24 reishia cla
15	35	26.5	41	Q5FU93_LACAC	Q5fi93 lactobacill
16	35	26.5	44	Q8G001_BRUSU	Q8g001 brucella su
17	35	26.5	49	Q5C039_SCHJA	Q5c039 schistosoma
18	34.5	26.1	44	Q8U2U2_PYROC	Q8u2u2 pyrococcus
19	34.5	26.1	44	Q7S6Q7_NEUCR	Q7s6q7 neurospora
20	34	25.8	15	PLAS_MICAE	P10625 microcystis
21	34	25.8	18	Q9XJQ5_9CAUD	Q9xjq5 bacterioph
22	34	25.8	30	Q83B13_COXBU	Q83b13 coxiella bu
23	34	25.8	42	Q5V7J5_HALWA	Q5v7j5 haloarcula
24	34	25.8	46	Q9NYL8_HUMAN	Q9nyl8 homo sapien
25	34	25.8	47	Q70UJ3_9BASI	Q70uj3 uncultured
26	33	25.0	18	Q63506_RAT	Q63506 rattus norv
27	33	25.0	20	Q9K5Y2_BACHD	Q9k5y2 bacillus ha
28	33	25.0	30	Q14579_HUMAN	Q14579 homo sapien
29	33	25.0	32	Q4XWD9_PLACH	Q4xwd9 plasmodium
30	33	25.0	33	Q8DWB4_STRMU	Q8dwb4 streptococ
31	33	25.0	34	Q4XE03_PLACH	Q4xe03 plasmodium

32	33	25.0	37	2	Q84TL9_BRARP	Q84tl9 brassica ra
33	33	25.0	41	2	Q8BX0_SHEON	Q8bx0 shewanella
34	33	25.0	41	2	Q9X065_THEMA	Q9x065 thermotoga
35	33	25.0	43	2	Q4XQ9_PLACH	Q4xq9 plasmodium
36	33	25.0	44	2	Q4W2C5_MYZAU	Q4w2c5 myzopoda au
37	33	25.0	44	2	Q928G6_LISIN	Q928g6 listeria in
38	33	25.0	47	2	Q5XDQ6_STRP6	Q5xdq6 streptococ
39	33	25.0	48	2	Q4XVJ5_PLACH	Q4xvj5 plasmodium
40	33	25.0	49	2	Q45960_CLOBU	Q45960 clostridium
41	33	25.0	50	2	Q4X9P8_PLACH	Q4x9p8 plasmodium
42	32.5	24.6	22	2	Q6VQ25_9NEOP	Q6vq25 heliconius
43	32.5	24.6	32	2	Q8TGT3_YEAST	Q8tgt3 saccharomyc
44	32.5	24.6	35	2	Q8ZWX8_PYRAE	Q8zwx8 pyrobaculum
45	32.5	24.6	46	2	Q5V3C5_HALWA	Q5v3c5 haloarcula
46	32.5	24.6	49	2	Q71ID3_LACDL	Q71id3 lactobacill
47	32.5	24.6	50	2	Q4XNE0_PLACH	Q4xne0 plasmodium
48	32.5	24.6	50	2	Q50701_BORBU	Q50701 borrelia bu
49	32	24.2	22	2	Q5BT20_SCHJA	Q5bt20 schistosoma
50	32	24.2	27	2	Q9GIC1_9PHAE	Q9gic1 sargassum m

ALIGNMENTS

RESULT 1

Q7M3G0\_BOVIN  
ID Q7M3G0\_BOVIN PRELIMINARY; PRT; 25 AA.  
AC Q7M3G0;  
DT 01-MAR-2004 (TREMBLrel. 26, Created)  
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE L-ascorbate peroxidase (BC 1.11.1.11) (Fragment).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
OC Pecora; Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
[1]  
RP PROTEIN SEQUENCE.  
RX MEDLINE=98113338; PubMed=9446780; DOI=10.1006/bbrc.1997.7946;  
RT Wada N., Kinoshita S., Matsuo M., Amako K., Miyake C., Asada K.;  
RA "Purification and molecular properties of ascorbate peroxidase from  
RT bovine eye."  
RL Biochem. Biophys. Res. Commun. 242:256-261(1998).  
DR PIR; PC4445; PC4445.  
DR GO; GO:0016888; F:L-ascorbate peroxidase activity; IEA.  
FT NON\_TER 1 1  
FT NON\_TER 25 25  
SQ SEQUENCE 25 AA; 2942 MW; 6355FFAF335709A8 CRC64;

Query Match 34.1%; Score 45; DB 2; Length 25;  
Best Local Similarity 50.0%; Pred. No. 40;  
Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 11 VKSCPDIAKEVFDN 24

DB 8 LENCRAIKELFEN 21

RESULT 2

Q4RC18\_TETNG  
ID Q4RC18\_TETNG PRELIMINARY; PRT; 48 AA.  
AC Q4RC18;  
DT 13-SEP-2005 (TREMBLrel. 31, Created)  
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)  
DE Chromosome 5 SCAF18819, whole genome shotgun sequence.  
DE (Fragment)  
GN ORFNames=GSTENG00039457001;  
OS Tetraodon nigroviridis (Green puffer).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;





"Unique physiological and pathogenic features of *Leptospira interrogans* revealed by whole-genome sequencing."



RA Schnitzler P., Soltan J.B., Fischer M., Reisner H., Scholz J.,  
 RA Delius H., Darai G.;  
 RT "Molecular cloning and physical mapping of the genome of insect  
 RT iridescent virus type 6: further evidence for circular permutation of  
 RT the viral genome.";  
 RL Virology 160:66-74 (1987).  
 RN [10]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=89073752; PubMed=3201750;  
 RA Fischer M., Schnitzler P., Delius H., Darai G.;  
 RT "Identification and characterization of the repetitive DNA element in  
 RT the genome of insect iridescent virus type 6.";  
 RL Virology 167:485-496 (1988).  
 RN [11]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=92196996; PubMed=1549908;  
 RA Handermann M., Schnitzler P., Roosen-Wolff A.P., Raab K.,  
 RA Sonntag K.C., Darai G.;  
 RT "Identification and mapping of origins of DNA replication within the  
 RT DNA sequences of the genome of insect iridescent virus type 6.";  
 RL Virus Genes 6:19-32 (1992).  
 RN [12]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=93260401; PubMed=8492091;  
 RA Schwaesser R., Raab K., Schnitzler P., Janssen W., Darai G.;  
 RT "Identification of the gene encoding the major capsid protein of  
 RT insect iridescent virus type 6 by polymerase chain reaction.";  
 RL J. Gen. Virol. 74:873-879 (1993).  
 RN [13]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=94167241; PubMed=8121799;  
 RA Schnitzler P., Hug M., Handermann M., Janssen W., Koonin E.V.,  
 RA Delius H., Darai G.;  
 RT "Identification of genes encoding zinc finger proteins, non-histone  
 RT chromosomal HMG protein homologue, and a putative GTP phosphohydrolase  
 RT in the genome of Chilo iridescent virus.";  
 RL Nucleic Acids Res. 22:158-166 (1994).  
 RN [14]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=99383793; PubMed=10456793; DOI=10.1023/A:1008072319875;  
 RA Muller K., Ridona C.A., Darai G.;  
 RT "Identification of a gene cluster within the genome of Chilo  
 RT iridescent virus encoding enzymes involved in viral DNA replication  
 RT and processing.";  
 RL Virus Genes 18:243-264 (1999).  
 RN [15]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=21342589; PubMed=11448171; DOI=10.1006/viro.2001.0963;  
 RA Jakob N.J., Mueller K., Bahr U., Darai G.;  
 RT "Analysis of the first complete DNA sequence of an invertebrate  
 RT iridovirus: coding strategy of the genome of Chilo iridescent virus.";  
 RL Virology 286:182-196 (2001).  
 DR EMBL; AF303741; AAK81959.1; -; Genomic DNA.  
 SQ SEQUENCE 41 AA; 4692 MW; BCC7EC950BC6FB09 CRC64;

Query Match 27.3%; Score 36; DB 2; Length 41;  
 Best Local Similarity 52.6%; Pred. No. 1.4e+03;  
 Matches 10; Conservative 2; Mismatches 3; Indels 4; Gaps 1;

QY 4 DVLETFVTKSCPDAIKEVF 22  
 :|||:|  
 Db 14 EILETKQVKK----IKEVF 28

RESULT 12  
 Q87JQ4 VIBPA  
 ID Q87JQ4 VIBPA PRELIMINARY; PRT; 43 AA.  
 AC Q87JQ4;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Hypothetical protein VPA0194.  
 GN OrderedLocusNames=VPA0194;

OS Vibrio parahaemolyticus.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
 OC Vibrionaceae; Vibrio.  
 OX NCBI\_TaxID=670;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=RMD 2210633 / Serotype O3:K6;  
 RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;  
 RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,  
 RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,  
 RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;  
 RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism  
 RT distinct from that of V. cholerae.";  
 RL Lancet 361:743-749 (2003).  
 DR EMBL; BA000032; BAC61537.1; -; Genomic DNA.  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 43 AA; 4813 MW; B65EB8D43C1E79A CRC64;

Query Match 27.3%; Score 36; DB 2; Length 43;  
 Best Local Similarity 42.9%; Pred. No. 1.4e+03;  
 Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 5 VLETFVTKSCPDAI 18  
 :|||:|  
 Db 21 VFDLFTIKRPNAL 34

RESULT 13  
 Q570AV ARATH  
 ID Q570AV ARATH PRELIMINARY; PRT; 45 AA.  
 AC Q570AV;  
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
 DE Hypothetical protein At5g55120.  
 GN Names=At5g55120;  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsid.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Totoki Y., Seki M., Ishida J., Nakajima M., Enju A., Kamiya A.,  
 RA Narusaka M., Shin-i T., Nakagawa M., Sakamoto N., Oishi K., Kohara Y.,  
 RA Kobayashi M., Toyoda A., Sakaki Y., Sakurai T., Iida K., Akiyama K.,  
 RA Satou M., Toyoda T., Konagaya A., Carninci P., Kawai J.,  
 RA Hayashizaki Y., Shinozaki K.;  
 RT "Large-scale analysis of RIKEN Arabidopsis full-length (RAPL) cDNAs.";  
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK220803; BAD94066.1; -; mRNA.  
 KW Hypothetical protein.  
 SQ SEQUENCE 45 AA; 5017 MW; 479C66D474235F2D CRC64;

Query Match 27.3%; Score 36; DB 2; Length 45;  
 Best Local Similarity 35.3%; Pred. No. 1.5e+03;  
 Matches 6; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 8 TPTVTKSCPDAIKEVFDN 24  
 :|||:|  
 Db 29 SFTIVHCPSVKEAVSN 45

RESULT 14  
 Q86B24 9CAEN  
 ID Q86B24 9CAEN PRELIMINARY; PRT; 37 AA.  
 AC Q86B24;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Nuclear Receptor g (Fragment).  
 GN Name=NRg;  
 OS Reishia clavigera.

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OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Muricoidea; Muricidae; Relishia.
OX NCBI_TaxID=128433;
[1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Ganglion;
RC Takahashi Y., Kuroki S., Kato K., Kurokawa T., Takahashi S., Sato M.,
RA Horiguchi T., Iguchi T., Miyata T., Miura T.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family.
DR EMBL; AB077035; BAC66483.1; -; mRNA.
DR HSSP; P22829; ICIT.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:004872; F:receptor activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00105; zf-C4; 1.
DR ProDom; PD00035; Znf_C4; 1.
DR SMART; SM00399; Znf_C4; 1.
KW DNA-binding; Metal-Binding; Nuclear protein; Receptor; Transcription;
KW Transcription regulation; Zinc; Zinc-finger.
FT NON_TER 1
FT TER 37
SQ SEQUENCE 37 AA; 4447 MW; 5D33991EB159B073 CRC64;

Query Match 26.5%; Score 35; DB 2; Length 37;
Best Local Similarity 41.2%; Pred. No. 1.7e+03;
Matches 7; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 9 FTVKSCPDAIKEVFNK 25
Db 1 FTCECKGPFKRVQNK 17

RESULT 15
QSFJ93 LACAC
ID QSFJ93 LACAC PRELIMINARY; PRT; 41 AA.
AC QSFJ93;
DT 10-MAY-2005 (TREMBLrel. 30, Created)
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=LBA1406;
OS Lactobacillus acidophilus.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1579;
[1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=NCFM;
RC Altermann E., Russell W.M., Azcarate-Peril M.A., Barrangou R.,
RA Buck B.L., McAuliffe O., Souther N., Dobson A., Duong T., Callanan M.,
RA Luck S., Hamrick A., Cano R., Klaenhammer T.R.;
RT "Complete genome sequence of the probiotic lactic acid bacterium
RT Lactobacillus acidophilus NCFM.";
RL Proc. Natl. Acad. Sci. U.S.A. 102:3906-3912(2005).
DR EMBL; CP000033; AA043231.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 41 AA; 4883 MW; 1344C5BBI43B64F1 CRC64;

Query Match 26.5%; Score 35; DB 2; Length 41;
Best Local Similarity 55.6%; Pred. No. 1.9e+03;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 15 PDAIKEVFD 23
Db 24 PESLKELFD 32

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RESULT 16
Q8G001 BRUSU
ID Q8G001 BRUSU PRELIMINARY; PRT; 44 AA.
AC Q8G001;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=BR1316;
OS Brucella suis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29461;
[1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=1330 / Biovar 1;
RX MEDLINE=22247741; PubMed=12271122; DOI=10.1073/pnas.192319099;
RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
RA Read T.D., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
RA Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J.A.,
RA Van Aken S.E., Riedmuller S., Tettelin H., Gill S.R., White O.,
RA Salzberg S.L., Hoover D.B., Lindler L.E., Hailing S.M., Boyle S.M.,
RA Frazer C.M.;
RT "The Brucella suis genome reveals fundamental similarities between
RT animal and plant pathogens and symbionts.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
DR EMBL; AE014291; AAN30233.1; -; Genomic DNA.
DR TIGR; BR1316; -.
SQ SEQUENCE 44 AA; 4670 MW; A38180FD364DB2FB CRC64;

Query Match 26.5%; Score 35; DB 2; Length 44;
Best Local Similarity 41.2%; Pred. No. 2.1e+03;
Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 5 VLETFVKSQDAIKEY 21
Db 12 VLCAFTLASCANTVRGV 28

RESULT 17
QSC039 SCHJA
ID QSC039 SCHJA PRELIMINARY; PRT; 49 AA.
AC QSC039;
DT 10-MAY-2005 (TREMBLrel. 30, Created)
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
DE Hypothetical protein.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
[1]
RN NUCLEOTIDE SEQUENCE.
RP Han Z.;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY811097; AAX26986.1; -; mRNA.
DR InterPro; IPR011986; LigA.
KW Hypothetical protein.
SQ SEQUENCE 49 AA; 5542 MW; 4818867A695E7AFF CRC64;

Query Match 26.5%; Score 35; DB 2; Length 49;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 14 CPDAIKEY 21
Db 41 CPDCVKDI 48

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RESULT 18
Q8U2U2 PYRFU
ID Q8U2U2 PYRFU PRELIMINARY; PRT; 44 AA.
AC Q8U2U2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein PF0737.
GN OrderedLocusNames=PF0737;
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Vcl / DSM 3638 / ATCC 43587 / JCM 8422;
RA Weiss R.B., Dunn D.M., Robb E.T., Brown J.R.;
RT "The complete sequence of the Pyrococcus furiosus genome."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE010192; AAL80861.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 44 AA; 5284 MW; 479C3074528E272E CRC64;

Query Match 26.1%; Score 34.5; DB 2; Length 44;
Best Local Similarity 40.0%; Pred. No. 2.4e+03;
Matches 10; Conservative 2; Mismatches 10; Indels 3; Gaps 1;

QY 1 PKKDVLTFTVK--SCPDAIKEYVFNK 25
DB 2 PKGFSLETVTLKK---RALEILDEK 23

RESULT 19
Q7S6Q7 NEUCR
ID Q7S6Q7 NEUCR PRELIMINARY; PRT; 44 AA.
AC Q7S6Q7;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Predicted protein.
GN Names=NCU05533.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Iankiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann R., Barrett R., Gnerre S.,
RA Kamal M., Kamvysellis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA Kyrstofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmari S.A.,
RA Desouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Sailer S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa."
RL Nature 010-0(2003).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABX01000322; EAA31259.1; -; Genomic DNA.
SQ SEQUENCE 44 AA; 5283 MW; 5D58B345C3059404 CRC64;

Query Match 26.1%; Score 34.5; DB 2; Length 44;
Best Local Similarity 39.3%; Pred. No. 2.4e+03;
Matches 11; Conservative 5; Mismatches 9; Indels 3; Gaps 2;
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QY 1 PKKDVLTFTVK--SCPDAIKEYVFNK 25
DB 2 PEKKLTFNFTVRMTAPDPNKKKDEDNK 29

RESULT 20
PLAS MICAE
ID PLAS MICAE STANDARD; PRT; 15 AA.
AC P10625;
DT 01-JUN-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Plastocyanin (Fragment).
GN Name=petE;
OS Microcystis aeruginosa.
OC Bacteria; Cyanobacteria; Chroococcales; Microcystis.
OX NCBI_TaxID=1126;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=89134784; PubMed=2537099;
RA Tan S., Ho K.-K.;
RT "Purification of an acidic plastocyanin from Microcystis aeruginosa."
RL Biochim. Biophys. Acta 973:111-117(1989).
CC -1- FUNCTION: Participates in electron transfer between P700 and the
CC cytochrome b6-f complex in photosystem I.
CC -1- SIMILARITY: Contains 1 plastocyanin-like domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC PIR; S03353; S03353.
CC HAMAP; MF_00566; -; 1.
CC InterPro; IPR000923; BlueCu 1.
CC PROSITE; PS00196; COPPER BLUE; PARTIAL.
CC Copper; Direct protein sequencing; Electron transport; Metal-binding;
CC Transport.
CC NON_TER 15 15
CC SEQUENCE 15 AA; 1555 MW; 32B6D4662F44F969 CRC64;

Query Match 25.8%; Score 34; DB 1; Length 15;
Best Local Similarity 72.7%; Pred. No. 9.6e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 EFTTVKSCPD 17
DB 1 EFTTVKMGDA 11

RESULT 21
Q9XJQ5 9CAUD
ID Q9XJQ5 9CAUD PRELIMINARY; PRT; 18 AA.
AC Q9XJQ5;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE N1H protein.
GN Name=n1h;
OS Bacteriophage 21.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=10743;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20092464; PubMed=10628842; DOI=10.1007/s004380051122;
RA Karch H., Schmidt H., Janetzki-Mittmann C., Scheef J., Kroeger M.;
RT "Shiga toxins even when different are encoded at identical positions
RT in the genomes of related temperate bacteriophages."
RL Mol. Gen. Genet. 262:600-607(1999).
DR EMBL; AJ237660; CAB39992.1; -; Genomic DNA.
SQ SEQUENCE 18 AA; 1975 MW; 2A8A468527FDBBB8 CRC64;
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Query Match      25.8%; Score 34; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 TFTVKSCPD 16
   |||: ||
Db 2 TFSVKTIPT 10

RESULT 22
Q83B13 COXBU
ID Q83B13 COXBU PRELIMINARY; PRT; 30 AA.
AC Q83B13
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=CBU1707;
OS Coxiella burnetii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Coxiellaceae; Coxiella.
OX NCBI_TaxID=777;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Nine Mile phase I / RSA 493;
RX MEDLINE=22608657; PubMed=12704232; DOI=10.1073/pnas.0931379100;
RA Seshadri R., Paulsen I.T., Eisen J.A., Read T.D., Nelson K.E.,
RA Nelson W.C., Ward N.L., Tettelin H., Davidsen T.M., Beanan M.J.,
RA DeBoy R.T., Daugherty S.C., Brinkac L.M., Madupu R., Dodson R.J.,
RA Khouri H.M., Lee K.H., Carty H.A., Scanlan D., Heinzen R.A.,
RA Thompson H.A., Samuel J.E., Fraser C.M., Heidelberg J.P.;
RT "Complete genome sequence of the Q-fever pathogen, Coxiella
   burnetii.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:5455-5460(2003).
DR EMBL; AB016965; AA091202.1; -; Genomic_DNA.
DR TIGR; CRU1707; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 30 AA; 3223 MW; 79F932AF90F0F2A CRC64;

Query Match      25.8%; Score 34; DB 2; Length 30;
Best Local Similarity 46.7%; Pred. No. 1.9e+03;
Matches 7; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

QY 10 TVKSC--PDAIKEVP 22
   :|: | |||: :|
Db 6 SVRGCLLPDAIQIGF 20

RESULT 23
Q5V7J5 HALMA
ID Q5V7J5 HALMA PRELIMINARY; PRT; 42 AA.
AC Q5V7J5;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=pNG5041;
OS Haloarcula marismortui (Halo bacterium marismortui).
OG Plasmid pNG500.
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Haloarcula.
OX NCBI_TaxID=2238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 43049;
RX PubMed=15520287; DOI=10.1101/gr.2700304;
RA Baliga N.S., Bonneau R., Facciotti M.T., Pan M., Glusman G.,
RA Deutsch E.W., Shannon P., Chiu Y., Weng R.S., Gan R.R., Hung P.,
RA Date S.V., Marcotte E., Hood L., Ng W.V.;
RT "Genome sequence of Haloarcula marismortui: a halophilic archaeon from
   the Dead Sea.";
RL Genome Res. 14:2221-2234(2004).

DR EMBL; AY596294; AAV44462.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein; Plasmid.
SQ SEQUENCE 42 AA; 5161 MW; 105FD4C99987D57C CRC64;

Query Match      25.8%; Score 34; DB 2; Length 42;
Best Local Similarity 26.1%; Pred. No. 2.7e+03;
Matches 6; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 3 KDVLETFVKSCPDAIKEVFDNK 25
   :|: |: | :| :| :|
Db 14 RELIESQRENTVVDDIHDLFENK 36

RESULT 24
Q9NYL8 HUMAN
ID Q9NYL8 HUMAN PRELIMINARY; PRT; 46 AA.
AC Q9NYL8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Ran binding protein 2 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA McCarthy N.F., Lindeman R.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF237700; AAF64155.1; -; mRNA.
FT NON_TER 1
FT NON_TER 46
SQ SEQUENCE 46 AA; 5051 MW; 5CF49EED493DDEBB CRC64;

Query Match      25.8%; Score 34; DB 2; Length 46;
Best Local Similarity 63.6%; Pred. No. 3e+03;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 KDVLETFVKKS 13
   |: | | | |
Db 17 KEVETFKANS 27

RESULT 25
Q70UJ3 9BASI
ID Q70UJ3 9BASI PRELIMINARY; PRT; 47 AA.
AC Q70UJ3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Laccase (EC 1.10.3.2) (Fragment).
GN Name=lac;
OS uncultured basidiomycete.
OC Eukaryota; Fungi; Basidiomycota; environmental samples.
OX NCBI_TaxID=175244;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Luis P., Walther G., Kellner H., Martin F., Buscot F.;
RT "Diversity of laccase genes from basidiomycetes in a forest soil.";
RL Soil Biol. Biochem. 36:1025-1036(2004).
DR EMBL; AJ540270; CAD62533.1; -; Genomic_DNA.
DR HSSP; Q9Y780; 1A65.
DR GO; GO:0008471; F:laccase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR011707; Cu-oxidase_3.
DR Pfam; PF07732; Cu-oxidase_3; 1.
KW Oxidoreductase.
FT NON_TER 1
FT NON_TER 47
SQ SEQUENCE 47 AA; 5506 MW; ACFB3288EF50FAB1 CRC64;

Query Match      25.8%; Score 34; DB 2; Length 47;

```

Best Local Similarity 50.0%; Pred. No. 3.1e+03;  
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 10 TVKSCPDAIKEVFD 23  
|:|:|:|:|  
Db 18 SVTQCPIVQKESFD 31

RESULT 26  
Q63506 RAT PRELIMINARY; PRT; 18 AA.  
AC Q63506  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Rat asialoglycoprotein receptor RHL1 (Fragment).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=87257885; Pubmed=3600647;  
RA McPhaul M., Berg P.;  
RT "Identification and characterization of cDNA clones encoding two  
RT homologous proteins that are part of the asialoglycoprotein  
RT receptor.";  
RL Mol. Cell. Biol. 7:1841-1847(1987).  
DR EMBL; M16349; AAA42039.1; -; mRNA.  
GO; GO:0004872; F:receptor activity; IEA.  
KW Receptor.  
FT NON\_TER  
SQ SEQUENCE 18 AA; 1988 MW; 43474B8AB145735C CRC64;

Query Match 25.0%; Score 33; DB 2; Length 18;  
Best Local Similarity 75.0%; Pred. No. 1.6e+03;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 VKSCPDAI 18  
|:|:|:|:|  
Db 6 VQSCPSAI 13

RESULT 27  
Q9K5Y2 BACHD PRELIMINARY; PRT; 29 AA.  
AC Q9K5Y2  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE BH3954 protein.  
GN OrderedLocusNames=BH3954;  
OS Bacillus halodurans.  
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=86665;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C-125 / JCM 9153;  
RX MEDLINE=20512582; Pubmed=11058132; DOI=10.1093/nar/28.21.4317;  
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,  
RA Fuji F., Hiramata C., Nakamura Y., Ogasawara N., Kuhara S.,  
RA Horikoshi K.;  
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus  
RT halodurans and genomic sequence comparison with Bacillus subtilis.";  
RL Nucleic Acids Res. 28:4317-4331(2000).  
DR EMBL; BA000004; BAB07673.1; -; Genomic\_DNA.  
DR FIR; B84144; B84144.  
KW Complete proteome.  
SQ SEQUENCE 29 AA; 3647 MW; 8C1526D4AF5FB264 CRC64;

Query Match 25.0%; Score 33; DB 2; Length 29;  
Best Local Similarity 42.9%; Pred. No. 2.6e+03;

Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
QY 9 FTVKSCPDAIKEVF 22  
|:|:|:|:|  
Db 3 FVLKGPDPYFEKVF 16

RESULT 28  
Q14579 HUMAN PRELIMINARY; PRT; 30 AA.  
AC Q14579  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Humer (Fragment).  
GN Name=mer5;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Oberbaumer I.;  
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.  
DR EMBL; X85129; CAA59443.1; -; mRNA.  
DR FIR; S55462; S55462.  
DR HSSP; B32119; IQMV.  
FT NON\_TER  
SQ SEQUENCE 30 AA; 3334 MW; 5713AF472692E46E CRC64;

Query Match 25.0%; Score 33; DB 2; Length 30;  
Best Local Similarity 53.8%; Pred. No. 2.7e+03;  
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 10 TVKSCPDAIKEVF 22  
|:|:|:|:|  
Db 13 TIKPSPAASKEVF 25

RESULT 29  
Q4XWD9 PLACH PRELIMINARY; PRT; 32 AA.  
AC Q4XWD9  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Hypothetical protein (Fragment).  
GN ORFNames=PC105305.00.0;  
OS Plasmodium chabaudi.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5825;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,  
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,  
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,  
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,  
RA Bidwell S.B., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,  
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;  
RT "A comprehensive survey of the Plasmodium life cycle by genomic,  
RT transcriptomic, and proteomic analyses.";  
RL Science 307:82-86(2005).  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; CAJ01002657; CAH78772.1; -; Genomic\_DNA.  
KW Hypothetical protein.  
FT NON\_TER  
SQ SEQUENCE 32 AA; 4013 MW; 2906341BFEBFB6E CRC64;

Query Match 25.0%; Score 33; DB 2; Length 32;  
Best Local Similarity 85.7%; Pred. No. 2.9e+03;







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RL  Nat. Biotechnol. 20:1118-1123 (2002).
DR  EMBL; AE015885; AAN57494.1; -; Genomic_DNA.
DR  TIGR; SO4531; -.
KW  Complete proteome; Hypothetical protein.
SQ  SEQUENCE 41 AA; 4596 MW; 3F6B72512E9CA13 CRC64;

Query Match 25.0%; Score 33; DB 2; Length 41;
Best Local Similarity 35.3%; Pred. No. 3.8e+03;
Matches 6; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 2 KKVLETFVTKSCPDAL 18
    | : | : | : |
Db 8 KYTIFEGISAIYCPDAV 24

RESULT 34
Q9X065.THEMA
ID Q9X065.THEMA PRELIMINARY; PRT; 41 AA.
AC Q9X065;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=TW0970;
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MSB8 / DSM 3109 / ATCC 43589;
RX MEDLINE=99287316; PubMed=10360571; DOI=10.1038/20601;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L.A., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.L.,
RA Heidelberg J.F., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
RT genome sequence of Thermotoga maritima.";
RL Nature 399:323-329 (1999).
DR EMBL; AE001759; AAU36049.1; -; Genomic_DNA.
DR PIR; G72312; G72312.
DR TIGR; TW0970; -.
DR InterPro; IPR010095; TspaseT teng_C.
DR Pfam; PF07282; Transposase_35; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 41 AA; 4586 MW; 7E52C021810E2023 CRC64;

Query Match 25.0%; Score 33; DB 2; Length 41;
Best Local Similarity 54.5%; Pred. No. 3.8e+03;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 DVLETFVTKSC 14
    : ||||| : |
Db 23 EVLETHTSQTC 33

RESULT 35
Q4XGQ9.PLACH
ID Q4XGQ9.PLACH PRELIMINARY; PRT; 43 AA.
AC Q4XGQ9;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PC401678.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berrihan M., Florens L., Janssen C.S., Pain A., Christophides G.K.,

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RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RA "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86 (2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAJ01006357; CAH83908.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 43 AA; 4914 MW; 6A0EBAB7BC302A1E CRC64;

Query Match 25.0%; Score 33; DB 2; Length 43;
Best Local Similarity 35.0%; Pred. No. 3.9e+03;
Matches 7; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 2 KKVLETFVTKSCPDALKEV 21
    || : : | : | : |
Db 8 KKIIKEFHLCFCFQICSV 27

RESULT 36
Q4W2C5.MYZAU
ID Q4W2C5.MYZAU PRELIMINARY; PRT; 44 AA.
AC Q4W2C5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Putative thyrotropin beta chain (Fragment).
GN Name=tbh;
OS Myzopoda aurita (old world sucker-footed bat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Chiroptera; Microchiroptera;
OC Myzopodidae; Myzopoda.
OX NCBI_TaxID=155038;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bick G.N., Jacobs D.S., Matthee C.R.;
RT "A phylogenetic perspective of the evolution of echolocation and
RT historical biogeography of extant bats (Chiroptera).";
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ865655; CAI28439.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 44
SQ SEQUENCE 44 AA; 5045 MW; C7EC3B2E3B2B7520 CRC64;

Query Match 25.0%; Score 33; DB 2; Length 44;
Best Local Similarity 33.3%; Pred. No. 4e+03;
Matches 6; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 5 VLETFVTKSCPDALKEVF 22
    ||| : | : | : |
Db 24 VYETVEIPGCGHVSPVF 41

RESULT 37
Q928G6.LISIN
ID Q928G6.LISIN PRELIMINARY; PRT; 44 AA.
AC Q928G6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Lin2569 protein.
GN OrderedLocNames=lin2569;
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CLIP 11262 / Serovar 6a;

```



Query Match 25.0%; Score 33; DB 2; Length 49;  
 Best Local Similarity 41.7%; Pred. No. 4.5e+03;  
 Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 13 SCPDAIKKVFQDN 24  
 Db |||:|:|:  
 6 SIPDEVKQFFED 17

Search completed: January 20, 2006, 17:33:48  
 Job time : 56.321 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:21:43 ; Search time 44.8889 Seconds  
(without alignments)  
176.187 Million cell updates/sec

Title: US-10-619-323-6

Perfect score: 95

Sequence: 1 PKXDVLETFVKSCPDAL 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 1130394

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

A\_Geneseq\_21.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*  
9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	95	100.0	18	8	Adj57563 Human CD9
2	95	100.0	25	8	Adj57562 Human CD9
3	61	64.2	30	6	ABU05051 Human exp
4	49	51.6	10	6	ABU03385 Human exp
5	46	48.4	44	4	AAM83184 Human imm
6	36	37.9	34	3	AAY92549 Human exp
7	36	37.9	34	3	AAB02778 Human TGF
8	36	37.9	36	2	AAB03057 Fragment
9	36	37.9	36	3	AAB09511 Human TGF
10	36	37.9	46	8	ADS06580 Staphyloc
11	35	36.8	41	4	AAU20329 Human nov
12	34	35.8	15	5	ABP58897 Human DNA
13	34	35.8	17	9	ADV59436 G protein
14	34	35.8	17	9	ADV57877 G protein
15	34	35.8	17	9	ADV58632 G protein
16	34	35.8	18	9	ADV59442 G protein
17	34	35.8	18	9	ADV57883 G protein
18	34	35.8	18	9	ADV58638 G protein
19	34	35.8	20	9	ADV59441 G protein
20	34	35.8	20	9	ADV58637 G protein
21	34	35.8	20	9	ADV57882 G protein
22	34	35.8	34	3	AAY92548 Finger 2
23	34	35.8	34	3	AAB02777 Human TGF
24	34	35.8	36	2	AAB03056 Fragment

25	34	35.8	36	3	AAB09510 Human TGF
26	34	35.8	38	4	ABB39942 Peptide #
27	34	35.8	38	4	AAM33561 Peptide #
28	34	35.8	38	4	AAM73359 Human bon
29	34	35.8	38	4	AAM60687 Human bra
30	34	35.8	38	4	ABG55075 Human liv
31	34	35.8	38	5	ABG43212 Human pep
32	34	35.8	42	3	AAG55485 Arabidops
33	33	34.7	24	7	ADI32847 Peptide 1
34	33	34.7	40	4	ABB41573 Peptide #
35	33	34.7	40	4	AAM35365 Peptide #
36	33	34.7	40	4	AAM75253 Human bon
37	33	34.7	40	4	AAM62444 Human bra
38	33	34.7	40	4	ABG57015 Human liv
39	33	34.7	40	5	ABG44901 Human pep
40	33	34.7	49	2	AAY11424 Human 5'
41	32	33.7	18	9	ADY63982 Human MCS
42	32	33.7	21	4	AAU08273 Human com
43	32	33.7	23	8	ADH35039 Glycopept
44	32	33.7	27	4	AAU08250 Human com
45	32	33.7	28	4	AAB07404 Synthetic
46	32	33.7	28	5	AAB15758 Pda8d pep
47	32	33.7	28	5	AAB076766 Pda8d pep
48	32	33.7	28	5	ABG75545 Optimised
49	32	33.7	32	2	AAR38439 Human tra
50	32	33.7	33	3	AAB16941 Bacteriop

#### ALIGNMENTS

##### RESULT 1

ADJ57563

ID ADJ57563 standard; peptide; 18 AA.

XX AC ADJ57563;

XX DT 06-MAY-2004 (first entry)

XX DE Human CD9 fibronectin-binding domain peptide fragment.

XX KW Human; CD9; antithrombotic; antiarteriosclerotic; vasotropic;  
XX KW haemostatic; antiangiogenic; cytostatic.

XX OS Homo sapiens.

XX PN WO2004007685-A2.

XX PD 22-JAN-2004.

XX PF 14-JUL-2003; 2003WO-US022050.

XX PR 12-JUL-2003; 2002US-0395864P.

XX PA (UYTE-) UNIV TENNESSEE RES FOUND.

XX PI Jennings LK, Longhurst CM, Cook GA, Bao J, Zhang C, White WM;

XX PI Crossno JT, Lu Y;

XX WPI; 2004-122924/12.

XX DR Interfering with CD9 binding to fibronectin by binding a fibronectin-binding domain of the CD9 protein or polypeptide, useful in treating thrombosis, atherosclerosis, restenosis, bleeding disorders, angiogenesis and cancers.

XX PS Claim 7; SEQ ID NO 6; 136pp; English.

XX CC The present sequence is that of a peptide fragment from the fibronectin-binding domain of human CD9 ADJ57563. The peptide, or an antibody that binds to it, is used in claimed methods for: interfering with CD9 binding to fibronectin; modifying adhesion, motility or spreading of a CD9-expressing cell on fibronectin; inhibiting proliferation or survival of

CC CD9-expressing cells; modifying pericellular fibronectin matrix assembly;  
 CC modifying invasiveness of a cell through a collagen and/or laminin matrix  
 CC ; and modifying cell-to-cell interaction. The methods are based on the  
 CC finding that increased CD9 expression is implicated in (i) decreased  
 CC adhesiveness of cells to extracellular matrix (via alpha5-beta-1  
 CC integrin) and/or decreased cell invasiveness and/or decreased  
 CC pericellular fibronectin matrix assembly, and/or (ii) increased cell  
 CC motility, spreading, proliferation, cell survival against apoptosis,  
 CC and/or cell-to-cell contacts. Conditions or disease states involving  
 CC proliferation or survival of CD9-expressing cells can be treated, e.g.  
 CC thrombosis, atherosclerosis, vein graft failure, restenosis, transplant  
 CC arteriopathy, bleeding disorders, angiogenesis, and primary and  
 CC metastatic cancers including breast cancer, prostate cancer, colon  
 CC cancer, melanoma, ovarian cancer, neuroblastoma, glioma and glioblastoma.  
 XX  
 SQ Sequence 18 AA;

Query Match 100.0%; Score 95; DB 8; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLETFVKSCPDAl 18  
 |||||  
 Db 1 PKKDVLETFVKSCPDAl 18

RESULT 2  
 ADJ57562  
 ID ADJ57562 standard; peptide; 25 AA.  
 XX  
 AC ADJ57562;

DT 06-MAY-2004 (first entry)

DE Human CD9 fibronectin-binding domain peptide fragment.

XX Human; CD9; antithrombotic; antiarteriosclerotic; vasotropic;  
 KW haemostatic; antiangiogenic; cycostatic.

XX Homo sapiens.

XX WO2004007685-A2.

XX 22-JAN-2004.

PF 14-JUL-2003; 2003WO-US022050.

PR 12-JUL-2002; 2002US-0395864P.

XX (UYTE-) UNIV TENNESSEE RES FOUND.

XX Jennings LK, Longhurst CM, Cook GA, Bao J, Zhang C, White MM;  
 PI Crossano JT, Lu Y;

XX WPI; 2004-122924/12.

XX Interfering with CD9 binding to fibronectin by binding a fibronectin-  
 PT binding domain of the CD9 protein or polypeptide, useful in treating  
 PT thrombosis, atherosclerosis, restenosis, bleeding disorders, angiogenesis  
 PT and cancers.

PS Claim 7; SEQ ID NO 5; 126pp; English.

XX The present sequence is that of a peptide fragment from the fibronectin-  
 CC binding domain of human CD9 ADJ57562. The peptide, or an antibody that  
 CC binds to it, is used in claimed methods for: interfering with CD9 binding  
 CC to fibronectin; modifying adhesion, motility or spreading of a CD9-  
 CC expressing cell on fibronectin; inhibiting proliferation or survival of  
 CC CD9-expressing cells; modifying pericellular fibronectin matrix assembly;  
 CC modifying invasiveness of a cell through a collagen and/or laminin matrix  
 CC ; and modifying cell-to-cell interaction. The methods are based on the  
 CC finding that increased CD9 expression is implicated in (i) decreased  
 CC adhesiveness of cells to extracellular matrix (via alpha5-beta-1

CC integrin) and/or decreased cell invasiveness and/or decreased  
 CC pericellular fibronectin matrix assembly, and/or (ii) increased cell  
 CC motility, spreading, proliferation, cell survival against apoptosis,  
 CC and/or cell-to-cell contacts. Conditions or disease states involving  
 CC proliferation or survival of CD9-expressing cells can be treated, e.g.  
 CC thrombosis, atherosclerosis, vein graft failure, restenosis, transplant  
 CC arteriopathy, bleeding disorders, angiogenesis, and primary and  
 CC metastatic cancers including breast cancer, prostate cancer, colon  
 CC cancer, melanoma, ovarian cancer, neuroblastoma, glioma and glioblastoma.  
 XX  
 SQ Sequence 25 AA;

Query Match 100.0%; Score 95; DB 8; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLETFVKSCPDAl 18  
 |||||  
 Db 1 PKKDVLETFVKSCPDAl 18

RESULT 3

ABU05051  
 ID ABU05051 standard; protein; 30 AA.  
 XX

AC ABU05051;

XX 29-JAN-2003 (first entry)

XX Human expressed protein tag (EPT) #1717.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
 KW protease; protease inhibitor; transporter; cytoskeletal protein;  
 KW receptor; transcription factor; cancer; MHC;  
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX Homo sapiens.

XX WO200278524-A2.

XX 10-OCT-2002.

XX 28-MAR-2002; 2002WO-US009671.

XX 28-MAR-2001; 2001US-0279495P.

PR 21-MAY-2001; 2001US-0292544P.

PR 08-AUG-2001; 2001US-0310801P.

PR 01-OCT-2001; 2001US-0326370P.

PR 04-DEC-2001; 2001US-0336780P.

PR 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCOS INC.

XX Chicx RM, Tomlinson AJ, Urban RG;

XX WPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
 PT cytoskeletal proteins, receptors or transcription factors), useful for  
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
 PT leukemia.

XX Example 2; SEQ ID NO 1717; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a  
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
 CC transporter, cytoskeletal protein, receptor or transcription factor. The  
 CC polypeptide is useful as an immunogenic composition for eliciting in a  
 CC mammal an immunogenic response directed against any of the purified  
 CC polypeptide. The purified polypeptide, or the antibody that binds to this  
 CC polypeptide, is useful for treating cancer. The polypeptide is also  
 CC useful for identifying compounds that binds to a naturally processed

CC class I or class II MHC-binding polypeptide. The polypeptides and  
 CC polynucleotides are particularly useful for treating or preventing  
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
 CC lymphoma or leukaemia. These are also useful for screening agents for  
 CC treating the above mentioned diseases. This sequence represents an  
 CC expressed protein tag (EPT) isolated from human tissue for translational  
 CC profiling. Note: This sequence does not appear in the printed  
 CC specification but was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 CC  
 XX SQ Sequence 30 AA;

Query Match 64.2%; Score 61; DB 6; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 0.014;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLFTTVK 12  
 |||||  
 Db 19 PKKDVLFTTVK 30

RESULT 4  
 ABU03385  
 ID ABU03385 standard; protein; 10 AA.  
 XX AC ABU03385;  
 XX  
 DT 29-JAN-2003 (first entry)  
 XX  
 DE Human expressed protein tag (EPT) #165.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
 KW protease; protease inhibitor; transporter; cytoskeletal protein;  
 KW receptor; transcription factor; cancer; MHC;  
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX Homo sapiens.

XX WO200278524-A2.

XX 10-OCT-2002.

XX 28-MAR-2002; 2002WO-US009671.

XX 28-MAR-2001; 2001US-0279495P.

XX 21-MAY-2001; 2001US-0292544P.

XX 08-AUG-2001; 2001US-0310801P.

XX 01-OCT-2001; 2001US-0326370P.

XX 04-DEC-2001; 2001US-0336780P.

XX 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCO INC.

XX Chicx RM, Tomlinson AJ, Urban RG;

XX WPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
 PT cytoskeletal proteins, receptors or transcription factors), useful for  
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
 PT leukemia.

XX Claim 10; SEQ ID NO 165; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a  
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
 CC transporter, cytoskeletal protein, receptor or transcription factor. The  
 CC polypeptide is useful as an immunogenic composition for eliciting in a  
 CC mammal an immunogenic response directed against any of the purified  
 CC polypeptide. The purified polypeptide, or the antibody that binds to this  
 CC polypeptide, is useful for treating cancer. The polypeptide is also  
 CC useful for identifying compounds that binds to a naturally processed

CC class I or class II MHC-binding polypeptide. The polypeptides and  
 CC polynucleotides are particularly useful for treating or preventing  
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
 CC lymphoma or leukaemia. These are also useful for screening agents for  
 CC treating the above mentioned diseases. This sequence represents an  
 CC expressed protein tag (EPT) isolated from human tissue for translational  
 CC profiling. Note: This sequence does not appear in the printed  
 CC specification but was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 CC  
 XX SQ Sequence 10 AA;

Query Match 51.6%; Score 49; DB 6; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.39;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KDVLFTTVK 12  
 |||||  
 Db 1 KDVLFTTVK 10

RESULT 5  
 AAM83184  
 ID AAM83184 standard; protein; 44 AA.  
 XX AC AAM83184;  
 XX  
 DT 07-NOV-2001 (first entry)  
 XX  
 DE Human immune/haematopoietic antigen SEQ ID NO:10777.

XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;  
 KW cytostatic; gene therapy; vaccine; metastasis.

XX Homo sapiens.

XX WO200157182-A2.

XX 09-AUG-2001.

XX 17-JAN-2001; 2001WO-US001354.

XX 31-JAN-2000; 2000US-0179065P.

XX 04-FEB-2000; 2000US-0180628P.

XX 24-FEB-2000; 2000US-0184664P.

XX 02-MAR-2000; 2000US-0186350P.

XX 16-MAR-2000; 2000US-0189874P.

XX 17-MAR-2000; 2000US-0190076P.

XX 18-APR-2000; 2000US-0198123P.

XX 19-MAY-2000; 2000US-0205515P.

XX 07-JUN-2000; 2000US-0209467P.

XX 28-JUN-2000; 2000US-0214886P.

XX 30-JUN-2000; 2000US-0215135P.

XX 07-JUL-2000; 2000US-0216647P.

XX 07-JUL-2000; 2000US-0216880P.

XX 11-JUL-2000; 2000US-0217487P.

XX 14-JUL-2000; 2000US-0218290P.

XX 26-JUL-2000; 2000US-0220963P.

XX 26-JUL-2000; 2000US-0220964P.

XX 14-AUG-2000; 2000US-0224518P.

XX 14-AUG-2000; 2000US-0224519P.

XX 14-AUG-2000; 2000US-0225213P.

XX 14-AUG-2000; 2000US-0225214P.

XX 14-AUG-2000; 2000US-0225266P.

XX 14-AUG-2000; 2000US-0225267P.

XX 14-AUG-2000; 2000US-0225268P.

XX 14-AUG-2000; 2000US-0225270P.

XX 14-AUG-2000; 2000US-0225447P.

XX 14-AUG-2000; 2000US-0225757P.

XX 14-AUG-2000; 2000US-0225758P.

XX 14-AUG-2000; 2000US-0225759P.

XX 18-AUG-2000; 2000US-0226279P.







KW amyotrophic lateral sclerosis; Alzheimer's disease; Parkinson's disease;  
 KW Huntington's disease; ischaemic stroke; acute brain injury; basopaenia;  
 KW acute spinal cord injury; multiple sclerosis; eosinopaenia; lymphopaenia;  
 KW monocystopaenia; neutropaenia; anaemia; thrombocytopaenia; neuroblastoma;  
 KW antibody; obesity; therapy; transforming growth factor beta; TGFbeta3;  
 KW growth factor; hybrid protein.

OS Homo sapiens.  
 XX  
 XX WO9708196-A1.  
 XX  
 PD 06-MAR-1997.  
 XX  
 XX 27-AUG-1996; 96WO-US014065.  
 XX  
 XX 28-AUG-1995; 95US-00519777.  
 XX  
 XX (UNIW ) UNIV WASHINGTON.  
 XX  
 XX Johnson EM, Milbrandt JD, Kotzbauer PT, Lampe PA;  
 PI WPI; 1997-179176/16.  
 XX  
 XX A novel growth factor Neurturin - used to treat neuro-degenerative and  
 PT haematopoietic cell degeneration diseases, e.g. Alzheimer's disease and  
 PT eosinopenia.  
 XX  
 XX Claim 92; Fig 18; 206pp; English.

XX AAW30355-W30377 represent growth factor fragments that are used in a  
 CC hybrid polypeptide of the invention. These sequences form a hybrid with  
 CC the human neurturin (NT) fragment shown in AAW30354. NT promotes the  
 CC growth and differentiation of haematopoietic and neuronal cells, and  
 CC their stem cells. The NT gene and protein are used to prevent or treat  
 CC neurodegenerative diseases e.g. peripheral neuropathy, amyotrophic  
 CC lateral sclerosis, Alzheimer's disease, Parkinson's disease, Huntington's  
 CC disease, ischaemic stroke, acute brain injury, acute spinal cord injury,  
 CC nervous system tumours, multiple sclerosis and infection; and  
 CC haematopoietic cell degenerative diseases, e.g. eosinopaenia, basopaenia,  
 CC lymphopaenia, monocystopaenia, neutropaenia, anaemia, thrombocytopaenia  
 CC and stem cell insufficiencies. The NT protein and gene are also useful to  
 CC treat neuroblastomas. Antibodies against NT and oligonucleotides (used as  
 CC either probes or primers, corresponding to an exon of pre-pro-NT gene or  
 CC flanking a target sequence) can be used for detecting NT in a sample or  
 CC detecting mutations in the NT gene. Antisense sequences of the NT gene  
 CC are used to treat diseases promoted by NT expression e.g. obesity

XX Sequence 36 AA;  
 SQ  
 Query Match 37.9%; Score 36; DB 2; Length 36;  
 Best Local Similarity 50.0%; Pred. No. 2.3e+02;  
 Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKKDVLETFVTKSC 14  
 || : | ||||  
 Db 20 PKVEQLSNMVKSC 33  
 RESULT 9  
 AAB09511  
 ID AAB09511 standard; peptide; 36 AA.  
 XX  
 AC AAB09511;  
 XX  
 XX 11-SEP-2000 (first entry)  
 XX  
 XX Human TGF-beta 3 finger 2 subdomain.

XX TGF-beta superfamily; transforming growth factor-beta;  
 KW developmental regulation; finger 2 subdomain; basic region;  
 KW protein refolding; stability; solubility; osteogenic protein; OP;  
 KW bone morphogenetic protein; BMP; growth/differentiation factor; GDF;  
 KW inhibin; tissue morphogenesis; regeneration; bone; dental tissue;

KW connective tissue; cartilage; vulnary.

XX Homo sapiens.  
 XX WO200020607-A2.

XX 13-APR-2000.  
 XX  
 XX 07-OCT-1999; 99WO-US023371.  
 XX  
 XX 07-OCT-1998; 98US-0103418P.  
 PR 16-AUG-1999; 99US-00374958.

XX (STYC ) STRYKER CORP.  
 XX  
 XX Oppermann H, Tai M, McCartney J;  
 PI WPI; 2000-303787/26.

XX Transforming growth factor-beta superfamily member mutant induces tissue  
 PT morphogenesis in e.g. bone, non-mineralized skeletal tissue, dental  
 PT tissue and connective tissue and comprises a substitution in a region of  
 PT the finger 2 domain.

XX Disclosure; Fig 1; 162pp; English.  
 XX  
 XX The invention relates to mutant TGF-beta (transforming growth factor-  
 CC beta) superfamily members. These mutants comprise one or more amino acid  
 CC substitutions in the base region of the finger 2 subdomain, and a C-  
 CC terminal residue selected from Arg, Ile, Leu, Ser and Ala. In the finger  
 CC 2 subdomain, basic residues (e.g., Arg, Lys), or residues containing an  
 CC amide group (e.g., Gln, Asn), are substituted with acidic residues (e.g.,  
 CC Glu, Asp) or residues containing a hydroxyl group (e.g., Ser, Thr). TGF-  
 CC beta superfamily proteins regulate developmental processes and include  
 CC proteins such as the osteogenic proteins (OPs), bone morphogenetic  
 CC proteins (BMPs), growth/differentiation factors (GDFs) and inhibins.

XX Specific examples of TGF-beta superfamily mutants encompassed by the  
 CC invention are the finger 2 subdomain mutants of human osteogenic protein-  
 CC 1 (OP-1) (AAB09576-B09615). Mutant TGF-beta proteins are used for  
 CC inducing tissue morphogenesis in bone, non-mineralised skeletal tissue,  
 CC dental tissue, connective tissue, brain, liver and nerve tissue. The  
 CC proteins can be used in conjunction with a biocompatible matrix e.g.,  
 CC collagen, hydroxyapatite or carboxymethylcellulose for regenerating bone,  
 CC cartilage and/or other mineralised skeletal or connective tissues e.g.,  
 CC ligament, tendon, muscle, fibrocartilage, joint capsule and  
 CC intervertebral discs. The OP-1 mutants can be used to repair diseased or  
 CC damaged mammalian tissue and to prevent or substantially inhibit  
 CC immune/inflammatory response-mediated tissue damage and scar tissue  
 CC formation following an injury. Compared to the wild-type TGF-beta  
 CC superfamily members, the mutant proteins have improved in vitro refolding  
 CC properties in a pH range of 6-9, increased solubility in aqueous solution  
 CC and improved stability and/or activity. Sequences AAB09481-B09516  
 CC represent wild-type finger 2 subdomains from a variety of TGF-beta  
 CC superfamily proteins referred to in the specification

XX Sequence 36 AA;  
 SQ  
 Query Match 37.9%; Score 36; DB 3; Length 36;  
 Best Local Similarity 50.0%; Pred. No. 2.3e+02;  
 Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKKDVLETFVTKSC 14  
 || : | ||||  
 Db 20 PKVEQLSNMVKSC 33

RESULT 10  
 ADS06580  
 ID ADS06580 standard; protein; 46 AA.  
 XX  
 AC ADS06580;  
 XX  
 XX 04-NOV-2004 (first entry)



```
PR 08-SEP-2000; 2000US-02332081P.
PR 12-SEP-2000; 2000US-0231368P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234397P.
PR 25-SEP-2000; 2000US-0234398P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249444P.
PR 17-NOV-2000; 2000US-0249445P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249397P.
PR 17-NOV-2000; 2000US-0249399P.
PR 17-NOV-2000; 2000US-0249300P.

PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 11-DEC-2000; 2000US-0251990P.
PR 05-JAN-2001; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI. 2001-457726/49.
XX N-PSDB; AAS32432.
XX
XX Isolated polypeptide for treating, preventing and prognosing disorders
XX related to the endocrine system including endocrine disorders,
XX reproductive disorders, and gastrointestinal disorders and also for
XX testing and detection e.g. diagnosis.
XX
XX Claim 11; SEQ ID NO 386; 558pp; English.
XX
XX The invention relates to cDNAs encoding novel human endocrine antigens or
XX a fragment having biological activity, a domain, an epitope, full length
XX protein, variant, allelic variant or a species homologue of the
XX cDNA/antigen. The DNAs and polypeptides are useful for preventing,
XX treating or ameliorating a medical condition when administered (e.g. by
XX gene therapy or antisense-therapy). Identifying mutations in the genes
XX coding for the antigens is useful for diagnosing a pathological condition
XX or a susceptibility to a pathological condition. The DNAs, antigens and
XX antibodies raised against the antigens useful for treating, preventing
XX and/or prognosing disorders related to the endocrine system or hormone
XX imbalance or reproductive disorders, cancers of endocrine tissues,
XX disorders of the pancreas (e.g. diabetes mellitus), the adrenal glands
XX (e.g. hirsutism), ovaries, the thyroid (e.g. hyperthyroidism), the
XX hypothalamus and testes (e.g. vanishing testes syndrome), many examples
XX of diseases and disorders are given in the specification. The present
XX sequence represents an endocrine antigen of the invention. Note: the
XX sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 41 AA;
SQ
Query Match 36.8%; Score 35; DB 4; Length 41;
Best Local Similarity 31.2%; Pred. NO. 3.9e+02;
Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 1 PKQDVLETFYVKSCPD 16
Db |::|::|::|
5 PHREIFYFTLRAPD 20
RESULT 12
ABP58897
ID ABP58897 standard; peptide; 15 AA.
XX
XX AC ABP58897;
XX
XX 10-APR-2003 (first entry)
XX
XX Human DNA binding protein 28.27 N-terminal peptide.
XX
XX Human; DNA binding protein 28.27; recombinant production; gene therapy;
XX malignant tumour; cancer; blood disease; human immunodeficiency virus;
XX HIV infection; immune disorder; inflammatory condition; cytostatic;
XX antinflammatory; immunomodulator; N-terminal peptide;
```

KW enzyme linked immunosorbent assay; ELISA.  
XX Homo sapiens.  
XX CNL361152-A.  
XX 31-JUL-2002.  
XX 26-DEC-2000; 2000CN-00135944.  
XX 26-DEC-2000; 2000CN-00135944.  
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
XX Mao Y, Xie Y;  
XX WPI; 2002-751571/82.  
XX New polypeptide human DNA binding 28.27 and polynucleotides encoding this  
PT polypeptide.  
XX Example 5; Page 18 (Disclosure); 33pp; Chinese.  
XX The invention relates to human DNA binding protein 28.27 (ABP8896) and  
CC nucleic acids encoding it (AB257649). The protein has a molecular weight  
CC of 28.27 kD. The invention also relates to a method for the recombinant  
CC production of the protein, an antagonist of the protein, and the use of  
CC the protein, gene and antagonist in therapeutic applications. DNA binding  
CC protein 28.27 can be used in the treatment of a variety of diseases such  
CC as malignant tumours, blood diseases, HIV (human immunodeficiency virus)  
CC infection, immune disorders and inflammatory conditions. The present  
CC sequence represents the 15 N-terminal amino acids of human DNA binding  
CC protein 28.27 used in ELISA (enzyme linked immunosorbent assay) in an  
XX exemplification of the invention  
XX  
SQ Sequence 15 AA;  
Query Match 35.8%; Score 34; DB 5; Length 15;  
Best Local Similarity 50.0%; Pred. No. 1.9e+02;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 7 EPTFTVKSCPD 16  
DB || : : |||  
6 ETLSLNKRCPD 15  
RESULT 13  
ADV59436  
ID ADV59436 standard; peptide; 17 AA.  
XX  
XX ADV59436;  
XX  
XX DT 10-MAR-2005 (first entry)  
XX  
XX DE G protein coupled receptor peptide SEQ ID NO 6941.  
XX diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;  
KW food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.  
KW  
XX Unidentified.  
XX WO2004111636-A2.  
XX  
XX 23-DEC-2004.  
XX  
XX 17-JUN-2004; 2004WO-EP051158.  
XX  
XX 17-JUN-2003; 2003EP-00101775.  
XX 17-JUN-2003; 2003US-0479061P.  
XX  
XX (VIBV-) VIB VZW.  
XX (UYGE-) UNIV GENT.  
XX  
XX Kas K, Vandekerckhove J, Krols L;  
PI

PI Kas K, Vandekerckhove J, Krols L;  
XX WPI; 2005-057893/06.  
XX  
XX Identifying a peptide combo which corresponds with a family of proteins,  
PT useful for diagnosing a variety of diseases, drug development or in  
PT agriculture, comprises generating peptides by applying a digest on the  
PT family of protein.  
XX  
XX Example; SEQ ID NO 6941; 265pp; English.  
XX  
XX The invention relates to a method of identifying a peptide combo which  
CC corresponds with a family of proteins where each of the members of the  
CC peptide combo is derived from a unique protein from the family. The  
CC peptide combo is useful for quantifying specific known splice variants of  
CC one or more particular proteins in a sample, for diagnosing complex  
CC genetic diseases such as cancer, obesity, diabetes, asthma and  
CC inflammation, neuropsychiatric disorders such as depression, for  
CC quantifying one to several hundreds of protein disease markers  
CC simultaneously leading to a more accurate diagnostic sub-classification,  
CC for determining the extent of protein modification in a particular sample  
CC of proteins, for tissue-typing analysis, for prenatal testing to detect  
CC the presence of a congenital disease or for quantitating protein levels  
CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases  
CC or neurological diseases, as biomarkers preclinical drug development,  
CC development of improved animal models, biomarkers related with  
CC toxicology, clinical drug development, guidance marketed drugs,  
CC prognostic or diagnostic disease markers, drug target validation and  
CC selection, monitoring protein splicing, drug lead profiling, pathway  
CC analysis, answering basic disease biology questions, and in the fields of  
CC food and feed, cosmetics, agriculture and animal breeding. The present  
CC sequence represents a peptide from a G-protein coupled receptor peptide  
CC combo.  
XX  
XX Sequence 17 AA;  
SQ  
Query Match 35.8%; Score 34; DB 9; Length 17;  
Best Local Similarity 60.0%; Pred. No. 2.1e+02;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 7 EPTFTVKSCPD 16  
DB || : : |||  
7 ETGEVQACPD 16  
RESULT 14  
ADV57877  
ID ADV57877 standard; peptide; 17 AA.  
XX  
XX ADV57877;  
XX  
XX DT 10-MAR-2005 (first entry)  
XX  
XX DE G protein coupled receptor peptide SEQ ID NO 5381.  
XX diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;  
KW food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.  
KW  
XX Unidentified.  
XX WO2004111636-A2.  
XX  
XX 23-DEC-2004.  
XX  
XX 17-JUN-2004; 2004WO-EP051158.  
XX  
XX 17-JUN-2003; 2003EP-00101775.  
XX 17-JUN-2003; 2003US-0479061P.  
XX  
XX (VIBV-) VIB VZW.  
XX (UYGE-) UNIV GENT.  
XX  
XX Kas K, Vandekerckhove J, Krols L;  
PI

XX WPI; 2005-057893/06.  
DR  
XX  
PT Identifying a peptide combo which corresponds with a family of proteins,  
PT useful for diagnosing a variety of diseases, drug development or in  
PT agriculture, comprises generating peptides by applying a digest on the  
PT family of protein.  
XX  
XX  
PS Example; SEQ ID NO 5381; 265pp; English.  
XX  
XX  
CC The invention relates to a method of identifying a peptide combo which  
CC corresponds with a family of proteins where each of the members of the  
CC peptide combo is derived from a unique protein from the family. The  
CC peptide combo is useful for quantifying specific known splice variants of  
CC one or more particular proteins in a sample, for diagnosing complex  
CC genetic diseases such as cancer, obesity, diabetes, asthma and  
CC inflammation, neuropsychiatric disorders such as depression, for  
CC quantifying one to several hundreds of protein disease markers  
CC simultaneously leading to a more accurate diagnostic sub-classification,  
CC for determining the extent of protein modification in a particular sample  
CC of proteins, for tissue-typing analysis, for prenatal testing to detect  
CC the presence of a congenital disease or for quantitating protein levels  
CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases  
CC or neurological diseases, as biomarkers, preclinical drug development,  
CC development of improved animal models, biomarkers related with  
CC toxicology, clinical drug development, guidance marketed drugs,  
CC prognostic or diagnostic disease markers, drug target validation and  
CC selection, monitoring protein splicing, drug lead profiling, pathway  
CC analysis, answering basic disease biology questions, and in the fields of  
CC food and feed, cosmetics, agriculture and animal breeding. The present  
CC sequence represents a peptide from a G-protein coupled receptor peptide  
CC combo.  
XX  
XX  
SQ Sequence 17 AA;  
Query Match 35.8%; Score 34; DB 9; Length 17;  
Best Local Similarity 60.0%; Pred. No. 2.1e+02;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 7 ETFTVKSCPD 16  
||| :|||  
Db 7 ETGEVQACPD 16  
||| :|||  
RESULT 15  
ADV58632  
ID ADV58632 standard; peptide; 17 AA.  
XX  
AC ADV58632;  
XX  
DT 10-MAR-2005 (first entry)  
XX  
DE G protein coupled receptor peptide SEQ ID NO 6137.  
XX  
KW diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;  
KW food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.  
XX  
OS Unidentified.  
XX  
PN WO2004111636-A2.  
XX  
PD 23-DEC-2004.  
XX  
PF 17-JUN-2004; 2004WO-EP051158.  
XX  
PR 17-JUN-2003; 2003EP-00101775.  
PR 17-JUN-2003; 2003US-0479061P.  
XX  
PA (VIBV-) VIB VZW.  
PA (UYGE-) UNIV GENT.  
XX  
PI Kas K, Vandekerckhove J, Krols L;  
XX WPI; 2005-057893/06.

DR WPI; 2005-057893/06.  
XX  
PT Identifying a peptide combo which corresponds with a family of proteins,  
PT useful for diagnosing a variety of diseases, drug development or in  
PT agriculture, comprises generating peptides by applying a digest on the  
PT family of protein.  
XX  
XX  
PS Example; SEQ ID NO 6137; 265pp; English.  
XX  
XX  
CC The invention relates to a method of identifying a peptide combo which  
CC corresponds with a family of proteins where each of the members of the  
CC peptide combo is derived from a unique protein from the family. The  
CC peptide combo is useful for quantifying specific known splice variants of  
CC one or more particular proteins in a sample, for diagnosing complex  
CC genetic diseases such as cancer, obesity, diabetes, asthma and  
CC inflammation, neuropsychiatric disorders such as depression, for  
CC quantifying one to several hundreds of protein disease markers  
CC simultaneously leading to a more accurate diagnostic sub-classification,  
CC for determining the extent of protein modification in a particular sample  
CC of proteins, for tissue-typing analysis, for prenatal testing to detect  
CC the presence of a congenital disease or for quantitating protein levels  
CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases  
CC or neurological diseases, as biomarkers, preclinical drug development,  
CC development of improved animal models, biomarkers related with  
CC toxicology, clinical drug development, guidance marketed drugs,  
CC prognostic or diagnostic disease markers, drug target validation and  
CC selection, monitoring protein splicing, drug lead profiling, pathway  
CC analysis, answering basic disease biology questions, and in the fields of  
CC food and feed, cosmetics, agriculture and animal breeding. The present  
CC sequence represents a peptide from a G-protein coupled receptor peptide  
CC combo.  
XX  
XX  
SQ Sequence 17 AA;  
Query Match 35.8%; Score 34; DB 9; Length 17;  
Best Local Similarity 60.0%; Pred. No. 2.1e+02;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 7 ETFTVKSCPD 16  
||| :|||  
Db 7 ETGEVQACPD 16  
||| :|||  
RESULT 16  
ADV59442  
ID ADV59442 standard; peptide; 18 AA.  
XX  
AC ADV59442;  
XX  
DT 10-MAR-2005 (first entry)  
XX  
DE G protein coupled receptor peptide SEQ ID NO 6947.  
XX  
KW diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;  
KW food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.  
XX  
OS Unidentified.  
XX  
PN WO2004111636-A2.  
XX  
PD 23-DEC-2004.  
XX  
PF 17-JUN-2004; 2004WO-EP051158.  
XX  
PR 17-JUN-2003; 2003EP-00101775.  
PR 17-JUN-2003; 2003US-0479061P.  
XX  
PA (VIBV-) VIB VZW.  
PA (UYGE-) UNIV GENT.  
XX  
PI Kas K, Vandekerckhove J, Krols L;  
XX WPI; 2005-057893/06.

XX Identifying a peptide combo which corresponds with a family of proteins,  
 PT useful for diagnosing a variety of diseases, drug development or in  
 PT agriculture, comprises generating peptides by applying a digest on the  
 PT family of protein.  
 XX  
 XX

PS Example; SEQ ID NO 6947; 265pp; English.

XX The invention relates to a method of identifying a peptide combo which  
 CC corresponds with a family of proteins where each of the members of the  
 CC peptide combo is derived from a unique protein from the family. The  
 CC peptide combo is useful for quantifying specific known splice variants of  
 CC one or more particular proteins in a sample, for diagnosing complex  
 CC genetic diseases such as cancer, obesity, diabetes, asthma and  
 CC inflammation, neuropsychiatric disorders such as depression, for  
 CC quantifying one to several hundreds of protein disease markers  
 CC simultaneously leading to a more accurate diagnostic sub-classification,  
 CC for determining the extent of protein modification in a particular sample  
 CC of proteins, for tissue-typing analysis, for prenatal testing to detect  
 CC the presence of a congenital disease or for quantitating protein levels  
 CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases  
 CC or neurological diseases, as biomarkers preclinical drug development,  
 CC development of improved animal models, biomarkers related with  
 CC toxicology, clinical drug development, guidance marketed drugs,  
 CC prognostic or diagnostic disease markers, drug target validation and  
 CC selection, monitoring protein splicing, drug lead profiling, pathway  
 CC analysis, answering basic disease biology questions, and in the fields of  
 CC food and feed, cosmetics, agriculture and animal breeding. The present  
 CC sequence represents a peptide from a G-protein coupled receptor peptide  
 CC combo.  
 XX  
 XX

SQ Sequence 18 AA;

Query Match 35.8%; Score 34; DB 9; Length 18;  
 Best Local Similarity 60.0%; Pred. No. 2.3e+02;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 ETFTVKSCPD 16  
 |||:|:|  
 Db 7 ETGEVQACPD 16

RESULT 17

ADV57883  
 ID ADV57883 standard; peptide; 18 AA.

AC ADV57883;

DT 10-MAR-2005 (first entry)

DE G protein coupled receptor peptide SEQ ID NO 5387.

DE diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;  
 KW food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.

XX Unidentified.

XX WO2004111636-A2.

XX 23-DEC-2004.

XX 17-JUN-2004; 2004WO-EP051158.

XX 17-JUN-2003; 2003EP-00101775.

XX 17-JUN-2003; 2003US-0479061P.

XX (VIBV-) VIB VZW.

XX (UYGB-) UNIV GENT.

XX Kas K, Vandekerckhove J, Krols L;

XX WPI; 2005-057893/06.

XX

PT Identifying a peptide combo which corresponds with a family of proteins,  
 PT useful for diagnosing a variety of diseases, drug development or in  
 PT agriculture, comprises generating peptides by applying a digest on the  
 PT family of protein.  
 XX  
 XX

PS Example; SEQ ID NO 5387; 265pp; English.

XX The invention relates to a method of identifying a peptide combo which  
 CC corresponds with a family of proteins where each of the members of the  
 CC peptide combo is derived from a unique protein from the family. The  
 CC peptide combo is useful for quantifying specific known splice variants of  
 CC one or more particular proteins in a sample, for diagnosing complex  
 CC genetic diseases such as cancer, obesity, diabetes, asthma and  
 CC inflammation, neuropsychiatric disorders such as depression, for  
 CC quantifying one to several hundreds of protein disease markers  
 CC simultaneously leading to a more accurate diagnostic sub-classification,  
 CC for determining the extent of protein modification in a particular sample  
 CC of proteins, for tissue-typing analysis, for prenatal testing to detect  
 CC the presence of a congenital disease or for quantitating protein levels  
 CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases  
 CC or neurological diseases, as biomarkers preclinical drug development,  
 CC development of improved animal models, biomarkers related with  
 CC toxicology, clinical drug development, guidance marketed drugs,  
 CC prognostic or diagnostic disease markers, drug target validation and  
 CC selection, monitoring protein splicing, drug lead profiling, pathway  
 CC analysis, answering basic disease biology questions, and in the fields of  
 CC food and feed, cosmetics, agriculture and animal breeding. The present  
 CC sequence represents a peptide from a G-protein coupled receptor peptide  
 CC combo.  
 XX  
 XX

SQ Sequence 18 AA;

Query Match 35.8%; Score 34; DB 9; Length 18;  
 Best Local Similarity 60.0%; Pred. No. 2.3e+02;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 ETFTVKSCPD 16  
 |||:|:|  
 Db 7 ETGEVQACPD 16

RESULT 18

ADV58638

ID ADV58638 standard; peptide; 18 AA.

AC ADV58638;

DT 10-MAR-2005 (first entry)

DE G protein coupled receptor peptide SEQ ID NO 6143.

DE diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;  
 KW food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.

XX Unidentified.

XX WO2004111636-A2.

XX 23-DEC-2004.

XX 17-JUN-2004; 2004WO-EP051158.

XX 17-JUN-2003; 2003EP-00101775.

XX 17-JUN-2003; 2003US-0479061P.

XX (VIBV-) VIB VZW.

XX (UYGB-) UNIV GENT.

XX Kas K, Vandekerckhove J, Krols L;

XX WPI; 2005-057893/06.

PT Identifying a peptide combo which corresponds with a family of proteins,



PT useful for diagnosing a variety of diseases, drug development or in  
PT agriculture, comprises generating peptides by applying a digest on the  
PT family of protein.  
XX  
XX Example; SEQ ID NO 6143; 265pp; English.  
XX  
XX The invention relates to a method of identifying a peptide combo which  
CC corresponds with a family of proteins where each of the members of the  
CC peptide combo is derived from a unique protein from the family. The  
CC peptide combo is useful for quantifying specific known splice variants of  
CC one or more particular proteins in a sample, for diagnosing complex  
CC genetic diseases such as cancer, obesity, diabetes, asthma and  
CC inflammation, neuropsychiatric disorders such as depression, for  
CC quantifying one to several hundreds of protein disease markers  
CC simultaneously leading to a more accurate diagnostic sub-classification,  
CC for determining the extent of protein modification in a particular sample  
CC of proteins, for tissue-typing analysis, for prenatal testing to detect  
CC the presence of a congenital disease or for quantitating protein levels  
CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases  
CC or neurological diseases, as biomarkers preclinical drug development,  
CC development of improved animal models, biomarkers related with  
CC toxicology, clinical drug development, guidance marketed drugs,  
CC prognostic or diagnostic disease markers, drug target validation and  
CC selection, monitoring protein splicing, drug lead profiling, pathway  
CC analysis, answering basic disease biology questions, and in the fields of  
CC food and feed, cosmetics, agriculture and animal breeding. The present  
CC sequence represents a peptide from a G-protein coupled receptor peptide  
CC combo.  
XX  
XX Sequence 18 AA;  
SQ  
Query Match 35.8%; Score 34; DB 9; Length 18;  
Best Local Similarity 60.0%; Pred. No. 2.3e+02;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 7 ETFTVKSCPD 16  
||| : : : :  
Db 7 ETGEVQACPD 16  
RESULT 19  
ADV59441  
ID ADV59441 standard; peptide; 20 AA.  
XX  
XX ADV59441;  
AC  
XX 10-MAR-2005 (first entry)  
DT  
XX G protein coupled receptor peptide SEQ ID NO 6946.  
DE  
XX diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;  
KW food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.  
KW  
XX Unidentified.  
OS  
XX WO2004111636-A2.  
PN  
XX 23-DEC-2004.  
PD  
XX 17-JUN-2004; 2004WO-EP051158.  
XX  
XX 17-JUN-2003; 2003EP-00101775.  
PR  
XX 17-JUN-2003; 2003US-0479061P.  
PR  
XX (VIBV-) VIB VZW.  
PA  
PA (UYGE-) UNIV GENT.  
XX  
XX Kas K, Vandekerckhove J, Krols L;  
PI  
XX WPI; 2005-057893/06.  
DR  
XX Identifying a peptide combo which corresponds with a family of proteins,  
PT useful for diagnosing a variety of diseases, drug development or in  
PT agriculture, comprises generating peptides by applying a digest on the

PT agriculture, comprises generating peptides by applying a digest on the  
PT family of protein.  
XX  
XX Example; SEQ ID NO 6946; 265pp; English.  
XX  
XX The invention relates to a method of identifying a peptide combo which  
CC corresponds with a family of proteins where each of the members of the  
CC peptide combo is derived from a unique protein from the family. The  
CC peptide combo is useful for quantifying specific known splice variants of  
CC one or more particular proteins in a sample, for diagnosing complex  
CC genetic diseases such as cancer, obesity, diabetes, asthma and  
CC inflammation, neuropsychiatric disorders such as depression, for  
CC quantifying one to several hundreds of protein disease markers  
CC simultaneously leading to a more accurate diagnostic sub-classification,  
CC for determining the extent of protein modification in a particular sample  
CC of proteins, for tissue-typing analysis, for prenatal testing to detect  
CC the presence of a congenital disease or for quantitating protein levels  
CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases  
CC or neurological diseases, as biomarkers preclinical drug development,  
CC development of improved animal models, biomarkers related with  
CC toxicology, clinical drug development, guidance marketed drugs,  
CC prognostic or diagnostic disease markers, drug target validation and  
CC selection, monitoring protein splicing, drug lead profiling, pathway  
CC analysis, answering basic disease biology questions, and in the fields of  
CC food and feed, cosmetics, agriculture and animal breeding. The present  
CC sequence represents a peptide from a G-protein coupled receptor peptide  
CC combo.  
XX  
XX Sequence 20 AA;  
SQ  
Query Match 35.8%; Score 34; DB 9; Length 20;  
Best Local Similarity 60.0%; Pred. No. 2.6e+02;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 7 ETFTVKSCPD 16  
||| : : : :  
Db 10 ETGEVQACPD 19  
RESULT 20  
ADV58637  
ID ADV58637 standard; peptide; 20 AA.  
XX  
XX ADV58637;  
AC  
XX 10-MAR-2005 (first entry)  
DT  
XX G protein coupled receptor peptide SEQ ID NO 6142.  
DE  
XX diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;  
KW food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.  
KW  
XX Unidentified.  
OS  
XX WO2004111636-A2.  
PN  
XX 23-DEC-2004.  
PD  
XX 17-JUN-2004; 2004WO-EP051158.  
XX  
XX 17-JUN-2003; 2003EP-00101775.  
PR  
XX 17-JUN-2003; 2003US-0479061P.  
PR  
XX (VIBV-) VIB VZW.  
PA  
PA (UYGE-) UNIV GENT.  
XX  
XX Kas K, Vandekerckhove J, Krols L;  
PI  
XX WPI; 2005-057893/06.  
DR  
XX Identifying a peptide combo which corresponds with a family of proteins,  
PT useful for diagnosing a variety of diseases, drug development or in  
PT agriculture, comprises generating peptides by applying a digest on the



PT family of protein.  
XX  
PS Example; SEQ ID NO 6142; 265pp; English.  
XX  
CC The invention relates to a method of identifying a peptide combo which  
CC corresponds with a family of proteins where each of the members of the  
CC peptide combo is derived from a unique protein from the family. The  
CC peptide combo is useful for quantifying specific known splice variants of  
CC one or more particular proteins in a sample, for diagnosing complex  
CC genetic diseases such as cancer, obesity, diabetes, asthma and  
CC inflammation, neuropsychiatric disorders such as depression, for  
CC quantifying one to several hundreds of protein disease markers  
CC simultaneously leading to a more accurate diagnostic sub-classification,  
CC for determining the extent of protein modification in a particular sample  
CC of proteins, for tissue-typing analysis, for prenatal testing to detect  
CC the presence of a congenital disease or for quantitating protein levels  
CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases  
CC or neurological diseases, as biomarkers preclinical drug development,  
CC development of improved animal models, biomarkers related with  
CC toxicology, clinical drug development, guidance marketed drugs,  
CC prognostic or diagnostic disease markers, drug target validation and  
CC selection, monitoring protein splicing, drug lead profiling, pathway  
CC analysis, answering basic disease biology questions, and in the fields of  
CC food and feed, cosmetics, agriculture and animal breeding. The present  
CC sequence represents a peptide from a G-protein coupled receptor peptide  
CC combo.  
XX  
SQ Sequence 20 AA;  
  
Query Match 35.8%; Score 34; DB 9; Length 20;  
Best Local Similarity 60.0%; Pred. No. 2.6e+02;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
  
QY 7 ETFTVKSCPD 16  
||| |::|||  
Db 10 ETGEVQACPD 19  
  
RESULT 21  
ADV57882  
ID ADV57882 standard; peptide; 20 AA.  
XX  
AC ADV57882;  
XX  
DT 10-MAR-2005 (first entry)  
XX  
DE G protein coupled receptor peptide SEQ ID NO 5386.  
XX  
XX diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;  
XX food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.  
XX Unidentified.  
XX  
XX WO2004111636-A2.  
XX  
XX 23-DEC-2004.  
XX  
XX 17-JUN-2004; 2004WO-EP051158.  
XX  
XX 17-JUN-2003; 2003EP-00101775.  
XX  
XX 17-JUN-2003; 2003US-0479061P.  
XX  
XX (VIBV-) VIB VZW  
XX (UYGB-) UNIV GENT.  
XX  
XX Kas K, Vandekerckhove J, Kroels L;  
XX  
XX WPI; 2005-057893/06.  
XX  
XX Identifying a peptide combo which corresponds with a family of proteins,  
XX useful for diagnosing a variety of diseases, drug development or in  
XX agriculture, comprises generating peptides by applying a digest on the  
XX family of protein.

XX  
PS Example; SEQ ID NO 5386; 265pp; English.  
XX  
CC The invention relates to a method of identifying a peptide combo which  
CC corresponds with a family of proteins where each of the members of the  
CC peptide combo is derived from a unique protein from the family. The  
CC peptide combo is useful for quantifying specific known splice variants of  
CC one or more particular proteins in a sample, for diagnosing complex  
CC genetic diseases such as cancer, obesity, diabetes, asthma and  
CC inflammation, neuropsychiatric disorders such as depression, for  
CC quantifying one to several hundreds of protein disease markers  
CC simultaneously leading to a more accurate diagnostic sub-classification,  
CC for determining the extent of protein modification in a particular sample  
CC of proteins, for tissue-typing analysis, for prenatal testing to detect  
CC the presence of a congenital disease or for quantitating protein levels  
CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases  
CC or neurological diseases, as biomarkers preclinical drug development,  
CC development of improved animal models, biomarkers related with  
CC toxicology, clinical drug development, guidance marketed drugs,  
CC prognostic or diagnostic disease markers, drug target validation and  
CC selection, monitoring protein splicing, drug lead profiling, pathway  
CC analysis, answering basic disease biology questions, and in the fields of  
CC food and feed, cosmetics, agriculture and animal breeding. The present  
CC sequence represents a peptide from a G-protein coupled receptor peptide  
CC combo.  
XX  
SQ Sequence 20 AA;  
  
Query Match 35.8%; Score 34; DB 9; Length 20;  
Best Local Similarity 60.0%; Pred. No. 2.6e+02;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
  
QY 7 ETFTVKSCPD 16  
||| |::|||  
Db 10 ETGEVQACPD 19  
  
RESULT 22  
AAY92548  
ID AAY92548 standard; peptide; 34 AA.  
XX  
AC AAY92548;  
XX  
DT 10-AUG-2000 (first entry)  
XX  
DE Finger 2 subdomain of TGF-beta2.  
XX  
XX finger 2 subdomain; BMP; TGF-beta family; protein refolding;  
XX fusion protein; osteopathic; antibacterial; cytostatic.  
XX Homo sapiens.  
XX  
XX WO200020449-A2.  
XX  
XX 13-APR-2000.  
XX  
XX 07-OCT-1999; 99WO-US023372.  
XX  
XX 07-OCT-1998; 98US-0103418P.  
XX  
XX 16-AUG-1999; 99US-00375333.  
XX  
XX (STYC ) STRYKER CORP.  
XX  
XX Oppermann H, Tai M, McCartney J;  
XX  
XX WPI; 2000-303743/26.  
XX  
XX A biologically active TGF-beta family member fusion protein competent to  
XX refold, comprising a C-terminal linked TGF-beta family protein.  
XX Disclosure; Page 131; 160pp; English.  
XX  
XX AAY92519-53 are C-terminal residues of the finger 2 subdomain of various

CC known members of the BMP and TGF-beta families, starting with the first  
 CC residue following the cysteine doublet. Novel proteins comprise  
 CC biologically active TGF-beta family member fusion proteins competent to  
 CC refold under suitable refolding conditions. The fusion proteins comprise:  
 CC (1) a TGF-beta family protein C-terminal seven cysteine domain,  
 CC comprising finger 1, finger 2 and heel subdomains; and (2) a heterologous  
 CC leader sequence domain operatively linked to the C-terminal domain.  
 CC Truncations, heterodimers and mutants of these fusion proteins and  
 CC methods of purifying the heterodimers are also claimed. The TGF-beta  
 CC family proteins can be used to induce the full cascade of morphogenic  
 CC events which culminate in skeletal tissue formation, including cartilage  
 CC and endochondral bone formation. They are useful in the binding of fibrin  
 CC and fibronectin to the implanted matrix, chemotaxis of cells,  
 CC proliferation of fibroblasts, differentiation into chondroblasts,  
 CC cartilage formation, vascular invasion, bone formation, remodeling, and  
 CC bone marrow differentiation. The proteins have improved physical  
 CC properties such as solubility and stability, improved biological  
 CC activity, including altered receptor binding and improved targeting  
 CC capabilities

XX Sequence 34 AA;

Query Match 35.8%; Score 34; DB 3; Length 34;  
 Best Local Similarity 50.0%; Pred. No. 4.7e+02;  
 Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKQVLETFTVKSC 14  
 DB 18 PKIEQLSNMIVKSC 31

RESULT 23  
 AAB02777  
 ID AAB02777 standard; protein; 34 AA.

XX AAB02777;  
 XX  
 XX 22-AUG-2000 (first entry)  
 DT Human TGF-beta2 finger 2 sub-domain sequence SEQ ID NO:30.  
 DE  
 XX Tumour growth factor beta; TGF-beta; morphogenic protein; BMP; OP;  
 KW bone morphogenic protein; osteogenic protein; mutant; modified;  
 KW finger 2 sub-domain; finger 1 domain; heel domain; chimeric protein;  
 KW osteogenic; proliferative; antiinflammatory; tissue morphogenesis;  
 KW tissue repair; regeneration; proliferation; differentiation.

XX Homo sapiens.

XX WO200020591-A2.

XX 13-APR-2000.

XX 07-OCT-1999; 99WO-US023370.

XX 07-OCT-1998; 98US-0103418P.

XX 16-AUG-1999; 99US-00374936.

XX (STYC ) STRYKER CORP.

XX Oppermann H, Tai M, McCartney J;

XX WPI; 2000-303776/26.

XX Novel TGF-beta superfamily mutant chimeric protein, useful for inducing  
 PT tissue morphogenesis in e.g. bone, comprises a dimer consisting of one  
 PT monomer containing domains from two family members.

XX Disclosure; Page 120; 149pp; English.

XX The present invention describes a tumour growth factor beta (TGF-beta)  
 CC superfamily chimeric protein (I) derived from at least 2 different  
 CC members of the superfamily comprising a dimer with one monomer that

CC contains a finger 2 domain derived from a first family member and a  
 CC finger 1 domain and heel domain, both derived from a second family  
 CC member. The monomer further comprises a conserved C-terminal cysteine  
 CC skeleton. (I) has osteogenic, proliferative and antiinflammatory  
 CC activities. The TGF-beta superfamily chimeric proteins (I) are useful for  
 CC inducing tissue morphogenesis (i.e. molecules capable of tissue repair  
 CC and regeneration and/or inhibiting inflammation) in bone, non-mineralised  
 CC skeletal tissue, dental tissue, connective tissue, brain, liver and nerve  
 CC and for inducing the proliferation and differentiation of uncommitted  
 CC progenitor cells in a tissue-specific manner to support new tissue  
 CC formation. AAB29887 to AAA29897 and AAB02748 to AAB02824 represent  
 CC sequences used in the exemplification of the present invention

XX Sequence 34 AA;

Query Match 35.8%; Score 34; DB 3; Length 34;  
 Best Local Similarity 50.0%; Pred. No. 4.7e+02;  
 Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKQVLETFTVKSC 14  
 DB 18 PKIEQLSNMIVKSC 31

RESULT 24  
 AAW30356  
 ID AAW30356 standard; peptide; 36 AA.

XX AAW30356;

XX 11-FEB-1998 (first entry)

XX Fragment #2 of growth factor TGFbeta2.

XX Neurturin; human; haematopoietic cell; neuronal cell; stem cell; NT gene;  
 KW neurodegenerative disease; peripheral neuropathy; nervous system tumour;  
 KW amyotrophic lateral sclerosis; Alzheimer's disease; Parkinson's disease;  
 KW Huntington's disease; ischaemic stroke; acute brain injury; basopaenia;  
 KW acute spinal cord injury; multiple sclerosis; eosinopaenia; lymphopaenia;  
 KW monocytopenaia; neutropaenia; anaemia; thrombocytopaenia; neuroblastoma;  
 KW antibody; obesity; therapy; transforming growth factor beta; TGFbeta2;  
 KW growth factor; hybrid protein.

XX Homo sapiens.

XX WO9708196-A1.

XX 06-MAR-1997.

XX 27-AUG-1996; 96WO-US014065.

XX 28-AUG-1995; 95US-00519777.

XX (UNIW ) UNIV WASHINGTON.

XX Johnson EM, Milbrandt JD, Kotzbauer PT, Lampe PA;

XX WPI; 1997-179176/16.

XX A novel growth factor Neurturin - used to treat neuro-degenerative and  
 PT haematopoietic cell degeneration diseases, e.g. Alzheimer's disease and  
 PT eosinopenia.

XX Claim 92; Fig 18; 206pp; English.

XX AAW30355-W30377 represent growth factor fragments that are used in a  
 CC hybrid polypeptide of the invention. These sequences form a hybrid with  
 CC the human neurturin (NT) fragment shown in AAW30354. NT promotes the  
 CC growth and differentiation of haematopoietic and neuronal cells, and  
 CC their stem cells. The NT gene and protein are used to prevent or treat  
 CC neurodegenerative diseases e.g. peripheral neuropathy, amyotrophic  
 CC lateral sclerosis, Alzheimer's disease, Parkinson's disease, Huntington's  
 CC disease, ischaemic stroke, acute brain injury, acute spinal cord injury,

CC nervous system tumours, multiple sclerosis and infection; and  
 CC haematopoietic cell degenerative diseases, e.g. eosinopaenia, basopaenia,  
 CC lymphopaenia, monocytopenia, neutropaenia, anaemia, thrombocytopaenia,  
 CC and stem cell insufficiencies. The NT protein and gene are also useful to  
 CC treat neuroblastomas. Antibodies against NT and oligonucleotides (used as  
 CC either probes or primers, corresponding to an exon of pre-pro-NT gene or  
 CC flanking a target sequence) can be used for detecting NT in a sample or  
 CC detecting mutations in the NT gene. Antisense sequences of the NT gene  
 CC are used to treat diseases promoted by NT expression e.g. obesity  
 XX  
 SQ Sequence 36 AA;

Query Match 35.8%; Score 34; DB 2; Length 36;  
 Best Local Similarity 50.0%; Pred. No. 5e+02;  
 Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKKDVLFTFTVKSC 14  
 ||| : ||||  
 Db 20 PKIEQLSNMIVKSC 33

RESULT 25  
 AAB09510  
 ID AAB09510 standard; peptide; 36 AA.

XX AAB09510;

XX 11-SEP-2000 (first entry)

XX Human TGF-beta 2 finger 2 subdomain.

XX TGF-beta superfamily; transforming growth factor-beta;  
 KW developmental regulation; finger 2 subdomain; basic region;  
 KW protein refolding; stability; solubility; osteogenic protein; OP;  
 KW bone morphogenetic protein; BMP; growth/differentiation factor; GDF;  
 KW inhibitor; tissue morphogenesis; regeneration; bone; dental tissue;  
 KW connective tissue; cartilage; vulvenerary.

XX Homo sapiens.

XX WO200020607-A2.

XX 13-APR-2000.

XX 07-OCT-1999; 99WO-US023371.

XX 07-OCT-1998; 98US-0103418P.

XX 16-AUG-1999; 99US-00374958.

XX (STYC ) STRYKER CORP.

XX Oppermann H, Tai M, McCartney J;

XX WPI; 2000-303787/26.

XX Transforming growth factor-beta superfamily member mutant induces tissue  
 PT morphogenesis in e.g. bone, non-mineralized skeletal tissue, dental  
 PT tissue and connective tissue and comprises a substitution in a region of  
 PT the finger 2 domain.

XX Disclosure; Fig 1; 162pp; English.

XX The invention relates to mutant TGF-beta (transforming growth factor-  
 CC beta) superfamily members. These mutants comprise one or more amino acid  
 CC substitutions in the base region of the finger 2 subdomain, and a C-  
 CC terminal residue selected from Arg, Ile, Leu, Ser and Ala. In the finger  
 CC 2 subdomain, basic residues (e.g., Arg, Lys), or residues containing an  
 CC amide group (e.g., Gln, Asn), are substituted with acidic residues (e.g.,  
 CC Glu, Asp) or residues containing a hydroxyl group (e.g., Ser, Thr). TGF-  
 CC beta superfamily proteins regulate developmental processes and include  
 CC proteins such as the osteogenic proteins (OPs), bone morphogenetic  
 CC proteins (BMPs), growth/differentiation factors (GDFs) and inhibitors.  
 CC Specific examples of TGF-beta superfamily mutants encompassed by the

CC invention are the finger 2 subdomain mutants of human osteogenic protein-  
 CC 1 (OP-1) (AAB09576-B09615). Mutant TGF-beta proteins are used for  
 CC inducing tissue morphogenesis in bone, non-mineralised skeletal tissue,  
 CC dental tissue, connective tissue, brain, liver and nerve tissue. The  
 CC proteins can be used in conjunction with a biocompatible matrix e.g.,  
 CC collagen, hydroxyapatite or carboxymethylcellulose for regenerating bone,  
 CC cartilage and/or other mineralised skeletal or connective tissues e.g.,  
 CC ligament, tendon, muscle, fibrocartilage, joint capsule and  
 CC intervertebral discs. The OP-1 mutants can be used to repair diseased or  
 CC damaged mammalian tissue and to prevent or substantially inhibit  
 CC immune/inflammatory response-mediated tissue damage and scar tissue  
 CC formation following an injury. Compared to the wild-type TGF-beta  
 CC superfamily members, the mutant proteins have improved in vitro refolding  
 CC properties in a pH range of 6-9, increased solubility in aqueous solution  
 CC and improved stability and/or activity. Sequences AAB09481-B09516  
 CC represent wild-type finger 2 subdomains from a variety of TGF-beta  
 CC superfamily proteins referred to in the specification  
 XX  
 SQ Sequence 36 AA;

Query Match 35.8%; Score 34; DB 3; Length 36;  
 Best Local Similarity 50.0%; Pred. No. 5e+02;  
 Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKKDVLFTFTVKSC 14

Db 20 PKIEQLSNMIVKSC 33

RESULT 26  
 ABB39942

ID ABB39942 standard; peptide; 38 AA.

XX ABB39942;

XX 04-FEB-2002 (first entry)

XX Peptide #7448 encoded by human foetal liver single exon probe.

XX Human; foetal liver; gene expression; single exon nucleic acid probe.

XX Homo sapiens.

XX WO200157277-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000669.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483447/52.

XX Human genome-derived single exon nucleic acid probes useful for analyzing  
 PT gene expression in human fetal liver.

XX Claim 27; SEQ ID NO 32577; 639pp + Sequence Listing; English.

XX The invention relates to a single exon nucleic acid probe for measuring  
 CC human gene expression in a sample derived from human foetal liver. The  
 CC single exon nucleic acid probes may be used for predicting, measuring and  
 CC displaying gene expression in samples derived from human fetal liver. The  
 CC present sequence is a peptide encoded by a single exon nucleic acid probe

CC of the invention. Note: The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 38 AA;

Query Match 35.8%; Score 34; DB 4; Length 38;  
Best Local Similarity 60.0%; Pred. No. 5.3e+02;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 LETFTVKSCP 15  
| :||| |||  
Db 15 LSSWTVASCP 24

RESULT 27

AAM33561  
ID AAM33561 standard; protein; 38 AA.

XX AC AAM33561;

XX DT 17-OCT-2001 (first entry)

XX Peptide #7598 encoded by probe for measuring placental gene expression.

XX DE Probe; microarray; human; placenta; antenatal diagnosis;

XX KW genetic disorder.

XX OS Homo sapiens.

XX PN WO200157272-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000663.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX PF WPI; 2001-488897/53.

XX PT Human genome-derived single exon nucleic acid probes useful for analyzing

XX PT gene expression in human placenta.

XX PS Claim 27; SEQ ID NO 33830; 654pp; English.

XX CC The present invention relates to single exon nucleic acid probes (SENP:

XX CC see AA131315-AA157546). The present sequence is a peptide encoded by one

XX CC such probe. The probes are useful for producing a microarray for

XX CC predicting, measuring and displaying gene expression in samples derived

XX CC from human placenta. The probes are useful for antenatal diagnosis of

XX CC human genetic disorders

XX SQ Sequence 38 AA;

Query Match 35.8%; Score 34; DB 4; Length 38;

Best Local Similarity 60.0%; Pred. No. 5.3e+02;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 LETFTVKSCP 15  
| :||| |||  
Db 15 LSSWTVASCP 24

RESULT 28

AAM73359

ID AAM73359 standard; protein; 38 AA.

XX AC AAM73359;

XX DT 06-NOV-2001 (first entry)

XX DE Human bone marrow expressed probe encoded protein SEQ ID NO: 33665.

XX KW Human; bone marrow expressed exon; gene expression analysis; probe;

XX KW microarray; cancer; leukaemia; lymphoma; myeloma.

XX OS Homo sapiens.

XX PN WO200157276-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000668.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX PD WPI; 2001-488900/53.

XX PT Human genome-derived single exon nucleic acid probes useful for analyzing

XX PT gene expression in human bone marrow.

XX PS Example 4; SEQ ID NO 33665; 658pp + Sequence Listing; English.

XX CC The present invention provides a number of single exon nucleic acid

XX CC probes which are derived from genomic sequences expressed in the human

XX CC bone marrow. They can be used to measure gene expression in bone marrow

XX CC samples, which may enable the improved diagnosis and treatment of cancers

XX CC such as lymphoma, leukaemia and myeloma. The present sequence is a

XX CC protein encoded by one of the probes of the invention

XX SQ Sequence 38 AA;

Query Match 35.8%; Score 34; DB 4; Length 38;

Best Local Similarity 60.0%; Pred. No. 5.3e+02;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 LETFTVKSCP 15  
| :||| |||  
Db 15 LSSWTVASCP 24

RESULT 29

AAM60687

ID AAM60687 standard; protein; 38 AA.

XX AC AAM60687;

XX DT 05-NOV-2001 (first entry)

XX DE Human brain expressed single exon probe encoded protein SEQ ID NO: 32792.

XX KW Human; brain expressed exon; gene expression analysis; probe; microarray;

XX KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.

XX OS Homo sapiens.

XX SQ





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PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 08-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.

PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 35.8%; Score 34; DB 3; Length 42;
Best Local Similarity 100.0%; Fred. No. 5.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 TVKSCP 15
Db 28 TVKSCP 33

RESULT 33
ADI32847
ID ADI32847 standard; peptide; 24 AA.
XX AC ADI32847;
XX DT 22-APR-2004 (first entry)
XX DE Peptide 1 related to human betaine homocysteine methyl transferase BHMT.
XX KW human; betaine homocysteine methyl transferase; BHMT; homocysteinaemia;
XX OS cardiovascular disease.
XX OS Unidentified.
XX PN CN1408854-A.
XX PD 09-APR-2003.
XX
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PF 24-SEP-2001; 2001CN-00142193.
XX
PR 24-SEP-2001; 2001CN-00142193.
XX
PA (HYGI-) INST HYGIENICS & ENVIRONMENTAL MEDICAL S.
XX
PI Qian L, Wu S;
XX
DR WPI; 2003-680504/65.
XX
XX Preparing and applying recombined human betaine homocysteine methyl
PT transferase.
XX
XX Example 1; Page 5; 6pp; Chinese.
XX
CC The invention relates to a novel method for preparing and applying
CC recombinant human betaine homocysteine methyl transferase (BHMT) to
CC biological technology which relates to efficient expression technology of
CC recombinant human BHMT. The recombinant human betaine homocysteine methyl
CC transferase of the invention may be used as a biological preparation for
CC treating homocysteinaemia and related cardiovascular diseases. The
CC current sequence is that of the peptide fragment 1 of the invention which
CC is related to human betaine homocysteine methyl transferase (BHMT).
XX
SQ Sequence 24 AA;

Query Match 34.7%; Score 33; DB 7; Length 24;
Best Local Similarity 85.7%; Pred. No. 4.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DVLETF 10
Db ||:||||
17 DVNETFT 23

RESULT 34
ABB41573
ID ABB41573 standard; peptide; 40 AA.
XX
AC ABB41573;
XX
DT 04-FEB-2002 (first entry)
XX
DE Peptide #9079 encoded by human foetal liver single exon probe.
XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
OS Homo sapiens.
XX
PN WO200157277-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000669.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
WPI; 2001-483447/52.
XX
Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human foetal liver.
XX
XX Claim 27; SEQ ID NO 34208; 639pp + Sequence Listing; English.

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XX
CC The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human foetal liver. The
CC present sequence is a peptide encoded by a single exon nucleic acid probe
CC of the invention. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 40 AA;

Query Match 34.7%; Score 33; DB 4; Length 40;
Best Local Similarity 60.0%; Pred. No. 8.2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LETFTVKSCP 15
Db :|||||
1 VSTFTVKQAP 10

RESULT 35
AAM35365
ID AAM35365 standard; protein; 40 AA.
XX
AC AAM35365;
XX
DT 17-OCT-2001 (first entry)
XX
DE Peptide #9402 encoded by probe for measuring placental gene expression.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000663.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
WPI; 2001-488897/53.
XX
Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
XX
XX Claim 27; SEQ ID NO 35634; 654pp; English.
XX
CC The present invention relates to single exon nucleic acid probes (SNP:
CC see AAI31315-AAI57546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders
XX
SQ Sequence 40 AA;

Query Match 34.7%; Score 33; DB 4; Length 40;
Best Local Similarity 60.0%; Pred. No. 8.2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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QY      6 LETFTVKSCP 15
      : |||||
Db      1 VSTFTVKQAP 10

RESULT 36
AAM75253
ID AAM75253 standard; protein; 40 AA.
XX
AC AAM75253;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 35559.
XX
KW Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma.
XX
OS Homo sapiens.
XX
PN WO200157276-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000668.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488900/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human bone marrow.
XX
PS Example 4; SEQ ID NO 35559; 658pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is a
CC protein encoded by one of the probes of the invention
XX
SQ Sequence 40 AA;

      Query Match      34.7%; Score 33; DB 4; Length 40;
      Best Local Similarity 60.0%; Pred. No. 8.2e+02;
      Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      6 LETFTVKSCP 15
      : |||||
Db      1 VSTFTVKQAP 10

RESULT 37
AAM62444
ID AAM62444 standard; protein; 40 AA.
XX
AC AAM62444;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 34549.

      Query Match      34.7%; Score 33; DB 4; Length 40;
      Best Local Similarity 60.0%; Pred. No. 8.2e+02;
      Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      6 LETFTVKSCP 15
      : |||||
Db      1 VSTFTVKQAP 10

RESULT 38
ABG57015
ID ABG57015 standard; peptide; 40 AA.
XX
AC ABG57015;
XX
DT 25-FEB-2003 (first entry)
XX
DE Human liver peptide, SEQ ID No 35663.
XX
KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
KW hypercholesterolaemia; coronary heart disease.
XX
OS Homo sapiens.
XX
PN WO200157273-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000664.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.

      Query Match      34.7%; Score 33; DB 4; Length 40;
      Best Local Similarity 60.0%; Pred. No. 8.2e+02;
      Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      6 LETFTVKSCP 15
      : |||||
Db      1 VSTFTVKQAP 10

The present invention provides a number of single exon nucleic acid
probes which are derived from genomic sequences expressed in the human
brain. They can be used to measure gene expression in brain cell samples,
which may enable the diagnosis and improved treatment of nervous system
diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
epilepsy and cancers. The present sequence is a protein encoded by one of
the probes of the invention
```

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PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488898/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human adult liver.
XX
XX Claim 27; SEQ ID NO 35663; 658pp; English.
XX
XX The invention relates to a single exon nucleic acid probe (SENP) (I) for
XX measuring human gene expression in a sample derived from human adult
XX liver, comprising one of 13109 defined nucleotide sequences given in the
XX specification (or complements/ fragments). The probe hybridises at high
XX stringency to a nucleic acid molecule expressed in the human adult liver.
XX (I) may be used for predicting, measuring and displaying gene expression
XX in samples derived from human adult liver. The genes identified may be
XX involved in genetic liver diseases such as cirrhosis,
XX hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
XX associated with coronary heart disease. ABG47348-ABG59930 represent human
XX liver single exon encoded peptides of the invention. Note: The sequence
XX information for this patent does not appear in the printed specification
XX but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 40 AA;
XX
XX Query Match 34.7%; Score 33; DB 4; Length 40;
XX Best Local Similarity 60.0%; Pred: No. 8.2e+02;
XX Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 6 LETFTVKSCP 15
XX : ||||| |
XX Db 1 VSTFTVKQAP 10
XX
XX RESULT 39
XX ABG44901
XX ID ABG44901 standard; peptide; 40 AA.
XX
XX AC ABG44901;
XX
XX DT 19-AUG-2002 (first entry)
XX
XX DE Human peptide encoded by genome-derived single exon probe SEQ ID 34566.
XX
XX KW Human; single exon probe; asthma; lung cancer; COPD; ILD;
XX KW chronic obstructive pulmonary disease; interstitial lung disease;
XX KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
XX KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
XX KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
XX KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
XX KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
XX KW primary ciliary dyskinesia; pulmonary hypertension;
XX KW hyaline membrane disease.
XX
XX OS Homo sapiens.
XX
XX PN WO200186003-A2.
XX
XX PD 15-NOV-2001.
XX
XX PF 30-JAN-2001; 2001WO-US000665.
XX
XX PR 04-FEB-2000; 2000US-0180312P.
XX
XX PR 26-MAY-2000; 2000US-0207456P.
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PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2002-114183/15.
XX
XX Spatially-addressable set of single exon nucleic acid probes, used to
XX measure gene expression in human lung samples.
XX
XX Claim 27; SEQ ID NO 34566; 634pp; English.
XX
XX The invention relates to a spatially-addressable set of single exon
XX nucleic acid probes for measuring gene expression in a sample derived
XX from human lung comprising single exon nucleic acid probes having one of
XX 12614 nucleic acid sequences mentioned in the specification, or their
XX complements or the 12387 open reading frames derived from the 12614
XX probes. Also included are a microarray comprising the novel set of probes
XX; the novel set of probes which hybridise at high stringency to a nucleic
XX acid expressed in the human lung; measuring gene expression in a sample
XX derived from human lung, comprising (a) contacting the array with a
XX collection of detectably labeled nucleic acids derived from human lung
XX mRNA, and (b) measuring the label detectably bound to each probe of the
XX array; identifying exons in a eukaryotic genome, comprising (a)
XX algorithmically predicting at least one exon from genomic sequences of
XX the eukaryote; and (b) detecting specific hybridisation of detectably
XX labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
XX having a fragment identical to the predicted exon, the probe is included
XX in the above mentioned microarray; assigning exons to a single gene,
XX comprising (a) identifying exons from genomic sequence by the method
XX above and (b) measuring the expression of each of the exons in several
XX tissues and/or cell types using hybridisation to a single exon
XX microarrays having a probe with the exon, where a common pattern of
XX expression of the exons in the tissues and/or cell types indicates that
XX the exons should be assigned to a single gene; a peptide comprising one
XX of 12011 sequences, mentioned in the specification, or encoded by the
XX probes/open reading frames (ORF). The probes are used for gene expression
XX analysis, and for identifying exons in a gene, particularly using human
XX lung derived mRNA and for the study of lung diseases such as asthma, lung
XX cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
XX disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
XX tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
XX Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
XX histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
XX Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
XX dyskinesia, pulmonary hypertension and hyaline membrane disease. The
XX present sequence is a peptide/protein encoded by a single exon probe of
XX the invention. Note: The sequence data for this patent did not form part
XX of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 40 AA;
XX
XX Query Match 34.7%; Score 33; DB 5; Length 40;
XX Best Local Similarity 60.0%; Pred: No. 8.2e+02;
XX Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 6 LETFTVKSCP 15
XX : ||||| |
XX Db 1 VSTFTVKQAP 10
XX
XX RESULT 40
XX AAY11424
XX ID AAY11424 standard; protein; 49 AA.
XX
XX AC AAY11424;
XX
XX XX
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DT 21-JUN-1999 (first entry)  
 XX Human 5' EST secreted protein SEQ ID No 246.  
 DE , XX  
 DE Human; secreted protein; EST; expressed sequence tag; diagnosis;  
 XX forensic; gene therapy; chromosome mapping; signal peptide;  
 KW upstream regulatory sequence; cytokine activity; cell proliferation;  
 KW differentiation; haematopoiesis regulation; tissue growth regulation;  
 KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;  
 KW thrombolytic; anti-inflammatory; tumour inhibition.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO9906551-A2.  
 XX  
 XX 11-FEB-1999.  
 XX  
 XX 31-JUL-1998; 98WO-IB001235.  
 PF  
 XX 01-AUG-1997; 97US-00905133.  
 XX  
 XX (GEST ) GENSET.  
 PA  
 XX Dumas Milne Edwards J, Duclert A, Lacroix B;  
 PI  
 XX WPI; 1999-153781/13.  
 DR N-PSDB; AAX39490.  
 DR  
 XX New nucleic acids encoding human secreted - proteins obtained from cdNA  
 PT libraries prepared from substantia nigra, cerebellum, surrenals and fetal  
 PT brain tissue.  
 XX  
 PS Claim 34; Page 367; 434pp; English.  
 XX  
 CC AAX39440 to AAX39597 represent 5' expressed sequence tags (ESTs) for  
 CC human secreted proteins, and encode the proteins given in AAY11374 to  
 CC AAY11531, respectively. The proteins given represent the signal peptide  
 CC and an N-terminal fragment of a secreted protein. The nucleic acid  
 CC sequences can be used for producing secreted human gene products. They  
 CC can also be used to develop products for diagnosis and therapy. The  
 CC proteins obtained may have cytokine activity, cell  
 CC proliferation/differentiation activity, haematopoiesis regulating  
 CC activity, tissue growth regulating activity, reproductive hormone  
 CC regulating activity, chemotactic/chemokinetic activity, haemostatic and  
 CC thrombolytic activity, receptor/ligand activity, anti-inflammatory  
 CC activity, tumour inhibition activity or other activities. The products  
 CC can be used in forensic, gene therapy and chromosome mapping procedures.  
 CC The sequences can also be used for obtaining corresponding promoter  
 CC sequences. The nucleic acids encoding the signal peptide can be used for  
 CC directing extracellular secretion of a polypeptide or the insertion of a  
 CC polypeptide into a membrane, or importing a polypeptide into a cell  
 XX  
 SQ Sequence 49 AA;  
 Query Match 34.7%; Score 33; DB 2; Length 49;  
 Best Local Similarity 85.7%; Pred. No. 1e+03;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TPTVKSC 14  
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 Db 6 TPTFKSC 12

Search completed: January 20, 2006, 17:30:43  
 Job time : 46.8889 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2006, 17:26:44 ; Search time 12.4444 Seconds  
(without alignments)  
119.584 Million cell updates/sec

Title: US-10-619-323-6

Perfect score: 95

Sequence: 1 PKKDVLETFVTKSCPDAl 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 308952

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 50 summaries

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2: /cgn2\_6/ptodata/1/iaa/6 COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/H COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/RE COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	100.0	29	1	US-08-254-493-6
2	95	100.0	29	1	US-08-408-222B-6
3	36	37.9	31	1	US-08-486-057B-38
4	36	37.9	31	1	US-08-789-588-38
5	36	37.9	32	6	5262319-9
6	36	37.9	34	2	US-09-374-958C-31
7	36	37.9	34	2	US-09-374-936-31
8	36	37.9	42	2	US-09-848-664A-14
9	35	36.8	17	2	US-08-974-549A-100
10	35	36.8	17	2	US-08-912-951-100
11	35	36.8	17	2	US-09-402-181B-100
12	35	36.8	17	2	US-09-721-456-100
13	35	36.8	26	2	US-08-851-843A-140
14	35	36.8	26	2	US-08-974-549A-258
15	35	36.8	26	2	US-08-854-050-140
16	35	36.8	26	2	US-09-430-323-140
17	35	36.8	26	2	US-09-402-181B-258
18	35	36.8	26	2	US-09-721-456-258
19	35	36.8	26	2	US-09-766-253-140
20	35	36.8	26	2	US-10-054-295-140
21	35	36.8	26	2	US-09-438-486A-140
22	35	36.8	27	2	US-08-851-843A-162
23	35	36.8	27	2	US-08-974-549A-282
24	35	36.8	27	2	US-08-854-050-162
25	35	36.8	27	2	US-09-430-323-162
26	35	36.8	27	2	US-09-402-181B-282
27	35	36.8	27	2	US-09-721-456-282

28	35	36.8	27	2	US-09-766-253-162	Sequence 162, App
29	35	36.8	27	2	US-10-054-295-162	Sequence 162, App
30	35	36.8	27	2	US-09-438-486A-162	Sequence 162, App
31	35	36.8	32	2	US-09-082-358B-57	Sequence 57, Appl
32	35	36.8	34	2	US-08-974-549A-45	Sequence 45, Appl
33	35	36.8	34	2	US-08-912-951-45	Sequence 45, Appl
34	35	36.8	34	2	US-09-402-181B-45	Sequence 45, Appl
35	35	36.8	34	2	US-09-721-456-45	Sequence 45, Appl
36	35	36.8	34	2	US-09-042-460-46	Sequence 46, Appl
37	34	35.8	31	1	US-08-486-057B-20	Sequence 20, Appl
38	34	35.8	31	1	US-08-789-588-20	Sequence 20, Appl
39	34	35.8	34	2	US-09-374-958C-30	Sequence 30, Appl
40	34	35.8	34	2	US-09-374-936-30	Sequence 30, Appl
41	34	35.8	42	2	US-09-848-664A-13	Sequence 13, Appl
42	32	33.7	27	2	US-09-084-303B-240	Sequence 240, App
43	32	33.7	28	2	US-09-058-459-2	Sequence 2, Appli
44	32	33.7	28	2	US-09-127-926-2	Sequence 2, Appli
45	32	33.7	28	2	US-09-714-357-2	Sequence 2, Appli
46	32	33.7	28	2	US-10-057-552-2	Sequence 2, Appli
47	32	33.7	28	2	US-09-827-960-2	Sequence 2, Appli
48	32	33.7	28	2	US-09-837-886-2	Sequence 2, Appli
49	32	33.7	28	2	US-09-812-034-2	Sequence 2, Appli
50	32	33.7	34	2	US-09-374-958C-29	Sequence 29, Appl

## ALIGNMENTS

RESULT 1  
US-08-254-493-6  
; Sequence 6, Application US/08254493  
; Patent No. 5439886  
; GENERAL INFORMATION:  
; APPLICANT: IKEYAMA, SHUICHI  
; APPLICANT: KOYAMA, MASARU  
; APPLICANT: MIYAKE, MASAYUKI  
; APPLICANT: SENOO, MASAHARU  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND  
; TITLE OF INVENTION: PRODUCTION THEREOF  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
; STREET: 130 WATER STREET  
; CITY: BOSTON  
; STATE: MASSACHUSETTS  
; COUNTRY: US  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/254,493  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/865552  
; FILING DATE: 09-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 0799996-1991  
; FILING DATE: 12-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 085396-1991  
; FILING DATE: 17-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 0223321-1992  
; FILING DATE: 07-FEB-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: RESNICK, DAVID S.  
; REGISTRATION NUMBER: 34235  
; REFERENCE/DOCKET NUMBER: 41777  
; TELECOMMUNICATION INFORMATION:

;/ TELEPHONE: (617) 523-3400  
;/ TELEFAX: (617) 523-6440  
;/ TELEX: 200251 STRE UR  
;/ INFORMATION FOR SEQ ID NO: 6:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 29 amino acids  
;/ TYPE: amino acid  
;/ STRANDEDNESS: single  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: protein  
US-08-254-493-6

Query Match 100.0%; Score 95; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 2.4e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLETFVKSCPDAl 18  
Db 5 PKKDVLETFVKSCPDAl 22

RESULT 2  
US-08-408-222B-6  
; Sequence 6, Application US/08408222B  
; Patent No. 5776727  
; GENERAL INFORMATION:  
; APPLICANT: Ikeyama, Shuichi  
; APPLICANT: Koyama, Masaru  
; APPLICANT: Miyake, Masauyuki  
; APPLICANT: Senoo, Masaharu  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dike, Bronstein, Roberts & Cushman  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/408,222B  
; FILING DATE: 22-MAR-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/254,493  
; FILING DATE: 06-JUN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP-079996-1991  
; FILING DATE: 12-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP-085396-1991  
; FILING DATE: 14-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP-022321-1992  
; FILING DATE: 07-FEB-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Reenick, David S.  
; REGISTRATION NUMBER: 34,235  
; REFERENCE/DOCKET NUMBER: 41777-DIV  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-523-3400  
; TELEFAX: 617-523-6440  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 29 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

US-08-408-222B-6

Query Match 100.0%; Score 95; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 2.4e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLETFVKSCPDAl 18  
Db 5 PKKDVLETFVKSCPDAl 22

RESULT 3  
US-08-486-057B-38  
; Sequence 38, Application US/08486057B  
; Patent No. 5650494  
; GENERAL INFORMATION:  
; APPLICANT: Cerletti, Nico  
; APPLICANT: McMaster, Gary K.  
; APPLICANT: Cox, David  
; APPLICANT: Schmitz, Albert  
; APPLICANT: Meyhack, Bernd  
; TITLE OF INVENTION: Process for Refolding Recombinantly  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Henry P. No. 5650494ak  
; STREET: 520 White Plains Road, P.O. Box 2005  
; CITY: Tarrytown  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10591-9005

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/486,057B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/201,703  
; FILING DATE: 25-FEB-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/960,309  
; FILING DATE: 13-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/621,502  
; FILING DATE: 03-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 8927546.5  
; FILING DATE: 06-DEC-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5650494ak, Henry P.  
; REGISTRATION NUMBER: 33200  
; REFERENCE/DOCKET NUMBER: 4-17861/+Cont3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908) 277-5110  
; TELEFAX: (908) 277-4306  
; INFORMATION FOR SEQ ID NO: 38:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 31 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-486-057B-38

Query Match 37.9%; Score 36; DB 1; Length 31;  
Best Local Similarity 50.0%; Pred. No. 32;  
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKKDVLETFVKSC 14

Db 15 PKVEQLSNMVKSC 28  
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RESULT 4  
US-08-789-588-38  
; Sequence 38, Application US/08789588  
; Patent No. 5922846  
; GENERAL INFORMATION:  
; APPLICANT: Cerletti, Nico  
; APPLICANT: McMaster, Gary K.  
; APPLICANT: Cox, David  
; APPLICANT: Schmitz, Albert  
; APPLICANT: Meyhack, Bernd  
; TITLE OF INVENTION: Process for Refolding Recombinantly  
; TITLE OF INVENTION: Produced TGF-beta-like Proteins  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Henry P. No. 5922846ak  
; STREET: 520 White Plains Road, P.O. Box 2005  
; CITY: Tarrytown  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10591-9005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08789,588  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/486,057  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: US 08/201,703  
; FILING DATE: 25-FEB-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/960,309  
; FILING DATE: 13-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/621,502  
; FILING DATE: 03-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 8927546.5  
; FILING DATE: 06-DEC-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5922846ak, Henry P.  
; REGISTRATION NUMBER: 33200  
; REFERENCE/DOCKET NUMBER: 4-17861/+Cont3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908) 277-5110  
; TELEFAX: (908) 277-4306  
; INFORMATION FOR SEQ ID NO: 38:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 31 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-789-588-38  
Query Match 37.9%; Score 36; DB 1; Length 31;  
Best Local Similarity 50.0%; Pred. No. 32;  
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
Qy 1 PKKDVLFTFTVKSC 14  
|| : | ||||  
Db 15 PKVEQLSNMVKSC 28  
|| : | ||||  
RESULT 5  
US-08-789-588-38  
; Sequence 38, Application US/08789588  
; Patent No. 5922846  
; GENERAL INFORMATION:  
; APPLICANT: Cerletti, Nico  
; APPLICANT: McMaster, Gary K.  
; APPLICANT: Cox, David  
; APPLICANT: Schmitz, Albert  
; APPLICANT: Meyhack, Bernd  
; TITLE OF INVENTION: Process for Refolding Recombinantly  
; TITLE OF INVENTION: Produced TGF-beta-like Proteins  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Henry P. No. 5922846ak  
; STREET: 520 White Plains Road, P.O. Box 2005  
; CITY: Tarrytown  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10591-9005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08789,588  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/486,057  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: US 08/201,703  
; FILING DATE: 25-FEB-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/960,309  
; FILING DATE: 13-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/621,502  
; FILING DATE: 03-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 8927546.5  
; FILING DATE: 06-DEC-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5922846ak, Henry P.  
; REGISTRATION NUMBER: 33200  
; REFERENCE/DOCKET NUMBER: 4-17861/+Cont3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908) 277-5110  
; TELEFAX: (908) 277-4306  
; INFORMATION FOR SEQ ID NO: 38:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 31 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-789-588-38  
Query Match 37.9%; Score 36; DB 1; Length 31;  
Best Local Similarity 50.0%; Pred. No. 32;  
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
Qy 1 PKKDVLFTFTVKSC 14  
|| : | ||||  
Db 15 PKVEQLSNMVKSC 28  
|| : | ||||  
RESULT 6  
US-09-374-958C-31  
; Sequence 31, Application US/09374958C  
; Patent No. 6677432  
; GENERAL INFORMATION:  
; APPLICANT: Stryker Corporation  
; TITLE OF INVENTION: Modified Proteins and DNAs of the TGF-beta Superfamily, Including  
; TITLE OF INVENTION: Modified Morphogenic Proteins  
; FILE REFERENCE: STK-076  
; CURRENT APPLICATION NUMBER: US/09/374,958C  
; CURRENT FILING DATE: 1999-08-16  
; NUMBER OF SEQ ID NOS: 90  
; SOFTWARE: PatentIn version 2.0  
; SEQ ID NO 31  
; LENGTH: 34  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: TGF-Beta3  
US-09-374-958C-31  
Query Match 37.9%; Score 36; DB 2; Length 34;  
Best Local Similarity 50.0%; Pred. No. 36;  
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
Qy 1 PKKDVLFTFTVKSC 14  
|| : | ||||  
Db 18 PKVEQLSNMVKSC 31  
|| : | ||||  
RESULT 7  
US-09-374-936-31  
; Sequence 31, Application US/09374936  
; Patent No. 6846906  
; GENERAL INFORMATION:  
; APPLICANT: Oppermann, Hermann  
; APPLICANT: Tai, Mei-Sheng

; APPLICANT: McCartney, John  
; TITLE OF INVENTION: Modified TGF-beta Superfamily Proteins  
; FILE REFERENCE: STK-077  
; CURRENT APPLICATION NUMBER: US/09/374,936  
; CURRENT FILING DATE: 1999-08-16  
; NUMBER OF SEQ ID NOS: 88  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 31  
; LENGTH: 34  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: TGF-Beta3  
US-09-374-936-31

Query Match 37.9%; Score 36; DB 2; Length 34;  
Best Local Similarity 50.0%; Pred. No. 36;  
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKKDVLFTTVKSC 14  
||| : | ||||  
Db 18 PKVEQLSNMVKSC 31

## RESULT 8

US-09-848-664A-14  
; Sequence 14, Application US/09848664A  
; Patent No. 6723344  
; GENERAL INFORMATION:  
; APPLICANT: Sakiyama-Elbert, Shelly E.  
; APPLICANT: Hubbell, Jeffrey A.  
; TITLE OF INVENTION: Controlled Release of No. 6723344-Heparin Binding Growth  
; TITLE OF INVENTION: Factors from Heparin Containing Matrices  
; FILE REFERENCE: ETH 108  
; CURRENT APPLICATION NUMBER: US/09/848,664A  
; CURRENT FILING DATE: 2001-05-03  
; PRIOR APPLICATION NUMBER: US/09/298,084A  
; PRIOR FILING DATE: 1999-04-22  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 42  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-848-664A-14

Query Match 37.9%; Score 36; DB 2; Length 42;  
Best Local Similarity 50.0%; Pred. No. 46;  
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKKDVLFTTVKSC 14  
||| : | ||||  
Db 26 PKVEQLSNMVKSC 39

## RESULT 9

US-08-974-549A-100  
; Sequence 100, Application US/08974549A  
; Patent No. 6166178  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.  
; APPLICANT: Morin, Gregg B.  
; APPLICANT: Harley, Calvin B.  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 727  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco

; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/974,549A  
; FILING DATE: 19-NOV-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/911,312  
; FILING DATE: 14-AUG-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/912,951  
; FILING DATE: 14-AUG-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/915,503  
; FILING DATE: 14-AUG-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US97/17618  
; FILING DATE: 01-OCT-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US97/17885  
; FILING DATE: 01-OCT-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph Ted  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002610US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 100:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..17  
; OTHER INFORMATION: /note= "telomerase RT finger motif A  
; OTHER INFORMATION: peptide from Saccharomyces  
; OTHER INFORMATION: cerevisiae EST2"  
US-08-974-549A-100

Query Match 36.8%; Score 35; DB 2; Length 17;  
Best Local Similarity 70.0%; Pred. No. 24;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18  
| | | | | : |  
Db 8 FDKVSCYDSI 17



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RESULT 10
US-08-912-951-100
; Sequence 100, Application US/08912951
; Patent No. 6475789
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; TITLE OF INVENTION: THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,951
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..17
; OTHER INFORMATION: /note= "telomerase RT finger motif A
; OTHER INFORMATION: peptide from Saccharomyces
; OTHER INFORMATION: cerevisiae EST2"
US-08-912-951-100

Query Match 36.8%; Score 35; DB 2; Length 17;
Best Local Similarity 70.0%; Pred. No. 24;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAI 18
DB 8 FDKVSCYDSI 17

RESULT 11
US-09-402-181B-100
; Sequence 100, Application US/09402181B
; Patent No. 6610839
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,181B
; FILING DATE: 29-Sep-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ausenhus, Scott L.
; REGISTRATION NUMBER: 42,271
; REFERENCE/DOCKET NUMBER: 015389-002620US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
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; NAME/KEY: Peptide
; LOCATION: 1..17
; OTHER INFORMATION: /note= "telomerase RT finger motif A
; peptide from Saccharomyces
; cerevisiae EST2"
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-09-402-181B-100

Query Match 36.8%; Score 35; DB 2; Length 17;
Best Local Similarity 70.0%; Pred. No. 24;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18
Db 8 FDKVSCYDSI 17

RESULT 12
US-09-721-456-100
; Sequence 100, Application US/09721456
; Patent No. 661710
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/721,456
; FILING DATE: 22-NOV-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
;
; NAME/KEY: Peptide
; LOCATION: 1..17
; OTHER INFORMATION: /note= "telomerase RT finger motif A
; peptide from Saccharomyces
; cerevisiae EST2"
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-09-402-181B-100

Query Match 36.8%; Score 35; DB 2; Length 17;
Best Local Similarity 70.0%; Pred. No. 24;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18
Db 8 FDKVSCYDSI 17

RESULT 13
US-08-851-843A-140
; Sequence 140, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. 6093809el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,843A
; FILING DATE: 06-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
;
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..17
; OTHER INFORMATION: /note= "telomerase RT finger motif A
; peptide from Saccharomyces
; cerevisiae EST2"
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-09-721-456-100

Query Match 36.8%; Score 35; DB 2; Length 17;
Best Local Similarity 70.0%; Pred. No. 24;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18
Db 8 FDKVSCYDSI 17
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;
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 140:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..26
; OTHER INFORMATION: /note= "motif 3(A) peptide from
; OTHER INFORMATION: Saccharomyces cerevisiae EST2p"
;
US-08-851-843A-140

Query Match 36.8%; Score 35; DB 2; Length 26;
Best Local Similarity 70.0%; Pred. No. 39;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 9 FTVKSCPDAL 18
Db 7 FDVKSCYDSI 16

RESULT 14
US-08-974-549A-258
; Sequence 258, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 258:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..26
; OTHER INFORMATION: /note= "motif 3(A) peptide from
; OTHER INFORMATION: Saccharomyces cerevisiae EST2p"
;
US-08-974-549A-258

Query Match 36.8%; Score 35; DB 2; Length 26;
Best Local Similarity 70.0%; Pred. No. 39;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 9 FTVKSCPDAL 18
Db 7 FDVKSCYDSI 16

RESULT 15
US-08-854-050-140
; Sequence 140, Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
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; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 140:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..26
; OTHER INFORMATION: /note= "motif 3(A) peptide from
; Saccharomyces cerevisiae EST2p"
;
; US-08-854-050-140
;
; Query Match 36.8%; Score 35; DB 2; Length 26;
; Best Local Similarity 70.0%; Pred. No. 39;
; Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
;
; QY 9 FTVKSCPDAL 18
; DB 7 FDVKSICYDSI 16
;
; RESULT 16
; US-09-430-323-140
; Sequence 140, Application US/09430323
; Patent No. 6309867
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. 6309867el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; US-08-854-050-140
;
; Query Match 36.8%; Score 35; DB 2; Length 26;
; Best Local Similarity 70.0%; Pred. No. 39;
; Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
;
; QY 9 FTVKSCPDAL 18
; DB 7 FDVKSICYDSI 16
;
; RESULT 17
; US-09-402-181B-258
; Sequence 258, Application US/09402181B
; Patent No. 6610839
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402.181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 258:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..26
OTHER INFORMATION: /note= "motif 3(A) peptide from Saccharomyces cerevisiae EST2p"
SEQUENCE DESCRIPTION: SEQ ID NO: 258:
US-09-402-181B-258
Query Match 36.8%; Score 35; DB 2; Length 26;
Best Local Similarity 70.0%; Pred. No. 39;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 9 FTVKSCPDAl 18
Db 7 FDVKSVCYDSI 16
RESULT 18
US-09-721-456-258
Sequence 258, Application US/09721456
Patent No. 661710
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California

COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-No. 6617110-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 258:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..26
OTHER INFORMATION: /note= "motif 3(A) peptide from Saccharomyces cerevisiae EST2p"
SEQUENCE DESCRIPTION: SEQ ID NO: 258:
US-09-721-456-258
Query Match 36.8%; Score 35; DB 2; Length 26;
Best Local Similarity 70.0%; Pred. No. 39;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 9 FTVKSCPDAl 18
Db 7 FDVKSVCYDSI 16
RESULT 19
US-09-766-253-140
Sequence 140, Application US/09766253
Patent No. 680880
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru

Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin  
Andrews, William H.  
TITLE OF INVENTION: No. 680880el Telomerase  
NUMBER OF SEQUENCES: 171  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION NUMBER: US/09/766,253  
FILING DATE: 19-Jan-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/846,017  
FILING DATE: 1997-04-25  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002920US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 140:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..26  
OTHER INFORMATION: /note= "motif 3(A) peptide from  
Saccharomyces cerevisiae EST2p"  
SEQUENCE DESCRIPTION: SEQ ID NO: 140:  
US-09-766-253-140

Query Match 36.8%; Score 35; DB 2; Length 26;  
Best Local Similarity 70.0%; Pred. No. 39;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 9 FTVKSCPDAl 18  
| | | | | | | |  
Db 7 FDKSCYDSI 16

RESULT 20  
US-10-054-295-140  
Sequence 140, Application US/10054295  
Patent No. 6921664  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin  
Andrews, William H.  
TITLE OF INVENTION: No. 6921664el Telomerase  
NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/054,295  
FILING DATE: 18-Jan-2002  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/854,050  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 140:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..26  
OTHER INFORMATION: /note= "motif 3(A) peptide from  
Saccharomyces cerevisiae EST2p"  
SEQUENCE DESCRIPTION: SEQ ID NO: 140:  
US-10-054-295-140

Query Match 36.8%; Score 35; DB 2; Length 26;  
Best Local Similarity 70.0%; Pred. No. 39;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 9 FTVKSCPDAl 18  
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Db 7 FDKSCYDSI 16

RESULT 21  
US-09-438-486A-140  
Sequence 140, Application US/09438486A  
Patent No. 6927285  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin  
Andrews, William H.  
TITLE OF INVENTION: GENE FOR HUMAN TELOMERASE REVERSE TRANSCRIPTASE AND  
TELOMERASE VARIANTS  
FILE REFERENCE: 018/062  
CURRENT APPLICATION NUMBER: US/09/438,486A  
CURRENT FILING DATE: 1999-11-12  
PRIOR APPLICATION NUMBER: 08/851,843

; PRIOR FILING DATE: 1997-05-06  
; PRIOR APPLICATION NUMBER: 08/846,017  
; PRIOR FILING DATE: 1997-04-25  
; PRIOR APPLICATION NUMBER: 08/844,419  
; PRIOR FILING DATE: 1997-04-18  
; PRIOR APPLICATION NUMBER: 08/724,643  
; PRIOR FILING DATE: 1996-10-01  
; NUMBER OF SEQ ID NOS: 223  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 140  
; LENGTH: 26  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant  
; OTHER INFORMATION: amino acid sequence  
US-09-438-486A-140

Query Match 36.8%; Score 35; DB 2; Length 26;  
Best Local Similarity 70.0%; Pred. No. 39;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 9 FTVKSCPDAL 18  
| | | | | | | |  
Db 7 FDKVSCYDSI 16

RESULT 22  
US-08-851-843A-162  
; Sequence 162, Application US/08851843A  
; Patent No. 6093809  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.  
; APPLICANT: Morin, Gregg B.  
; APPLICANT: Harley, Calvin  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: No. 6093809el Telomerase  
; NUMBER OF SEQUENCES: 225  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/851,843A  
; FILING DATE: 06-MAY-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002930US

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 162:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 27 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..27  
; OTHER INFORMATION: /note= "motif A peptide from  
; OTHER INFORMATION: Saccharomyces cerevisiae EST2"  
US-08-851-843A-162  
  
Query Match 36.8%; Score 35; DB 2; Length 27;  
Best Local Similarity 70.0%; Pred. No. 41;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 9 FTVKSCPDAL 18  
| | | | | | | |  
Db 8 FDKVSCYDSI 17  
  
RESULT 23  
US-08-974-549A-282  
; Sequence 282, Application US/08974549A  
; Patent No. 6166178  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.  
; APPLICANT: Morin, Gregg B.  
; APPLICANT: Harley, Calvin B.  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 727  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
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; FILING DATE: 19-NOV-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/911,312

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; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA: WO PCT/US97/17618
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 282:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..27
; OTHER INFORMATION: /note= "motif A peptide from
; OTHER INFORMATION: Saccharomyces cerevisiae EST2"
US-08-974-549A-282

Query Match 36.8%; Score 35; DB 2; Length 27;
Best Local Similarity 70.0%; Pred. No. 41;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAl 18
DB 8 FDKVSCYDSI 17

RESULT 24
US-08-854-050-162
; Sequence 162, Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536

; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 162:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..27
; OTHER INFORMATION: /note= "motif A peptide from
; OTHER INFORMATION: Saccharomyces cerevisiae EST2"
US-08-854-050-162

Query Match 36.8%; Score 35; DB 2; Length 27;
Best Local Similarity 70.0%; Pred. No. 41;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAl 18
DB 8 FDKVSCYDSI 17

RESULT 25
US-09-430-323-162
; Sequence 162, Application US/09430323
; Patent No. 6309867
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6309867el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09-430,323
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
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APPLICATION NUMBER: US/09/430,323  
FILING DATE: 29-Oct-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 162:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..27  
OTHER INFORMATION: /note= "motif A peptide from  
Saccharomyces cerevisiae EST2"  
SEQUENCE DESCRIPTION: SEQ ID NO: 162:  
US-09-430-323-162

Query Match 36.8%; Score 35; DB 2; Length 27;  
Best Local Similarity 70.0%; Pred. No. 41;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAI 18  
Db 8 FDKSCYDSI 17

RESULT 26  
US-09-402-181B-282  
Sequence 282, Application US/09402181B  
Patent No. 6610839  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin B.  
Andrews, William H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 633  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/402,181B

FILING DATE: 29-Sep-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ausenhus, Scott L.  
REGISTRATION NUMBER: 42,271  
REFERENCE/DOCKET NUMBER: 015389-002620US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 282:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..27  
OTHER INFORMATION: /note= "motif A peptide from  
Saccharomyces cerevisiae EST2"  
SEQUENCE DESCRIPTION: SEQ ID NO: 282:  
US-09-402-181B-282

Query Match 36.8%; Score 35; DB 2; Length 27;  
Best Local Similarity 70.0%; Pred. No. 41;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAI 18  
Db 8 FDKSCYDSI 17

RESULT 27  
US-09-721-456-282  
Sequence 282, Application US/09721456  
Patent No. 6617110  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin B.  
Andrews, William H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 727  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/721,456  
FILING DATE: 22-NOV-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,549A  
FILING DATE: 19-NOV-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph Ted  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 282:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1-27  
OTHER INFORMATION: /note= "motif A peptide from  
Saccharomyces cerevisiae EST2"  
SEQUENCE DESCRIPTION: SEQ ID NO: 282:  
US-09-721-456-282

Query Match 36.8%; Score 35; DB 2; Length 27;  
Best Local Similarity 70.0%; Pred. No. 41;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAl 18  
| | | | | | | |  
Db 8 FDKVSCYDSI 17

RESULT 28  
US-09-766-253-162  
Sequence 162, Application US/09766253  
Patent No. 6808880  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.

Harley, Calvin  
Andrews, William H.  
TITLE OF INVENTION: No. 6808880el Telomerase  
NUMBER OF SEQUENCES: 171  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/766,253  
FILING DATE: 19-Jan-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/846,017  
FILING DATE: 1997-04-25  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002920US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 162:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1-27  
OTHER INFORMATION: /note= "motif A peptide from  
Saccharomyces cerevisiae EST2"  
SEQUENCE DESCRIPTION: SEQ ID NO: 162:  
US-09-766-253-162  
Query Match 36.8%; Score 35; DB 2; Length 27;  
Best Local Similarity 70.0%; Pred. No. 41;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAl 18  
| | | | | | | |  
Db 8 FDKVSCYDSI 17

RESULT 29  
US-10-054-295-162  
Sequence 162, Application US/10054295  
Patent No. 6921664  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin  
Andrews, William H.  
TITLE OF INVENTION: No. 6921664el Telomerase  
NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor

;; CITY: San Francisco  
;; STATE: California  
;; COUNTRY: United States of America  
;; ZIP: 94111  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/10/054,295  
;; FILING DATE: 18-Jan-2002  
;; CLASSIFICATION: 536  
;;  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/854,050  
;; FILING DATE: <Unknown>  
;; APPLICATION NUMBER: US 08/846,017  
;; FILING DATE: 25-APR-1997  
;; APPLICATION NUMBER: US 08/844,419  
;; FILING DATE: 18-APR-1997  
;; APPLICATION NUMBER: US 08/724,643  
;; FILING DATE: 01-OCT-1996  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Apple, Randolph T.  
;; REGISTRATION NUMBER: 36,429  
;; REFERENCE/DOCKET NUMBER: 015389-002930US  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 576-0200  
;; TELEFAX: (415) 576-0300  
;; INFORMATION FOR SEQ ID NO: 162:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 27 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: <Unknown>  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; FEATURE:  
;; NAME/KEY: Peptide  
;; LOCATION: 1..27  
;; OTHER INFORMATION: /note= "motif A peptide from  
;; Saccharomyces cerevisiae EST2"  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 162:  
US-10-054-295-162

Query Match 36.8%; Score 35; DB 2; Length 27;  
Best Local Similarity 70.0%; Pred. No. 41;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAl 18  
| | | | | | | |  
Db 8 FDKVSCYDSI 17

RESULT 30  
US-09-438-486A-162  
; Sequence 162, Application US/09438486A  
; Patent No. 6927285  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: LINGNER, JOACHIM  
; APPLICANT: NAKAMURA, TORU  
; APPLICANT: CHAPMAN, KAREN B.  
; APPLICANT: MORIN, GREGG B.  
; APPLICANT: HARLEY, CALVIN  
; TITLE OF INVENTION: GENE FOR HUMAN TELOMERASE REVERSE TRANSCRIPTASE AND  
; TITLE OF INVENTION: TELOMERASE VARIANTS  
; FILE REFERENCE: 018/062  
; CURRENT APPLICATION NUMBER: US/09/438,486A  
; CURRENT FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: 08/851,843  
; PRIOR FILING DATE: 1997-05-06  
; PRIOR APPLICATION NUMBER: 08/846,017

;; PRIOR FILING DATE: 1997-04-25  
;; PRIOR APPLICATION NUMBER: 08/844,419  
;; COUNTRY: United States of America  
;; ZIP: 94111  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/10/054,295  
;; FILING DATE: 18-Jan-2002  
;; CLASSIFICATION: 536  
;;  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/854,050  
;; FILING DATE: <Unknown>  
;; APPLICATION NUMBER: US 08/846,017  
;; FILING DATE: 25-APR-1997  
;; APPLICATION NUMBER: US 08/844,419  
;; FILING DATE: 18-APR-1997  
;; APPLICATION NUMBER: US 08/724,643  
;; FILING DATE: 01-OCT-1996  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Apple, Randolph T.  
;; REGISTRATION NUMBER: 36,429  
;; REFERENCE/DOCKET NUMBER: 015389-002930US  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 576-0200  
;; TELEFAX: (415) 576-0300  
;; INFORMATION FOR SEQ ID NO: 162:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 27 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: <Unknown>  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; FEATURE:  
;; NAME/KEY: Peptide  
;; LOCATION: 1..27  
;; OTHER INFORMATION: /note= "motif A peptide from  
;; Saccharomyces cerevisiae EST2"  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 162:  
US-10-054-295-162

Query Match 36.8%; Score 35; DB 2; Length 27;  
Best Local Similarity 70.0%; Pred. No. 41;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAl 18  
| | | | | | | |  
Db 8 FDKVSCYDSI 17

RESULT 31  
US-09-082-358B-57  
; Sequence 57, Application US/09082358B  
; Patent No. 6469153  
; GENERAL INFORMATION:  
; APPLICANT: Goff, Stephen P.  
; APPLICANT: Li, Xingquiang  
; TITLE OF INVENTION: EIP-1, EIP-3 GENES, ENVELOPE-INTERACTING PROTEINS,  
; TITLE OF INVENTION: EIP-1, and EIP-3  
; FILE REFERENCE: 0575/54804  
; CURRENT APPLICATION NUMBER: US/09/082,358B  
; CURRENT FILING DATE: 1998-05-20  
; NUMBER OF SEQ ID NOS: 106  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 57  
; LENGTH: 32  
; TYPE: PRT  
; ORGANISM: murine  
US-09-082-358B-57

Query Match 36.8%; Score 35; DB 2; Length 32;  
Best Local Similarity 50.0%; Pred. No. 50;  
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 VLETFVKSCPD 16  
| | | | | | | |  
Db 4 VLASFQQACPD 15

RESULT 32  
US-08-974-549A-45  
; Sequence 45, Application US/08974549A  
; Patent No. 6166178  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.  
; APPLICANT: Morin, Gregg B.  
; APPLICANT: Harley, Calvin B.  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 727  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California

1 COUNTRY: USA  
2 ZIP: 94111-3834  
3 COMPUTER READABLE FORM:  
4 MEDIUM TYPE: Floppy disk  
5 COMPUTER: IBM PC compatible  
6 OPERATING SYSTEM: PC-DOS/MS-DOS  
7 SOFTWARE: PatentIn Release #1.0, Version #1.30  
8 CURRENT APPLICATION DATA:  
9 APPLICATION NUMBER: US/08/974,549A  
10 FILING DATE: 19-NOV-1997  
11 CLASSIFICATION: 536  
12 PRIOR APPLICATION DATA:  
13 APPLICATION NUMBER: US 08/724,643  
14 FILING DATE: 01-OCT-1996  
15 PRIOR APPLICATION DATA: US 08/844,419  
16 FILING DATE: 18-APR-1997  
17 PRIOR APPLICATION DATA:  
18 APPLICATION NUMBER: US 08/846,017  
19 FILING DATE: 25-APR-1997  
20 PRIOR APPLICATION DATA:  
21 APPLICATION NUMBER: US 08/851,843  
22 FILING DATE: 06-MAY-1997  
23 PRIOR APPLICATION DATA:  
24 APPLICATION NUMBER: US 08/854,050  
25 FILING DATE: 09-MAY-1997  
26 PRIOR APPLICATION DATA:  
27 APPLICATION NUMBER: US 08/911,312  
28 FILING DATE: 14-AUG-1997  
29 PRIOR APPLICATION DATA:  
30 APPLICATION NUMBER: US 08/912,951  
31 FILING DATE: 14-AUG-1997  
32 PRIOR APPLICATION DATA:  
33 APPLICATION NUMBER: US 08/915,503  
34 FILING DATE: 14-AUG-1997  
35 PRIOR APPLICATION DATA:  
36 APPLICATION NUMBER: WO PCT/US97/17618  
37 FILING DATE: 01-OCT-1997  
38 PRIOR APPLICATION DATA:  
39 APPLICATION NUMBER: WO PCT/US97/17885  
40 FILING DATE: 01-OCT-1997  
41 ATTORNEY/AGENT INFORMATION:  
42 NAME: Apple, Randolph Ted  
43 REGISTRATION NUMBER: 36,429  
44 REFERENCE/DOCKET NUMBER: 015389-002610US  
45 TELECOMMUNICATION INFORMATION:  
46 TELEPHONE: (415) 576-0200  
47 TELEFAX: (415) 576-0300  
48 INFORMATION FOR SEQ ID NO: 45:  
49 SEQUENCE CHARACTERISTICS:  
50 LENGTH: 34 amino acids  
51 TYPE: amino acid  
52 STRANDEDNESS:  
53 TOPOLOGY: linear  
54 MOLECULE TYPE: peptide  
55 FEATURE:  
56 NAME/KEY: Peptide  
57 LOCATION: 1..34  
58 OTHER INFORMATION: /note= "motif A peptide from  
59 OTHER INFORMATION: Saccharomyces cerevisiae EST2p"  
60 US-08-974-549A-45

Query Match 36.8%; Score 35; DB 2; Length 34;  
Best Local Similarity 70.0%; Pred. No. 53;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18  
Db 10 FDKSCYDSI 19

RESULT 33  
US-08-912-951-45

1 Sequence 45, Application US/08912951  
2 Patent No. 6475789  
3 GENERAL INFORMATION:  
4 APPLICANT: Cech, Thomas R.  
5 APPLICANT: Lingner, Joachim  
6 APPLICANT: Nakamura, Toru  
7 APPLICANT: Chapman, Karen B.  
8 APPLICANT: Morin, Gregg B.  
9 APPLICANT: Harley, Calvin  
10 APPLICANT: Andrews, William H.  
11 TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND  
12 TITLE OF INVENTION: THERAPEUTIC METHODS  
13 NUMBER OF SEQUENCES: 335  
14 CORRESPONDENCE ADDRESS:  
15 ADDRESSEE: Townsend and Townsend and Crew LLP  
16 STREET: Two Embarcadero Center, 8th Floor  
17 CITY: San Francisco  
18 STATE: California  
19 COUNTRY: United States of America  
20 ZIP: 94111  
21 COMPUTER READABLE FORM:  
22 MEDIUM TYPE: Floppy disk  
23 COMPUTER: IBM PC compatible  
24 OPERATING SYSTEM: PC-DOS/MS-DOS  
25 SOFTWARE: PatentIn Release #1.0, Version #1.30  
26 CURRENT APPLICATION DATA:  
27 APPLICATION NUMBER: US/08/912,951  
28 FILING DATE: 14-AUG-1997  
29 CLASSIFICATION: 435  
30 PRIOR APPLICATION DATA:  
31 APPLICATION NUMBER: US 08/854,050  
32 FILING DATE: 09-MAY-1997  
33 CLASSIFICATION: 435  
34 PRIOR APPLICATION DATA:  
35 APPLICATION NUMBER: US 08/851,843  
36 FILING DATE: 06-MAY-1997  
37 CLASSIFICATION: 435  
38 PRIOR APPLICATION DATA:  
39 APPLICATION NUMBER: US 08/846,017  
40 FILING DATE: 25-APR-1997  
41 CLASSIFICATION: 435  
42 PRIOR APPLICATION DATA:  
43 APPLICATION NUMBER: US 08/844,419  
44 FILING DATE: 18-APR-1997  
45 CLASSIFICATION: 435  
46 PRIOR APPLICATION DATA:  
47 APPLICATION NUMBER: US 08/724,643  
48 FILING DATE: 01-OCT-1996  
49 CLASSIFICATION: 435  
50 ATTORNEY/AGENT INFORMATION:  
51 NAME: Apple, Randolph T.  
52 REGISTRATION NUMBER: 36,429  
53 REFERENCE/DOCKET NUMBER: 015389-002600US  
54 TELECOMMUNICATION INFORMATION:  
55 TELEPHONE: (415) 576-0200  
56 TELEFAX: (415) 576-0300  
57 INFORMATION FOR SEQ ID NO: 45:  
58 SEQUENCE CHARACTERISTICS:  
59 LENGTH: 34 amino acids  
60 TYPE: amino acid  
61 STRANDEDNESS:  
62 TOPOLOGY: linear  
63 MOLECULE TYPE: peptide  
64 FEATURE:  
65 NAME/KEY: Peptide  
66 LOCATION: 1..34  
67 OTHER INFORMATION: /note= "motif A peptide from  
68 OTHER INFORMATION: Saccharomyces cerevisiae EST2p"  
69 US-08-912-951-45  
70 Query Match 36.8%; Score 35; DB 2; Length 34;  
71 Best Local Similarity 70.0%; Pred. No. 53;  
72 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy      9 FTVKSCPD1 18
      | | | | | | | |
Db     10 FDKVSCYDSI 19

RESULT 34
US-09-402-181B-45
; Sequence 45, Application US/09402181B
; Patent No. 6610839
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
;           Lingner, Joachim
;           Nakamura, Toru
;           Chapman, Karen B.
;           Morin, Gregg B.
;           Harley, Calvin B.
;           Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/402.181B
; FILING DATE: 29-Sep-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ausenhus, Scott L.
; REGISTRATION NUMBER: 42,271
; REFERENCE/DOCKET NUMBER: 015389-002620US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..34
; OTHER INFORMATION: /note= "motif A peptide from

; Saccharomyces cerevisiae EST2p"
; SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-402-181B-45
Query Match      36.8%; Score 35; DB 2; Length 34;
Best Local Similarity 70.0%; Pred. No. 53;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      9 FTVKSCPD1 18
      | | | | | | | |
Db     10 FDKVSCYDSI 19

RESULT 35
US-09-721-456-45
; Sequence 45, Application US/09721456
; Patent No. 6617110
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
;           Lingner, Joachim
;           Nakamura, Toru
;           Chapman, Karen B.
;           Morin, Gregg B.
;           Harley, Calvin B.
;           Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/721,456
; FILING DATE: 22-No. 6617110-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
```

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; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 34 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: <Unknown>
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   FEATURE:
;     NAME/KEY: Peptide
;     LOCATION: 1..34
;     OTHER INFORMATION: /note= "motif A peptide from
;       Saccharomyces cerevisiae EST2p"
;   SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-721-456-45

Query Match          36.8%; Score 35; DB 2; Length 34;
Best Local Similarity 70.0%; Pred. No. 53;
Matches 7; Conservative 1; Mismatches 0; Gaps 0;

QY 9 FTVKSCPDAL 18
Db 10 FDKSCYDSI 19

RESULT 36
US-09-042-460-46
; Sequence 46, Application US/09042460
; Patent No. 6767719
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; APPLICANT: Allsopp, Richard
; APPLICANT: Definno, Ronald
; APPLICANT: Greenberg, Roger
; TITLE OF INVENTION: Mouse Telomerase Reverse Transcriptase
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,460
; FILING DATE: 16-MAR-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/974,549
; FILING DATE: 19-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/974,584
; FILING DATE: 19-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/979,742
; FILING DATE: 26-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Einhorn, Gregory P.
; REGISTRATION NUMBER: 38,440
; REFERENCE/DOCKET NUMBER: 015389-0031100S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 34 amino acids
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-09-042-460-46

Query Match          36.8%; Score 35; DB 2; Length 34;
Best Local Similarity 70.0%; Pred. No. 53;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18
Db 10 FDKSCYDSI 19

RESULT 37
US-08-486-057B-20
; Sequence 20, Application US/08486057B
; Patent No. 5650494
; GENERAL INFORMATION:
; APPLICANT: Cerletti, Nico
; APPLICANT: McMaster, Gary K.
; APPLICANT: Cox, David
; APPLICANT: Schmitz, Albert
; APPLICANT: Meyhack, Bernd
; TITLE OF INVENTION: Process for Refolding Recombinantly
;   Produced TGP-beta-like Proteins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Henry P. No. 5650494ak
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,057B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/201,703
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; FILING DATE: 25-FEB-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/960,309  
; FILING DATE: 13-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/621,502  
; FILING DATE: 03-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 8927546.5  
; FILING DATE: 06-DEC-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5650494ak, Henry P.  
; REGISTRATION NUMBER: 33200  
; REFERENCE/DOCKET NUMBER: 4-17861/+/Cont3  
; TELEPHONE: (908) 277-5110  
; TELEFAX: (908) 277-4306  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 31 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-486-057B-20

Query Match 35.8%; Score 34; DB 1; Length 31;  
Best Local Similarity 50.0%; Pred. No. 71;  
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKKDVLFTFTVKSC 14  
||:|  
Db 15 PKIEQLSNMIVKSC 28  
||||

RESULT 38  
US-08-789-588-20  
; Sequence 20, Application US/08789588  
; Patent No. 5922846  
; GENERAL INFORMATION:  
; APPLICANT: Cerletti, Nico  
; APPLICANT: McMaster, Gary K.  
; APPLICANT: Cox, David  
; APPLICANT: Schmitz, Albert  
; APPLICANT: Meyhack, Bernd  
; TITLE OF INVENTION: Process for Refolding Recombinantly  
; TITLE OF INVENTION: Produced TGF-beta-like Proteins  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Henry P. No. 5922846ak  
; STREET: 520 White Plains Road, P.O. Box 2005  
; CITY: Tarrytown  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10591-9005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/789,588  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/486,057  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: US 08/201,703  
; FILING DATE: 25-FEB-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/960,309  
; FILING DATE: 13-OCT-1992  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/621,502  
; FILING DATE: 03-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 8927546.5  
; FILING DATE: 06-DEC-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5922846ak, Henry P.  
; REGISTRATION NUMBER: 33200  
; REFERENCE/DOCKET NUMBER: 4-17861/+/Cont3  
; TELEPHONE: (908) 277-5110  
; TELEFAX: (908) 277-4306  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 31 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-789-588-20

Query Match 35.8%; Score 34; DB 1; Length 31;  
Best Local Similarity 50.0%; Pred. No. 71;  
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKKDVLFTFTVKSC 14  
||:|  
Db 15 PKIEQLSNMIVKSC 28  
||||

RESULT 39  
US-09-374-958C-30  
; Sequence 30, Application US/09374958C  
; Patent No. 6677432  
; GENERAL INFORMATION:  
; APPLICANT: Stryker Corporation  
; TITLE OF INVENTION: Modified Proteins and DNAs of the TGF-beta Superfamily, Including  
; TITLE OF INVENTION: Modified Morphogenic Proteins  
; FILE REFERENCE: STK-076  
; CURRENT APPLICATION NUMBER: US/09/374,958C  
; CURRENT FILING DATE: 1999-08-16  
; NUMBER OF SEQ ID NOS: 90  
; SOFTWARE: PatentIn version 2.0  
; SEQ ID NO 30  
; LENGTH: 34  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: TGF-Beta2  
US-09-374-958C-30

Query Match 35.8%; Score 34; DB 2; Length 34;  
Best Local Similarity 50.0%; Pred. No. 79;  
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKKDVLFTFTVKSC 14  
||:|  
Db 18 PKIEQLSNMIVKSC 31  
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RESULT 40  
US-09-374-936-30  
; Sequence 30, Application US/09374936  
; Patent No. 6846906  
; GENERAL INFORMATION:  
; APPLICANT: Oppermann, Hermann  
; APPLICANT: Tai, Mei-Sheng  
; APPLICANT: McCartney, John  
; TITLE OF INVENTION: Modified TGF-beta Superfamily Proteins  
; FILE REFERENCE: STK-077  
; CURRENT APPLICATION NUMBER: US/09/374,936  
; CURRENT FILING DATE: 1999-08-16  
; NUMBER OF SEQ ID NOS: 88

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: TGF-Beta2
US-09-374-936-30
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Query Match      35.8%; Score 34; DB 2; Length 34;
Best Local Similarity 50.0%; Pred. No. 79;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
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QY      1 PKKDVLETFVVKSC 14
          |||:|
Db      18 PKIEQLSNMIVKSC 31
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Search completed: January 20, 2006, 17:35:33
Job time : 12.4444 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2006, 17:27:09 ; Search time 34.4444 Seconds  
(without alignments)  
218.350 Million cell updates/sec

Title: US-10-619-323-6  
Perfect score: 95  
Sequence: 1 PKKDVLETFVKSCPDAl 18  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues  
Total number of hits satisfying chosen parameters: 549595  
Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 50 summaries

Database : Published Applications AA Main:  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.psp:\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.psp:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.psp:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.psp:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.psp:\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.psp:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	100.0	18	4	US-10-619-323-6
2	95	100.0	25	4	US-10-619-323-5
3	61	64.2	30	5	US-10-473-127-1717
4	49	51.6	10	5	US-10-473-127-165
5	39	41.1	49	4	US-10-424-599-278211
6	39	41.1	50	4	US-10-424-599-165124
7	37	38.9	46	4	US-10-437-963-170639
8	36	37.9	42	3	US-09-848-664-14
9	36	37.9	46	4	US-10-724-972A-5875
10	35	36.8	17	4	US-10-044-692-100
11	35	36.8	17	4	US-10-044-539-100
12	35	36.8	17	4	US-10-325-810-100
13	35	36.8	17	5	US-10-877-124-100
14	35	36.8	17	5	US-10-877-022-100
15	35	36.8	17	5	US-10-877-146-100
16	35	36.8	26	3	US-09-843-676-140
17	35	36.8	26	3	US-09-766-253-140
18	35	36.8	26	3	US-09-438-486-140
19	35	36.8	26	4	US-10-053-758-140
20	35	36.8	26	4	US-10-054-295-140
21	35	36.8	26	4	US-10-054-611-140
22	35	36.8	26	4	US-10-325-810-258
23	35	36.8	26	5	US-10-877-124-258
24	35	36.8	26	5	US-10-877-022-258
25	35	36.8	26	5	US-10-877-146-258
26	35	36.8	27	3	US-09-843-676-162
27	35	36.8	27	3	US-09-766-253-162

ALIGNMENTS

RESULT 1

US-10-619-323-6  
; Sequence 6, Application US/10619323  
; Publication No. US20040136985A1  
; GENERAL INFORMATION:  
; APPLICANT: Jennings, Lisa K.  
; APPLICANT: Longhurst, Celia M.  
; APPLICANT: Cook, George A.  
; APPLICANT: Bao, Jianxiong  
; APPLICANT: Zhang, Chunxiang  
; APPLICANT: White, Melanie M.  
; APPLICANT: Crossno, Jr., Joseph T.  
; APPLICANT: Lu, Yi  
; TITLE OF INVENTION: METHODS OF MODIFYING BEHAVIOR OF CD9-EXPRESSING CELLS  
; FILE REFERENCE: 20609/241  
; CURRENT APPLICATION NUMBER: US/10/619,323  
; CURRENT FILING DATE: 2003-07-14  
; PRIOR APPLICATION NUMBER: 60/395,864  
; PRIOR FILING DATE: 2002-07-12  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: CD9 peptide

Query Match 100.0%; Score 95; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.7e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLETFVKSCPDAl 18

Db 1 PKKDVLETFVKSCPDAl 18

RESULT 2

US-10-619-323-5  
; Sequence 5, Application US/10619323  
; Publication No. US20040136985A1  
; GENERAL INFORMATION:  
; APPLICANT: Jennings, Lisa K.  
; APPLICANT: Longhurst, Celia M.

```
; APPLICANT: Cook, George A.
; APPLICANT: Bao, Jianxiong
; APPLICANT: Zhang, Chunxiang
; APPLICANT: White, Melanie M.
; APPLICANT: Crossno, Jr., Joseph T.
; APPLICANT: Lu, Yi
; TITLE OF INVENTION: METHODS OF MODIFYING BEHAVIOR OF CD9-EXPRESSING CELLS
; FILE REFERENCE: 20609/241
; CURRENT APPLICATION NUMBER: US/10/619,323
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: 60/395,864
; PRIOR FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CD9 peptide
US-10-619-323-5

Query Match 100.0%; Score 95; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKDVLTTFTVKSCPDAI 18
   |||||
Db 1 PKDVLTTFTVKSCPDAI 18

RESULT 3
US-10-473-127-1717
; Sequence 1717, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1717
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1717

Query Match 64.2%; Score 61; DB 5; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKDVLTTFTVK 12
   |||||
Db 19 PKDVLTTFTVK 30

RESULT 4
US-10-473-127-165
; Sequence 165, Application US/10473127
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; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 165
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-165

Query Match 51.6%; Score 49; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KDVLETTFTVK 12
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Db 1 KDVLETTFTVK 10

RESULT 5
US-10-424-599-278211
; Sequence 278211, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 278211
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(49)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_93248C.1.pcp
US-10-424-599-278211

Query Match 41.1%; Score 39; DB 4; Length 49;
Best Local Similarity 63.6%; Pred. No. 66;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 EFTVKSCTPA 17
   |||||
Db 9 EFTVKSCTPA 19

RESULT 6
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;
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; THERAPEUTIC METHODS
;
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/044,692
; FILING DATE: 11-Jan-2002
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/912,951
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
;
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..17
; OTHER INFORMATION: /note= "telomerase RT finger motif A
; peptide from Saccharomyces
; cerevisiae EST2"
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-044-692-100
Query Match 36.8%; Score 35; DB 4; Length 17;
Best Local Similarity 70.0%; Pred. No. 95;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAl 18
Db 8 FDKSCYDSI 17

RESULT 11
US-10-044-539-100
; Sequence 100, Application US/10044539
; Publication No. US2003010009A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.

;
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; THERAPEUTIC METHODS
;
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/044,539
; FILING DATE: 11-Jan-2002
; CLASSIFICATION: 435
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/912,951
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
;
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..17
; OTHER INFORMATION: /note= "telomerase RT finger motif A
; peptide from Saccharomyces
; cerevisiae EST2"
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-044-539-100
Query Match 36.8%; Score 35; DB 4; Length 17;
Best Local Similarity 70.0%; Pred. No. 95;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAl 18
Db 8 FDKSCYDSI 17

RESULT 12
US-10-325-810-100
; Sequence 100, Application US/10325810
; Publication No. US20030204069A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
;

```

Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin B.  
Andrews, William H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 633  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION NUMBER: US/10/325,810  
FILING DATE: 20-Dec-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/402,181  
FILING DATE: 29-Sep-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ausenhus, Scott L.  
REGISTRATION NUMBER: 42,271  
REFERENCE/DOCKET NUMBER: 015389-002620US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 100:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..17  
OTHER INFORMATION: /note= "telomerase RT finger motif A  
peptide from Saccharomyces  
cerevisiae EST2"  
SEQUENCE DESCRIPTION: SEQ ID NO: 100:  
US-10-325-810-100

Query Match 36.88; Score 35; DB 4; Length 17;  
Best Local Similarity 70.08; Pred. No. 95;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAl 18

Db 8 FDKSCVDSI 17  
RESULT 13  
US-10-877-124-100  
; Sequence 100, Application US/10877124  
; Publication No. US20040242529A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin B.  
; Andrews, William H.  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 727  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/877,124  
; FILING DATE: 24-Jun-2004  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/432,503  
; FILING DATE: 02-Nov-1999  
; APPLICATION NUMBER: 08/974,549  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; APPLICATION NUMBER: US 08/911,312  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: US 08/912,951  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: US 08/915,503  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: WO PCT/US97/17618  
; FILING DATE: 01-OCT-1997  
; APPLICATION NUMBER: WO PCT/US97/17885  
; FILING DATE: 01-OCT-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph Ted  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002610US  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 100:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; NAME/KEY: Peptide

; LOCATION: 1..17  
; OTHER INFORMATION: /note= "telomerase RT finger motif A  
; peptide from Saccharomyces  
; cerevisiae EST2"  
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:  
US-10-877-124-100

Query Match 36.8%; Score 35; DB 5; Length 17;  
Best Local Similarity 70.0%; Pred. No. 95;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAI 18  
| | | | | : |  
Db 8 FDKSCYDSI 17

RESULT 14  
US-10-877-022-100  
; Sequence 100, Application US/10877022  
; Publication No. US20040247613A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin B.  
; Andrews, William H.

; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 727  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834

## COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

## CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/877,022  
; FILING DATE: 24-Jun-2004  
; CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/432,503  
; FILING DATE: 02-Nov-1999  
; APPLICATION NUMBER: 08/974,549

; FILING DATE: <Unknown>

; APPLICATION NUMBER: US 08/844,419

; FILING DATE: 18-APR-1997

; APPLICATION NUMBER: US 08/846,017

; FILING DATE: 25-APR-1997

; APPLICATION NUMBER: US 08/851,843

; FILING DATE: 06-MAY-1997

; APPLICATION NUMBER: US 08/854,050

; FILING DATE: 09-MAY-1997

; APPLICATION NUMBER: US 08/911,312

; FILING DATE: 14-AUG-1997

; APPLICATION NUMBER: US 08/912,951

; FILING DATE: 14-AUG-1997

; APPLICATION NUMBER: US 08/915,503

; FILING DATE: 14-AUG-1997

; APPLICATION NUMBER: WO PCT/US97/17618

; FILING DATE: 01-OCT-1997

; APPLICATION NUMBER: WO PCT/US97/17885

; FILING DATE: 01-OCT-1997

## ATTORNEY/AGENT INFORMATION:

; NAME: Apple, Randolph Ted

; REGISTRATION NUMBER: 36,429

; REFERENCE/DOCKET NUMBER: 015389-002610US

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 100:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..17  
; OTHER INFORMATION: /note= "telomerase RT finger motif A  
; peptide from Saccharomyces  
; cerevisiae EST2"  
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:  
US-10-877-022-100

Query Match 36.8%; Score 35; DB 5; Length 17;  
Best Local Similarity 70.0%; Pred. No. 95;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAI 18  
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Db 8 FDKSCYDSI 17

RESULT 15  
US-10-877-146-100  
; Sequence 100, Application US/10877146  
; Publication No. US20050013825A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin B.  
; Andrews, William H.

; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 727  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834

## COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

## CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/877,146  
; FILING DATE: 24-Jun-2004  
; CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/432,503  
; FILING DATE: 02-Nov-1999  
; APPLICATION NUMBER: 08/974,549

; FILING DATE: <Unknown>

; APPLICATION NUMBER: US 08/844,419

; FILING DATE: 18-APR-1997

; APPLICATION NUMBER: US 08/846,017

; FILING DATE: 25-APR-1997

; APPLICATION NUMBER: US 08/851,843

; FILING DATE: 06-MAY-1997

; APPLICATION NUMBER: US 08/854,050

; FILING DATE: 09-MAY-1997

; APPLICATION NUMBER: US 08/911,312

; FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph Ted  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 100:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..17  
OTHER INFORMATION: /note= "telomerase RT finger motif A  
peptide from Saccharomyces  
cerevisiae EST2"  
SEQUENCE DESCRIPTION: SEQ ID NO: 100:  
US-10-877-146-100

Query Match 36.8%; Score 35; DB 5; Length 17;  
Best Local Similarity 70.0%; Pred. No. 95;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 9 FTVKSCPDAl 18  
| | | | | | | |  
Db 8 FDKVSCYDSI 17

RESULT 16  
US-09-843-676-140  
Sequence 140, Application US/09843676  
Patent No. US20020164786A1  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin  
Andrews, William H.  
TITLE OF INVENTION: No. US20020164786A1el Telomerase  
NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/843,676  
FILING DATE: 26-Apr-2001  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/854,050  
FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 140:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..26  
OTHER INFORMATION: /note= "motif 3(A) peptide from  
Saccharomyces cerevisiae EST2p"  
SEQUENCE DESCRIPTION: SEQ ID NO: 140:  
US-09-843-676-140

Query Match 36.8%; Score 35; DB 3; Length 26;  
Best Local Similarity 70.0%; Pred. No. 1.5e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 9 FTVKSCPDAl 18  
| | | | | | | |  
Db 7 FDKVSCYDSI 16

RESULT 17  
US-09-766-253-140  
Sequence 140, Application US/09766253  
Publication No. US20020187471A1  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin  
Andrews, William H.  
TITLE OF INVENTION: No. US20020187471A1el Telomerase  
NUMBER OF SEQUENCES: 171  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/766,253  
FILING DATE: 19-Jan-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/846,017  
FILING DATE: 1997-04-25  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002920US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 140:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..26  
OTHER INFORMATION: /note= "motif 3(A) peptide from  
Saccharomyces cerevisiae EST2p"  
SEQUENCE DESCRIPTION: SEQ ID NO: 140:  
US-09-766-253-140

Query Match 36.8%; Score 35; DB 3; Length 26;  
Best Local Similarity 70.0%; Pred. No. 1.5e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAI 18  
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DB 7 FDKKSCYDSI 16

RESULT 19  
US-09-438-486-140  
Sequence 140, Application US/09438486  
Publication No. US20030009019A1  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
APPLICANT: Lingner, Joachim  
APPLICANT: Nakamura, Toru  
APPLICANT: Chapman, Karen B.  
APPLICANT: Morin, Gregg B.  
APPLICANT: Harley, Calvin  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: No. US20030009019A1el Telomerase  
NUMBER OF SEQUENCES: 223  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/438,486  
FILING DATE: 12-NOV-1999  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002931US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 140:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..26  
OTHER INFORMATION: /note= "motif 3(A) peptide from  
Saccharomyces cerevisiae EST2p"  
US-09-438-486-140  
Query Match 36.8%; Score 35; DB 3; Length 26;  
Best Local Similarity 70.0%; Pred. No. 1.5e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 9 FTVKSCPDAI 18  
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DB 7 FDKKSCYDSI 16  
RESULT 19  
US-10-053-758-140  
Sequence 140, Application US/10053758  
Publication No. US20030032075A1  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
APPLICANT: Lingner, Joachim  
APPLICANT: Nakamura, Toru  
APPLICANT: Chapman, Karen B.  
APPLICANT: Morin, Gregg B.  
APPLICANT: Harley, Calvin  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: No. US20030032075A1el Telomerase  
NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/053,758  
FILING DATE: 18-Jan-2002  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/724,643



ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 140:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..26  
OTHER INFORMATION: /note= "motif 3(A) peptide from  
Saccharomyces cerevisiae EST2p"  
SEQUENCE DESCRIPTION: SEQ ID NO: 140:  
US-10-053-758-140

Query Match 36.8%; Score 35; DB 4; Length 26;  
Best Local Similarity 70.0%; Pred. No. 1.5e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAI 18  
| | | | | | | |  
Db 7 FDKSCYDSI 16

RESULT 20  
US-10-054-295-140  
Sequence 140, Application US/10054295  
Publication No. US20030044953A1  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin  
Andrews, William H.  
TITLE OF INVENTION: No. US20030044953A1el Telomerase  
NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/054,295  
FILING DATE: 18-Jan-2002  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/854,050  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US  
TELECOMMUNICATION INFORMATION:

REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 140:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..26  
OTHER INFORMATION: /note= "motif 3(A) peptide from  
Saccharomyces cerevisiae EST2p"  
SEQUENCE DESCRIPTION: SEQ ID NO: 140:  
US-10-054-295-140

Query Match 36.8%; Score 35; DB 4; Length 26;  
Best Local Similarity 70.0%; Pred. No. 1.5e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAI 18  
| | | | | | | |  
Db 7 FDKSCYDSI 16

RESULT 21  
US-10-054-611-140  
Sequence 140, Application US/10054611  
Publication No. US20030059787A1  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin  
Andrews, William H.  
TITLE OF INVENTION: No. US20030059787A1el Telomerase  
NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/054,611  
FILING DATE: 18-Jan-2002  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/854,050  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US  
TELECOMMUNICATION INFORMATION:

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;
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 140:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; MOLECULE TYPE: peptide
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..26
; OTHER INFORMATION: /note= "motif 3(A) peptide from
; Saccharomyces cerevisiae EST2p"
; SEQUENCE DESCRIPTION: SEQ ID NO: 140:
US-10-054-611-140

Query Match 36.8%; Score 35; DB 4; Length 26;
Best Local Similarity 70.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAl 18
Db 7 FDKSCYDSI 16

RESULT 22
US-10-325-810-258
; Sequence 258, Application US/10325810
; Publication No. US20030204069A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/325,810
; FILING DATE: 20-Dec-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,181
; FILING DATE: 29-Sep-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997

;
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Aussenhus, Scott L.
; REGISTRATION NUMBER: 42,271
; REFERENCE/DOCKET NUMBER: 015389-002620US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 258:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..26
; OTHER INFORMATION: /note= "motif 3(A) peptide from
; Saccharomyces cerevisiae EST2p"
; SEQUENCE DESCRIPTION: SEQ ID NO: 258:
US-10-325-810-258

Query Match 36.8%; Score 35; DB 4; Length 26;
Best Local Similarity 70.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAl 18
Db 7 FDKSCYDSI 16

RESULT 23
US-10-877-124-258
; Sequence 258, Application US/10877124
; Publication No. US20040242529A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/877,124
; FILING DATE: 24-Jun-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,503
; FILING DATE: 02-Nov-1999
; APPLICATION NUMBER: 08/974,549
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 14-AUG-1997
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;  
; FILING DATE: 25-APR-1997  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; APPLICATION NUMBER: US 08/911,312  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: US 08/912,951  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: US 08/915,503  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: WO PCT/US97/17618  
; FILING DATE: 01-OCT-1997  
; APPLICATION NUMBER: WO PCT/US97/17885  
; FILING DATE: 01-OCT-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph Ted  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002610US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 258:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 26 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..26  
; OTHER INFORMATION: /note= "motif 3(A) peptide from  
; Saccharomyces cerevisiae EST2p"  
; SEQUENCE DESCRIPTION: SEQ ID NO: 258:  
US-10-877-124-258  
  
Query Match 36.8%; Score 35; DB 5; Length 26;  
Best Local Similarity 70.0%; Pred. No. 1.5e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 9 FTVKSCPDAl 18  
Db 7 FDVKSCYDSI 16  
| | | | | | | |  
| | | | | | | |  
  
RESULT 24  
US-10-877-022-258  
; Sequence 258, Application US/10877022  
; Publication No US20040247613A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin B.  
; Andrews, William H.  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 727  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:

;  
; APPLICATION NUMBER: US/10/877,022  
; FILING DATE: 24-Jun-2004  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/432,503  
; FILING DATE: 02-Nov-1999  
; APPLICATION NUMBER: 08/974,549  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; APPLICATION NUMBER: US 08/911,312  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: US 08/912,951  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: US 08/915,503  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: WO PCT/US97/17618  
; FILING DATE: 01-OCT-1997  
; APPLICATION NUMBER: WO PCT/US97/17885  
; FILING DATE: 01-OCT-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph Ted  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002610US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 258:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 26 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..26  
; OTHER INFORMATION: /note= "motif 3(A) peptide from  
; Saccharomyces cerevisiae EST2p"  
; SEQUENCE DESCRIPTION: SEQ ID NO: 258:  
US-10-877-022-258  
  
Query Match 36.8%; Score 35; DB 5; Length 26;  
Best Local Similarity 70.0%; Pred. No. 1.5e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 9 FTVKSCPDAl 18  
Db 7 FDVKSCYDSI 16  
| | | | | | | |  
| | | | | | | |  
  
RESULT 25  
US-10-877-146-258  
; Sequence 258, Application US/10877146  
; Publication No US20050013825A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin B.  
; Andrews, William H.  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 727  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor  
City: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/877,146  
FILING DATE: 24-Jun-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/432,503  
FILING DATE: 02-Nov-1999  
APPLICATION NUMBER: 08/974,549  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph Ted  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 258:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..26  
OTHER INFORMATION: /note= "motif 3(A) peptide from Saccharomyces cerevisiae EST2p"  
SEQUENCE DESCRIPTION: SEQ ID NO: 258:  
US-10-877-146-258  
Query Match 36.8%; Score 35; DB 5; Length 26;  
Best Local Similarity 70.0%; Pred. No. 1.5e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 9 FTVKSCPDAl 18  
Db 7 FDKVSCYDSI 16  
RESULT 26  
US-09-843-676-162  
; Sequence 162, Application US/09843676  
; Patent No. US20020164786A1  
; GENERAL INFORMATION:  
; APPLICANT: Cecch, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin  
; Andrews, William H.  
TITLE OF INVENTION: NO. US20020164786A1el Telomerase  
NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/843,676  
FILING DATE: 26-Apr-2001  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 162:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..27  
OTHER INFORMATION: /note= "motif A peptide from Saccharomyces cerevisiae EST2"  
SEQUENCE DESCRIPTION: SEQ ID NO: 162:  
US-09-843-676-162  
Query Match 36.8%; Score 35; DB 3; Length 27;  
Best Local Similarity 70.0%; Pred. No. 1.6e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 9 FTVKSCPDAl 18  
Db 8 FDKVSCYDSI 17  
RESULT 27  
US-09-766-253-162  
; Sequence 162, Application US/09766253  
; Publication No. US20020187471A1  
; GENERAL INFORMATION:  
; APPLICANT: Cecch, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru

APPLICANT: Cecch, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin  
Andrews, William H.  
TITLE OF INVENTION: NO. US20020164786A1el Telomerase  
NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/843,676  
FILING DATE: 26-Apr-2001  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 162:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..27  
OTHER INFORMATION: /note= "motif A peptide from Saccharomyces cerevisiae EST2"  
SEQUENCE DESCRIPTION: SEQ ID NO: 162:  
US-09-843-676-162  
Query Match 36.8%; Score 35; DB 3; Length 27;  
Best Local Similarity 70.0%; Pred. No. 1.6e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 9 FTVKSCPDAl 18  
Db 8 FDKVSCYDSI 17  
RESULT 27  
US-09-766-253-162  
; Sequence 162, Application US/09766253  
; Publication No. US20020187471A1  
; GENERAL INFORMATION:  
; APPLICANT: Cecch, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru

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; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20020187471A1el Telomerase
; NUMBER OF SEQUENCES: 171
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/766,253
; FILING DATE: 19-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,017
; FILING DATE: 1997-04-25
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002920US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 162:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..27
; OTHER INFORMATION: /note= "motif A peptide from
; Saccharomyces cerevisiae EST2"
; SEQUENCE DESCRIPTION: SEQ ID NO: 162:
US-09-766-253-162
;
; Query Match 36.8%; Score 35; DB 3; Length 27;
; Best Local Similarity 70.0%; Pred. No. 1.6e+02;
; Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
;
; QY 9 FTVKSCPDAL 18
; DB 8 FDVKSCYDSI 17
;
; RESULT 28
; US-09-438-486-162
; Sequence 162, Application US/09438486
; Publication No. US20030009019A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. US20030009019A1el Telomerase
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
```

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; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/438,486
; FILING DATE: 12-NOV-1999
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002931US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 162:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..27
; OTHER INFORMATION: /note= "motif A peptide from
; Saccharomyces cerevisiae EST2"
; SEQUENCE DESCRIPTION: SEQ ID NO: 162:
US-09-438-486-162
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; Query Match 36.8%; Score 35; DB 3; Length 27;
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; Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
;
; QY 9 FTVKSCPDAL 18
; DB 8 FDVKSCYDSI 17
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; RESULT 29
; US-10-053-758-162
; Sequence 162, Application US/10053758
; Publication No. US20030032075A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
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;; TITLE OF INVENTION: No. US20030032075A1el Telomerase  
;; NUMBER OF SEQUENCES: 225  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Townsend and Townsend and Crew LLP  
;; STREET: Two Embarcadero Center, 8th Floor  
;; CITY: San Francisco  
;; STATE: California  
;; COUNTRY: United States of America  
;; ZIP: 94111  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.30  
;; CURRENT APPLICATION NUMBER: US/10/053,758  
;; FILING DATE: 18-Jan-2002  
;; CLASSIFICATION: 536  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/854,050  
;; FILING DATE: 09-MAY-1997  
;; APPLICATION NUMBER: US 08/851,843  
;; FILING DATE: 06-MAY-1997  
;; APPLICATION NUMBER: US 08/846,017  
;; FILING DATE: 25-APR-1997  
;; APPLICATION NUMBER: US 08/844,419  
;; FILING DATE: 18-APR-1997  
;; APPLICATION NUMBER: US 08/724,643  
;; FILING DATE: 01-OCT-1996  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Apple, Randolph T.  
;; REGISTRATION NUMBER: 36,429  
;; REFERENCE/DOCKET NUMBER: 015389-002930US  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 576-0200  
;; TELEFAX: (415) 576-0300  
;; INFORMATION FOR SEQ ID NO: 162:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 27 amino acids  
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;; STRANDEDNESS: <Unknown>  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
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;; NAME/KEY: Peptide  
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;; Saccharomyces cerevisiae EST2"  
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QY 9 FTVKSCPDAl 18  
Db 8 FDVKSCYDSI 17  
  
RESULT 30  
US-10-054-295-162  
; Sequence 162, Application US/10054295  
; Publication No. US20030044953A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin  
; Andrews, William H.  
; TITLE OF INVENTION: No. US20030044953A1el Telomerase

;; NUMBER OF SEQUENCES: 225  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Townsend and Townsend and Crew LLP  
;; STREET: Two Embarcadero Center, 8th Floor  
;; CITY: San Francisco  
;; STATE: California  
;; COUNTRY: United States of America  
;; ZIP: 94111  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
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;; APPLICATION NUMBER: US 08/846,017  
;; FILING DATE: 25-APR-1997  
;; APPLICATION NUMBER: US 08/844,419  
;; FILING DATE: 18-APR-1997  
;; APPLICATION NUMBER: US 08/724,643  
;; FILING DATE: 01-OCT-1996  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Apple, Randolph T.  
;; REGISTRATION NUMBER: 36,429  
;; REFERENCE/DOCKET NUMBER: 015389-002930US  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 576-0200  
;; TELEFAX: (415) 576-0300  
;; INFORMATION FOR SEQ ID NO: 162:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 27 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: <Unknown>  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; FEATURE:  
;; NAME/KEY: Peptide  
;; LOCATION: 1..27  
;; OTHER INFORMATION: /note= "motif A peptide from  
;; Saccharomyces cerevisiae EST2"  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 162:  
US-10-054-295-162  
  
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Best Local Similarity 70.0%; Pred. No. 1.6e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
QY 9 FTVKSCPDAl 18  
Db 8 FDVKSCYDSI 17  
  
RESULT 31  
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; Sequence 162, Application US/10054611  
; Publication No. US20030059787A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin  
; Andrews, William H.  
; TITLE OF INVENTION: No. US20030059787A1el Telomerase  
; NUMBER OF SEQUENCES: 225  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
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FILING DATE: 18-Jan-2002  
CLASSIFICATION DATA:  
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FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0300  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 162:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..27  
OTHER INFORMATION: /note= "motif A peptide from Saccharomyces cerevisiae EST2"  
SEQUENCE DESCRIPTION: SEQ ID NO: 162:  
US-10-054-611-162  
Query Match 36.8%; Score 35; DB 4; Length 27;  
Best Local Similarity 70.0%; Pred. No. 1.6e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 9 FTVKSCPDAI 18  
Db 8 FDKVSCYDSI 17  
RESULT 32  
US-10-325-810-282  
Sequence 282, Application US/10325810  
Publication No. US20030204069A1  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin B.  
Andrews, William H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 633  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California

COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
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FILING DATE: 20-Dec-2002  
CLASSIFICATION DATA:  
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APPLICATION NUMBER: US/09/402,181  
FILING DATE: 29-Sep-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ausenhus, Scott L.  
REGISTRATION NUMBER: 42,271  
REFERENCE/DOCKET NUMBER: 015389-002620US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 282:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..27  
OTHER INFORMATION: /note= "motif A peptide from Saccharomyces cerevisiae EST2"  
SEQUENCE DESCRIPTION: SEQ ID NO: 282:  
US-10-325-810-282  
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Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 9 FTVKSCPDAI 18  
Db 8 FDKVSCYDSI 17  
RESULT 33  
US-10-877-124-282  
Sequence 282, Application US/10877124  
Publication No. US20040242529A1  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.

Harley, Calvin B.  
Andrews, William H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 727  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/877,124  
FILING DATE: 24-Jun-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/432,503  
FILING DATE: 02-Nov-1999  
APPLICATION NUMBER: 08/974,549  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph Ted  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 282:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..27  
OTHER INFORMATION: /note= "motif A peptide from  
Saccharomyces cerevisiae EST2"  
SEQUENCE DESCRIPTION: SEQ ID NO: 282:

Query Match 36.8%; Score 35; DB 5; Length 27;  
Best Local Similarity 70.0%; Pred. No. 1.6e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0;

QY 9 FTVKSCPDAI 18  
Db 8 FDKVSCYDSI 17

RESULT 34  
US-10-877-022-282  
; Sequence 282, Application US/10877022  
; Publication No. US20040247613A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin B.  
; Andrews, William H.  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 727  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
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; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/432,503  
; FILING DATE: 02-Nov-1999  
; APPLICATION NUMBER: 08/974,549  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; APPLICATION NUMBER: US 08/911,312  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: US 08/912,951  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: US 08/915,503  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: WO PCT/US97/17618  
; FILING DATE: 01-OCT-1997  
; APPLICATION NUMBER: WO PCT/US97/17885  
; FILING DATE: 01-OCT-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph Ted  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002610US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 282:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 27 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..27  
; OTHER INFORMATION: /note= "motif A peptide from  
; Saccharomyces cerevisiae EST2"



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/ SEQUENCE DESCRIPTION: SEQ ID NO: 282:
/ US-10-877-022-282
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/ Query Match          36.8%; Score 35; DB 5; Length 27;
/ Best Local Similarity 70.0%; Pred. No. 1.6e+02;
/ Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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/ QY 9 FTVKSCPDAl 18
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/ Db 8 FDVKSVCDSI 17
/
/ RESULT 35
/ US-10-877-146-282
/ Sequence 282, Application US/10877146
/ Publication No. US20050013825A1
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/      Lingner, Joachim
/      Nakamura, Toru
/      Chapman, Karen B.
/      Morin, Gregg B.
/      Harley, Calvin B.
/      Andrews, William H.
/ TITLE OF INVENTION: Human Telomerase Catalytic Subunit
/ NUMBER OF SEQUENCES: 727
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/877,146
/ FILING DATE: 24-Jun-2004
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/432,503
/ FILING DATE: 02-Nov-1999
/ APPLICATION NUMBER: 08/974,549
/ FILING DATE: <Unknown>
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
/ APPLICATION NUMBER: US 08/851,843
/ FILING DATE: 06-MAY-1997
/ APPLICATION NUMBER: US 08/854,050
/ FILING DATE: 09-MAY-1997
/ APPLICATION NUMBER: US 08/911,312
/ FILING DATE: 14-AUG-1997
/ APPLICATION NUMBER: US 08/912,951
/ FILING DATE: 14-AUG-1997
/ APPLICATION NUMBER: US 08/915,503
/ FILING DATE: 14-AUG-1997
/ APPLICATION NUMBER: WO PCT/US97/17618
/ FILING DATE: 01-OCT-1997
/ APPLICATION NUMBER: WO PCT/US97/17885
/ FILING DATE: 01-OCT-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph Ted
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002610US
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 282:
/
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 27 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ FEATURE:
/ NAME/KEY: Peptide
/ LOCATION: 1..27
/ OTHER INFORMATION: /note= "motif A peptide from
/      Saccharomyces cerevisiae EST2"
/ SEQUENCE DESCRIPTION: SEQ ID NO: 282:
/ US-10-877-146-282
/
/ Query Match          36.8%; Score 35; DB 5; Length 27;
/ Best Local Similarity 70.0%; Pred. No. 1.6e+02;
/ Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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/ QY 9 FTVKSCPDAl 18
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/ Db 8 FDVKSVCDSI 17
/
/ RESULT 36
/ US-10-044-692-45
/ Sequence 45, Application US/10044692
/ Publication No. US20030096344A1
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/      Lingner, Joachim
/      Nakamura, Toru
/      Chapman, Karen B.
/      Morin, Gregg B.
/      Harley, Calvin
/      Andrews, William H.
/ TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT:
/      THERAPEUTIC METHODS
/ NUMBER OF SEQUENCES: 335
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, 8th Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: United States of America
/ ZIP: 94111
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
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/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
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/ FILING DATE: 11-Jan-2002
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/912,951
/ FILING DATE: <Unknown>
/ APPLICATION NUMBER: US 08/854,050
/ FILING DATE: 09-MAY-1997
/ APPLICATION NUMBER: US 08/851,843
/ FILING DATE: 06-MAY-1997
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph T.
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002600US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
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/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 45:
/ SEQUENCE CHARACTERISTICS:
/   LENGTH: 34 amino acids
/   TYPE: amino acid
/   STRANDEDNESS: <Unknown>
/   TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ FEATURE:
/   NAME/KEY: Peptide
/   LOCATION: 1..34
/ OTHER INFORMATION: /note= "motif A peptide from
/   Saccharomyces cerevisiae EST2p"
/ SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-10-044-692-45

Query Match      36.8%; Score 35; DB 4; Length 34;
Best Local Similarity 70.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      9 FTVKSCPDAL 18
Db      10 FDKSCYDSI 19

RESULT 37
US-10-044-539-45
/ Sequence 45, Application US/10044539
/ Publication No. US20030100093A1
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/   Lingner, Joachim
/   Nakamura, Toru
/   Chapman, Karen B.
/   Morin, Gregg B.
/   Harley, Calvin
/   Andrews, William H.
/ TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
/   THERAPEUTIC METHODS
/ NUMBER OF SEQUENCES: 335
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, 8th Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: United States of America
/ ZIP: 94111
/ COMPUTER READABLE FORM:
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/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/044,539
/ FILING DATE: 11-Jan-2002
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/912,951
/ FILING DATE: <Unknown>
/ APPLICATION NUMBER: US 08/854,050
/ FILING DATE: 09-MAY-1997
/ APPLICATION NUMBER: US 08/851,843
/ FILING DATE: 06-MAY-1997
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph T.
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-00260005

/
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 45:
/ SEQUENCE CHARACTERISTICS:
/   LENGTH: 34 amino acids
/   TYPE: amino acid
/   STRANDEDNESS: <Unknown>
/   TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ FEATURE:
/   NAME/KEY: Peptide
/   LOCATION: 1..34
/ OTHER INFORMATION: /note= "motif A peptide from
/   Saccharomyces cerevisiae EST2p"
/ SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-10-044-539-45

Query Match      36.8%; Score 35; DB 4; Length 34;
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Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      9 FTVKSCPDAL 18
Db      10 FDKSCYDSI 19

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/ Publication No. US20030204069A1
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/   Lingner, Joachim
/   Nakamura, Toru
/   Chapman, Karen B.
/   Morin, Gregg B.
/   Harley, Calvin B.
/   Andrews, William H.
/ TITLE OF INVENTION: Human Telomerase Catalytic Subunit
/ NUMBER OF SEQUENCES: 633
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
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/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/325,810
/ FILING DATE: 20-Dec-2002
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/402,181
/ FILING DATE: 29-Sep-1997
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
/ APPLICATION NUMBER: US 08/851,843
/ FILING DATE: 06-MAY-1997
/ APPLICATION NUMBER: US 08/854,050
/ FILING DATE: 09-MAY-1997
/ APPLICATION NUMBER: US 08/911,312
/ FILING DATE: 14-AUG-1997
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; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: US 08/915,503  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: WO PCT/US97/17885  
; FILING DATE: 01-OCT-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ausenhus, Scott L.  
; REGISTRATION NUMBER: 42,271  
; REFERENCE/DOCKET NUMBER: 015389-002620US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 45:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 34 amino acids  
; TYPE: amino acid  
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; Saccharomyces cerevisiae EST2p"  
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; Sequence 45, Application US/10877124  
; Publication No. US20040242529A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin B.  
; Andrews, William H.  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 727  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
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; FILING DATE: 02-Nov-1999  
; APPLICATION NUMBER: 08/974,549  
; FILING DATE: <Unknown>  
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; FILING DATE: 25-APR-1997  
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; FILING DATE: 06-MAY-1997  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
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; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: US 08/912,951  
; FILING DATE: 14-AUG-1997  
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; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: WO PCT/US97/17618  
; FILING DATE: 01-OCT-1997  
; APPLICATION NUMBER: WO PCT/US97/17885  
; FILING DATE: 01-OCT-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph Ted  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002610US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 45:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 34 amino acids  
; TYPE: amino acid  
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; SEQUENCE DESCRIPTION: SEQ ID NO: 45:  
US-10-877-124-45  
  
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; Sequence 45, Application US/10877022  
; Publication No. US20040247613A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin B.  
; Andrews, William H.  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 727  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
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; FILING DATE: 24-Jun-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,503
; FILING DATE: 02-Nov-1999
; APPLICATION NUMBER: 08/974,549
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
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; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
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; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17895
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
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; Saccharomyces cerevisiae EST2p"
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US-10-877-022-45

Query Match 36.8%; Score 35; DB 5; Length 34;
Best Local Similarity 70.0%; Pred. No. 2.1e+02;
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QY 9 FTVKSCPDAL 18
Db 10 FDVKSCTDSI 19

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Search completed: January 20, 2006, 17:38:20  
Job time : 35.4444 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:30:50 ; Search time 3.11111 Seconds  
(without alignments)  
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Title: US-10-619-323-6

Perfect score: 95  
Sequence: 1 PKKDVLETFVKSCPD1 18

Scoring table: BLOSUM62  
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Searched: 70606 seqs, 1013881 residues

Total number of hits satisfying chosen parameters: 41278

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : Published Applications AA New:\*\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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2	34	35.8	34	US-10-816-768-30	Sequence 30, Appl
3	32	33.7	34	US-10-816-768-29	Sequence 29, Appl
4	31	32.6	37	US-10-957-351-6	Sequence 6, Appl
5	30	31.6	35	US-10-957-351-34	Sequence 34, Appl
6	29.5	31.1	33	US-11-121-301-50	Sequence 50, Appl
7	29	30.5	44	US-10-986-501-356	Sequence 356, Appl
8	28	29.5	32	US-10-957-351-196	Sequence 196, Appl
9	28	29.5	35	US-10-957-351-112	Sequence 112, Appl
10	28	29.5	38	US-10-957-351-183	Sequence 183, Appl
11	28	29.5	44	US-10-467-657-1118	Sequence 1118, Appl
12	28	29.5	44	US-10-957-887B-278	Sequence 278, Appl
13	27	28.4	9	US-10-859-643-2	Sequence 2, Appl
14	27	28.4	9	US-10-859-643-254	Sequence 254, Appl
15	27	28.4	9	US-10-859-643-690	Sequence 690, Appl
16	27	28.4	9	US-11-097-864-2	Sequence 2, Appl
17	27	28.4	9	US-11-097-864-254	Sequence 254, Appl
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23	27	28.4	10	US-11-097-864-350	Sequence 350, Appl
24	27	28.4	10	US-11-097-912-350	Sequence 350, Appl
25	27	28.4	15	US-11-019-894A-28	Sequence 28, Appl

26	27	28.4	17	6	US-10-723-207-72	Sequence 72, Appl
27	27	28.4	19	6	US-10-503-575-192	Sequence 192, Appl
28	27	28.4	21	6	US-10-467-657-3848	Sequence 3848, Appl
29	27	28.4	30	6	US-10-467-657-5752	Sequence 5752, Appl
30	27	28.4	35	6	US-10-467-657-7362	Sequence 7362, Appl
31	27	28.4	35	6	US-10-467-657-8218	Sequence 8218, Appl
32	27	28.4	35	6	US-10-957-351-195	Sequence 195, Appl
33	27	28.4	35	7	US-11-121-301-23	Sequence 23, Appl
34	27	28.4	38	6	US-10-957-351-155	Sequence 155, Appl
35	27	28.4	47	7	US-11-123-896-453	Sequence 453, Appl
36	26.5	27.9	33	7	US-11-121-301-49	Sequence 49, Appl
37	26.5	27.9	43	6	US-10-467-657-2778	Sequence 2778, Appl
38	26	27.4	16	6	US-10-723-207-50	Sequence 50, Appl
39	26	27.4	16	7	US-11-054-515-2313	Sequence 2313, Appl
40	26	27.4	20	6	US-10-623-155-407	Sequence 407, Appl
41	26	27.4	20	6	US-10-623-155-518	Sequence 518, Appl
42	26	27.4	30	6	US-10-467-657-6636	Sequence 6636, Appl
43	26	27.4	30	6	US-10-467-657-8160	Sequence 8160, Appl
44	26	27.4	34	6	US-10-816-768-33	Sequence 33, Appl
45	26	27.4	43	6	US-10-957-887B-91	Sequence 91, Appl
46	26	27.4	44	6	US-10-957-887B-4	Sequence 4, Appl
47	26	27.4	44	6	US-10-957-887B-4	Sequence 4, Appl
48	25.5	26.8	13	6	US-10-511-559-223	Sequence 223, Appl
49	25.5	26.8	35	6	US-10-816-768-3	Sequence 3, Appl
50	25.5	26.8	37	7	US-11-033-039-169	Sequence 169, Appl

## ALIGNMENTS

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; GENERAL INFORMATION:  
; APPLICANT: Oppermann, Hermann  
; APPLICANT: Tai, Mei-Sheng  
; APPLICANT: McCartney, John  
; TITLE OF INVENTION: Modified TGF-beta Superfamily Proteins  
; FILE REFERENCE: STK-075  
; CURRENT APPLICATION NUMBER: US/10/816,768  
; CURRENT FILING DATE: 2004-04-02  
; NUMBER OF SEQ ID NOS: 124  
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; SEQ ID NO 31  
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RESULT 2  
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; Sequence 30, Application US/10816768  
; Publication No. US20050250936A1  
; GENERAL INFORMATION:  
; APPLICANT: Oppermann, Hermann  
; APPLICANT: Tai, Mei-Sheng  
; APPLICANT: McCartney, John  
; TITLE OF INVENTION: Modified TGF-beta Superfamily Proteins  
; FILE REFERENCE: STK-075  
; CURRENT APPLICATION NUMBER: US/10/816,768  
; CURRENT FILING DATE: 2004-04-02

; NUMBER OF SEQ ID NOS: 124  
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Db 18 PKIEQLSNMIVKSC 31

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; GENERAL INFORMATION:  
; APPLICANT: Oppermann, Hermann  
; APPLICANT: Tai, Mei-Sheng  
; APPLICANT: McCartney, John  
; TITLE OF INVENTION: Modified TGF-beta Superfamily Proteins  
; FILE REFERENCE: STK-075  
; CURRENT APPLICATION NUMBER: US/10/816,768  
; CURRENT FILING DATE: 2004-04-02  
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; GENERAL INFORMATION:  
; APPLICANT: Stemmer, Willem P. C.  
; APPLICANT: Perlrath, D. Victor  
; APPLICANT: Satyal, Sanjeev  
; APPLICANT: Avidia Research Institute  
; TITLE OF INVENTION: c-Met Kinase Binding Proteins  
; FILE REFERENCE: 022013-001400US  
; CURRENT APPLICATION NUMBER: US/10/957,351  
; CURRENT FILING DATE: 2004-09-30  
; PRIOR APPLICATION NUMBER: US 10/871,602  
; PRIOR FILING DATE: 2004-06-17  
; NUMBER OF SEQ ID NOS: 471  
; SOFTWARE: FastSeq for Windows Version 3.0  
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US-10-957-351-6

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; Sequence 34, Application US/10957351  
; Publication No. US20060008844A1  
; GENERAL INFORMATION:  
; APPLICANT: Stemmer, Willem P. C.  
; APPLICANT: Perlrath, D. Victor  
; APPLICANT: Satyal, Sanjeev  
; APPLICANT: Avidia Research Institute  
; TITLE OF INVENTION: c-Met Kinase Binding Proteins  
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US-11-121-301-50  
; Sequence 50, Application US/11121301  
; Publication No. US20050277176A1  
; GENERAL INFORMATION:  
; APPLICANT: MCCRAY, JR., PAUL B.  
; APPLICANT: SCHUTTE, BRIAN C.  
; APPLICANT: JIA, HONG PENG  
; APPLICANT: CASAVANT, THOMAS L.  
; TITLE OF INVENTION: HUMAN AND MOUSE b-DEFENSINS, ANTIMICROBIAL PEPTIDES  
; FILE REFERENCE: IOWA:041USDI  
; CURRENT APPLICATION NUMBER: US/11/121,301  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/323,991  
; PRIOR FILING DATE: 2001-09-21  
; PRIOR APPLICATION NUMBER: 10/252,734  
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; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: P2013P2C1
; CURRENT APPLICATION NUMBER: US/10/986,501
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US/10/621,363
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/969,730
; PRIOR FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: 09/774,639
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/238,291
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: PCT/US98/16235
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/056,371
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,732
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,366
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,364
; PRIOR FILING DATE: 1997-08-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 373
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 356
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-986-501-356

Query Match      30.5%; Score 29; DB 6; Length 44;
Best Local Similarity 38.5%; Pred. No. 95;
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY      6  LETFTVKSCPD 18
      :|| ||| :
Db      28  IQRTAVSCVDGV 40

RESULT 8
US-10-957-351-196
; Sequence 196, Application US/10957351
; Publication No. US20060008844A1
; GENERAL INFORMATION:
; APPLICANT: Stemmer, Willem P. C.
; APPLICANT: Perlroth, D. Victor
; APPLICANT: Satyal, Sanjeev
; APPLICANT: Avidia Research Institute
; TITLE OF INVENTION: c-Met Kinase Binding Proteins
; FILE REFERENCE: 022013-001400US
; CURRENT APPLICATION NUMBER: US/10/957,351
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: US 10/871,602
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 471
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 196
; LENGTH: 32

QY      11 VKSCPD 16
      || : |||
Db      23  VRDCPD 28

RESULT 9
US-10-957-351-112
; Sequence 112, Application US/10957351
; Publication No. US20060008844A1
; GENERAL INFORMATION:
; APPLICANT: Stemmer, Willem P. C.
; APPLICANT: Perlroth, D. Victor
; APPLICANT: Satyal, Sanjeev
; APPLICANT: Avidia Research Institute
; TITLE OF INVENTION: c-Met Kinase Binding Proteins
; FILE REFERENCE: 022013-001400US
; CURRENT APPLICATION NUMBER: US/10/957,351
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: US 10/871,602
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 471
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 112
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human LDL-receptor class A domain
US-10-957-351-112

Query Match      29.5%; Score 28; DB 6; Length 35;
Best Local Similarity 66.7%; Pred. No. 11e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      11 VKSCPD 16
      || : |||
Db      23  VRDCPD 28

RESULT 10
US-10-957-351-183
; Sequence 183, Application US/10957351
; Publication No. US20060008844A1
; GENERAL INFORMATION:
; APPLICANT: Stemmer, Willem P. C.
; APPLICANT: Perlroth, D. Victor
; APPLICANT: Satyal, Sanjeev
; APPLICANT: Avidia Research Institute
; TITLE OF INVENTION: c-Met Kinase Binding Proteins
; FILE REFERENCE: 022013-001400US
; CURRENT APPLICATION NUMBER: US/10/957,351
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: US 10/871,602
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 471
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 183
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human LDL-receptor class A domain
US-10-957-351-183
```

```
Query Match      29.5%; Score 28; DB 6; Length 38;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 VKSCPD 16
Db 24 VRQCPD 29

RESULT 11
US-10-467-657-1118
; Sequence 1118, Application US/10467657
; Publication No. US20050360581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1118
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1118

Query Match      29.5%; Score 28; DB 6; Length 44;
Best Local Similarity 38.9%; Pred. No. 1.4e+02;
Matches 7; Conservative 2; Mismatches 7; Indels 2; Gaps 1;

QY 1 PKKVLETFYTKS--CPD 16
Db 25 PRLAVLSVLSAASPCPD 42

RESULT 12
US-10-957-887B-278
; Sequence 278, Application US/10957887B
; Publication No. US20050272677A1
; GENERAL INFORMATION:
; APPLICANT: Friesen, Robert H. E.
; APPLICANT: Leenhouts, Cornelius J.
; APPLICANT: Hektor, Harm
; APPLICANT: van Esch, Johannes H.
; APPLICANT: Heeres, Andre
; TITLE OF INVENTION: DELIVERY OF A SUBSTANCE TO A PRE-DETERMINED SITE
; FILE REFERENCE: 2183-6668US
; CURRENT APPLICATION NUMBER: US/10/957,887B
; CURRENT FILING DATE: 2004-10-04
; PRIOR APPLICATION NUMBER: PCT/NL/00256
; PRIOR FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 278
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Sinorhizobium meliloti
US-10-957-887B-278

Query Match      29.5%; Score 28; DB 6; Length 44;
Best Local Similarity 38.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 PKKVLETFYTKS 13
Db 13 PRLAVLSVLSAASPCPD 42

Query Match      29.5%; Score 28; DB 6; Length 38;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 VKSCPD 16
Db 24 VRQCPD 29

RESULT 13
US-10-859-643-2
; Sequence 2, Application US/10859643
; Publication No. US20060002993A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 511582006203
; CURRENT APPLICATION NUMBER: US/10/859,643
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-859-643-2

Query Match      28.4%; Score 27; DB 6; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKSCPD 16
Db 2 VESCPD 7

RESULT 14
US-10-859-643-254
; Sequence 254, Application US/10859643
; Publication No. US20060002993A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 511582006203
; CURRENT APPLICATION NUMBER: US/10/859,643
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 254
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-859-643-254

Query Match      28.4%; Score 27; DB 6; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKSCPD 16
Db 2 VESCPD 7
```



```
RESULT 15
US-10-859-643-690
; Sequence 690, Application US/10859643
; Publication No. US2006002993A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 511582006203
; CURRENT APPLICATION NUMBER: US/10/859,643
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 690
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-859-643-690

Query Match      28.4%; Score 27; DB 6; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      11 VKSCPD 16
DB      2 VESCP 7

RESULT 16
US-11-097-864-2
; Sequence 2, Application US/11097864
; Publication No. US2005026592A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 511582006205
; CURRENT APPLICATION NUMBER: US/11/097,864
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-864-2

Query Match      28.4%; Score 27; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      11 VKSCPD 16
DB      2 VESCP 7

RESULT 17
US-11-097-864-254
; Sequence 254, Application US/11097864
; Publication No. US2005026592A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 511582006205
; CURRENT APPLICATION NUMBER: US/11/097,864
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 254
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-864-254

Query Match      28.4%; Score 27; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      11 VKSCPD 16
DB      2 VESCP 7

RESULT 18
US-11-097-864-690
; Sequence 690, Application US/11097864
; Publication No. US2005026592A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 511582006205
; CURRENT APPLICATION NUMBER: US/11/097,864
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 690
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-864-690

Query Match      28.4%; Score 27; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      11 VKSCPD 16
DB      2 VESCP 7
```

```
Db          2 VESCP 7

RESULT 19
US-11-097-912-2
; Sequence 2, Application US/11097912
; Publication No. US20050265921A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B
; FILE REFERENCE: 511582006204
; CURRENT APPLICATION NUMBER: US/11/097,912
; PRIOR FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-912-2

Query Match      28.4%; Score 27; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY          11 VKSCPD 16
|:|:|:
Db          2 VESCP 7

RESULT 20
US-11-097-912-254
; Sequence 254, Application US/11097912
; Publication No. US20050265921A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B
; FILE REFERENCE: 511582006204
; CURRENT APPLICATION NUMBER: US/11/097,912
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 254
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-912-254

Query Match      28.4%; Score 27; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY          11 VKSCPD 16
|:|:|:
Db          2 VESCP 7

RESULT 21
US-11-097-912-690
; Sequence 690, Application US/11097912
; Publication No. US20050265921A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B
; FILE REFERENCE: 511582006204
; CURRENT APPLICATION NUMBER: US/11/097,912
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 690
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-912-690

Query Match      28.4%; Score 27; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY          11 VKSCPD 16
|:|:|:
Db          2 VESCP 7

RESULT 22
US-10-859-643-350
; Sequence 350, Application US/10859643
; Publication No. US20060002993A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 511582006203
; CURRENT APPLICATION NUMBER: US/10/859,643
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 350
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-859-643-350

Query Match      28.4%; Score 27; DB 6; Length 10;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY          11 VKSCPD 16
```

Db 11 VKSCPD 8  
|:|:|:|:  
3 VESCPF 8

## RESULT 23

US-11-097-864-350  
; Sequence 350, Application US/11097864  
; Publication No. US20050265924A1  
; GENERAL INFORMATION:  
; APPLICANT: Challita-Bid, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Faris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B  
; FILE REFERENCE: 511582006205  
; CURRENT APPLICATION NUMBER: US/11/097,864  
; CURRENT FILING DATE: 2005-04-01  
; PRIOR APPLICATION NUMBER: US 10/062,109  
; PRIOR FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: US 10/005,480  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 765  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 350  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-11-097-864-350

Query Match 28.4%; Score 27; DB 7; Length 10;  
Best Local Similarity 66.7%; Pred. No. 41;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VKSCPD 16  
|:|:|:|:  
Db 3 VESCPF 8

## RESULT 24

US-11-097-912-350  
; Sequence 350, Application US/11097912  
; Publication No. US20050265921A1  
; GENERAL INFORMATION:  
; APPLICANT: Challita-Bid, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Faris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B  
; FILE REFERENCE: 511582006204  
; CURRENT APPLICATION NUMBER: US/11/097,912  
; CURRENT FILING DATE: 2005-04-01  
; PRIOR APPLICATION NUMBER: US 10/062,109  
; PRIOR FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: US 10/005,480  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 765  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 350  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-11-097-912-350

Query Match 28.4%; Score 27; DB 7; Length 10;  
Best Local Similarity 66.7%; Pred. No. 41;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VKSCPD 16  
|:|:|:|:  
Db 3 VESCPF 8

## RESULT 25

US-11-019-894A-28  
; Sequence 28, Application US/11019894A  
; Publication No. US20050245451A1  
; GENERAL INFORMATION:  
; APPLICANT: Pincus, Matthew R.  
; TITLE OF INVENTION: PEPTIDES SELECTIVELY LETHAL TO THE MALIGNANT AND TRANSFORMED  
; FILE REFERENCE: 1181-17 CIP A  
; CURRENT APPLICATION NUMBER: US/11/019,894A  
; CURRENT FILING DATE: 2004-12-21  
; PRIOR APPLICATION NUMBER: 10/386,737  
; PRIOR FILING DATE: 2003-03-12  
; PRIOR APPLICATION NUMBER: 09/827,683  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/195,102  
; PRIOR FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: 60/363,785  
; PRIOR FILING DATE: 2002-03-12  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 28  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: peptide; retro-inverso peptide analog of SEQ ID NO:1;  
; OTHER INFORMATION: all D-amino acids  
US-11-019-894A-28

Query Match 28.4%; Score 27; DB 7; Length 15;  
Best Local Similarity 50.0%; Pred. No. 63;  
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 6 LETFTVKSCP 15  
|:|:|:|:  
Db 5 LDSFTEQSLP 14

## RESULT 26

US-10-723-207-72  
; Sequence 72, Application US/10723207  
; Publication No. US20050250934A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Chang Yi  
; APPLICANT: Walfield, Alan M.  
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF  
; FILE REFERENCE: 1151-4153US2  
; CURRENT APPLICATION NUMBER: US/10/723,207  
; CURRENT FILING DATE: 2003-11-24  
; PRIOR APPLICATION NUMBER: 09/701,623  
; PRIOR FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: PCT/US99/13959  
; PRIOR FILING DATE: 1999-06-21  
; PRIOR APPLICATION NUMBER: 09/100,287  
; PRIOR FILING DATE: 1998-06-20  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 72  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide  
; OTHER INFORMATION: synthesized from amino acids with no genetic  
; OTHER INFORMATION: material as source  
US-10-723-207-72

```
Query Match      28.4%; Score 27; DB 6; Length 17;
Best Local Similarity 36.4%; Pred. No. 73;
Matches 4; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 3 KDVLFTFTVKS 13
   :|::|||:|
Db 3 RDIIDFTNES 13

RESULT 27
US-10-503-575-192
; Sequence 192, Application US/10503575
; Publication No. US20050244823A1
; GENERAL INFORMATION:
; APPLICANT: Drijfhout, Jan Wouter
; APPLICANT: van Veelen, Petrus Antonius
; APPLICANT: Koning, Frits
; TITLE OF INVENTION: NOVEL EPITOPES FOR CELIAC DISEASE AND AUTOIMMUNE DISEASES, METHOD
; TITLE OF INVENTION: DETECTING THOSE AND NOVEL NON-ANTIGENIC FOOD COMPOUNDS
; FILE REFERENCE: 2799/72843-PCT-US
; CURRENT APPLICATION NUMBER: US/10/503,575
; PRIOR FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: PCT/NL03/00077
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: EP 02075456.0
; PRIOR FILING DATE: 2002-02-04
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 192
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-503-575-192

Query Match      28.4%; Score 27; DB 6; Length 19;
Best Local Similarity 62.5%; Pred. No. 82;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 ETFTVKSC 14
   :|::|||
Db 1 DDFTGKSC 8

RESULT 28
US-10-467-657-3848
; Sequence 3848, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3848
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3848

Query Match      28.4%; Score 27; DB 6; Length 21;
Best Local Similarity 66.7%; Pred. No. 92;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 VKSCPD 16
   :|::|||
```

```
Db 9 LKPCPD 14
   :|::|||

RESULT 29
US-10-467-657-5752
; Sequence 5752, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5752
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5752

Query Match      28.4%; Score 27; DB 6; Length 30;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 TVKSCP 15
   :|::|||
Db 10 SVKACP 15

RESULT 30
US-10-467-657-7362
; Sequence 7362, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7362
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7362

Query Match      28.4%; Score 27; DB 6; Length 35;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

QY 5 VLETFTVKS--CPD 16
   |||:|::|||
Db 6 VLSVLSVASSPCPD 19
   :|::|||

RESULT 31
US-10-467-657-8218
; Sequence 8218, Application US/10467657
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; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASNAGNI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 8218  
; LENGTH: 35  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-8218

Query Match 28.4%; Score 27; DB 6; Length 35;  
Best Local Similarity 50.0%; Pred. No. 1.6e+02;  
Matches 7; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

QY 5 VLETFVTKS--CPD 16  
|||:|:|  
Db 6 VLSVLSVASSPCPD 19

RESULT 32  
US-10-957-351-195  
; Sequence 195, Application US/10957351  
; Publication No. US2006000844A1  
; GENERAL INFORMATION:  
; APPLICANT: Stemmer, Willem P. C.  
; APPLICANT: Perltroth, D. Victor  
; APPLICANT: Satyal, Sanjeev  
; APPLICANT: Avidia Research Institute  
; TITLE OF INVENTION: c-Met Kinase Binding Proteins  
; FILE REFERENCE: 022013-001400US  
; CURRENT APPLICATION NUMBER: US/10/957,351  
; CURRENT FILING DATE: 2004-09-30  
; PRIOR APPLICATION NUMBER: US 10/871,602  
; PRIOR FILING DATE: 2004-06-17  
; NUMBER OF SEQ ID NOS: 471  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 195  
; LENGTH: 35  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: human LDL-receptor class A domain  
US-10-957-351-195

Query Match 28.4%; Score 27; DB 6; Length 35;  
Best Local Similarity 66.7%; Pred. No. 1.6e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 VKSCPD 16  
|:|  
Db 23 VQCCPD 28

RESULT 33  
US-11-121-301-23  
; Sequence 23, Application US/11121301  
; Publication No. US20050277176A1  
; GENERAL INFORMATION:  
; APPLICANT: MCCRAY, JR., PAUL B.  
; APPLICANT: SCHUTTE, BRIAN C.  
; APPLICANT: JIA, HONG PENG  
; APPLICANT: CASAVANT, THOMAS L.

; TITLE OF INVENTION: HUMAN AND MOUSE b-DEFENSINS, ANTIMICROBIAL PEPTIDES  
; FILE REFERENCE: IOWA:041USD1  
; CURRENT APPLICATION NUMBER: US/11/121,301  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/323,991  
; PRIOR FILING DATE: 2001-09-21  
; PRIOR APPLICATION NUMBER: 10/252,734  
; PRIOR FILING DATE: 2002-09-23  
; NUMBER OF SEQ ID NOS: 82  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 35  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-121-301-23

Query Match 28.4%; Score 27; DB 7; Length 35;  
Best Local Similarity 44.4%; Pred. No. 1.6e+02;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 7 ETEFVKSCP 15  
:|:|:|  
Db 8 DTCRLKNCP 16

RESULT 34  
US-10-957-351-155  
; Sequence 155, Application US/10957351  
; Publication No. US2006000844A1  
; GENERAL INFORMATION:  
; APPLICANT: Stemmer, Willem P. C.  
; APPLICANT: Perltroth, D. Victor  
; APPLICANT: Satyal, Sanjeev  
; APPLICANT: Avidia Research Institute  
; TITLE OF INVENTION: c-Met Kinase Binding Proteins  
; FILE REFERENCE: 022013-001400US  
; CURRENT APPLICATION NUMBER: US/10/957,351  
; CURRENT FILING DATE: 2004-09-30  
; PRIOR APPLICATION NUMBER: US 10/871,602  
; PRIOR FILING DATE: 2004-06-17  
; NUMBER OF SEQ ID NOS: 471  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 155  
; LENGTH: 38  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: human LDL-receptor class A domain  
US-10-957-351-155

Query Match 28.4%; Score 27; DB 6; Length 38;  
Best Local Similarity 80.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 KSCPD 16  
|:|  
Db 26 KDCPD 30

RESULT 35  
US-11-123-896-453  
; Sequence 453, Application US/11123896  
; Publication No. US20050273861A1  
; GENERAL INFORMATION:  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Navarro Acevedo, Pedro A.  
; APPLICANT: Harvell, Leslie  
; APPLICANT: Cahoon, Rebecca  
; APPLICANT: McCutchen, Billy Fred  
; APPLICANT: Lu, Albert  
; APPLICANT: Herrmann, Rafael  
; APPLICANT: Wong, James  
; TITLE OF INVENTION: Defensin Polynucleotides and Methods of

```
; TITLE OF INVENTION: Use
; FILE REFERENCE: 35718/246703
; CURRENT APPLICATION NUMBER: US/11/123,896
; CURRENT FILING DATE: 2005-05-06
; PRIOR APPLICATION NUMBER: 60/300,152
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/300,241
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 453
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Arachis hypogaea
US-11-123-896-453

Query Match      28.4%; Score 27; DB 7; Length 47;
Best Local Similarity 62.5%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 FTVKSCPD 16
Db 15 FITGSCDD 22

RESULT 36
US-11-121-301-49
; Sequence 49, Application US/11121301
; Publication No. US20050277176A1
; GENERAL INFORMATION:
; APPLICANT: MCCRAY, JR., PAUL B.
; APPLICANT: SCHUTTIE, BRIAN C.
; APPLICANT: JIA, HONG PENG
; TITLE OF INVENTION: HUMAN AND MOUSE b-DEFENSINS, ANTIMICROBIAL PEPTIDES
; FILE REFERENCE: IOWA:041USD1
; CURRENT APPLICATION NUMBER: US/11/121,301
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/323,991
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 10/252,734
; PRIOR FILING DATE: 2002-09-23
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-121-301-49

Query Match      27.9%; Score 26.5; DB 7; Length 33;
Best Local Similarity 54.5%; Pred. No. 1.8e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 7 ETFTVKSCPD 17
Db 18 ETY-MHLCPD 27

RESULT 37
US-10-467-657-2778
; Sequence 2778, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11

; TITLE OF INVENTION: Use
; FILE REFERENCE: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2778
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2778

Query Match      27.9%; Score 26.5; DB 6; Length 43;
Best Local Similarity 53.8%; Pred. No. 2.5e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 3; Gaps 1;

QY 2 KKVLETFVKSC 14
Db 20 KKVLETFVKSC 29

RESULT 38
US-10-723-207-50
; Sequence 50, Application US/10723207
; Publication No. US20050250934A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; APPLICANT: Walfield, Alan M.
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
; TITLE OF INVENTION: ALLERGY
; FILE REFERENCE: 1151-4153US2
; CURRENT APPLICATION NUMBER: US/10/723,207
; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: 09/701,623
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/13959
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 09/100,287
; PRIOR FILING DATE: 1998-06-20
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
; OTHER INFORMATION: synthesized from amino acids with no genetic
; OTHER INFORMATION: material as source
US-10-723-207-50

Query Match      27.4%; Score 26; DB 6; Length 16;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 TFTVKSC 14
Db 10 TLTVTSC 16

RESULT 39
US-11-054-515-2313
; Sequence 2313, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind BlyS
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
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; PRIOR FILING DATE: 2002-11-14  
; PRIOR APPLICATION NUMBER: 60/331,469  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/340,817  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 3247  
; SEQ ID NO 2313  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-054-515-2313

Query Match 27.4%; Score 26; DB 7; Length 16;  
Best Local Similarity 31.2%; Pred. No. 1e+02;  
Matches 5; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 PKKDVLETFVTKSCPD 16  
DB 1 PFYDVLTSVLEFFPD 16

RESULT 40  
US-10-623-155-407  
; Sequence 407, Application US/10623155  
; Publication No. US20050261166A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Peckham, David W.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Fanger, Gary R.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.455C20  
; CURRENT APPLICATION NUMBER: US/10/623,155  
; CURRENT FILING DATE: 2003-07-17  
; NUMBER OF SEQ ID NOS: 560  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 407  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-623-155-407

Query Match 27.4%; Score 26; DB 6; Length 20;  
Best Local Similarity 71.4%; Pred. No. 1.3e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 LETFTVK 12  
DB 5 LENFTLK 11

Search completed: January 20, 2006, 17:38:44  
Job time : 4.1111 secs

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OM protein - protein search, using sw model

Run on: January 20, 2006, 17:23:49 ; Search time 6.66667 Seconds  
(without alignments)  
259.785 Million cell updates/sec

Title: US-10-619-323-6  
Perfect score: 95  
Sequence: 1 PKNDVLETFVKSCPDAL 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 11837

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 50 summaries

Database : PIR 80.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	35.8	15	S03353	plastocyanin - Mic
2	33	34.7	41	G72312	hypothetical prote
3	32	33.7	49	S72793	cysteine synthase
4	31	32.6	38	S12409	ribosomal protein
5	31	32.6	44	AD1753	Lactococcus lactis
6	31	32.6	50	AB0925	hypothetical prote
7	30	31.6	50	A81546	hypothetical prote
8	29	30.5	12	A61309	glycoprotein hormo
9	29	30.5	32	S11610	ribosomal protein
10	29	30.5	34	F95187	hypothetical prote
11	28	29.5	33	A06001	keratin, 55k, nucl
12	28	29.5	38	A70022	kalikrein - mouse
13	28	29.5	42	T07581	hypothetical prote
14	28	29.5	43	A34071	gag polyprotein -
15	28	29.5	44	T07537	hypothetical prote
16	28	29.5	45	S36709	B7 protein - equin
17	28	29.5	46	H71262	hypothetical prote
18	28	29.5	48	A32457	myeloperoxidase [E
19	27.5	28.9	36	1 WISNWA	alpha-amylase inh
20	27.5	28.9	41	C39558	matricoxin A - el
21	27	28.4	21	A60225	pyruvate dehydroge
22	27	28.4	33	S22603	ribosomal protein
23	27	28.4	37	T29808	hypothetical prote
24	27	28.4	39	T03344	gene e23 protein -
25	27	28.4	45	1 HPBO	hapctoglobin precu
26	27	28.4	45	JS0655	hypothetical 5K pr
27	27	28.4	48	T07305	hypothetical prote
28	27	28.4	48	AB1181	hypothetical prote
29	26.5	27.9	30	D70253	conserved hypothet

30	26.5	27.9	34	2	S65371	tRNA-guanine trans
31	26	27.4	19	2	PA0012	superoxide dismuta
32	26	27.4	23	2	D60583	glycoprotein hormo
33	26	27.4	27	2	C85939	hypothetical prote
34	26	27.4	30	2	A60914	pheromone-binding
35	26	27.4	33	2	C82312	hypothetical prote
36	26	27.4	35	2	S29726	lignin peroxidase
37	26	27.4	35	2	S29728	lignin peroxidase
38	26	27.4	35	2	S29729	manganese(II) pero
39	26	27.4	35	2	S29731	manganese(II) pero
40	26	27.4	36	2	S70092	hypothetical prote
41	26	27.4	38	2	I70018	kalikrein - mouse
42	26	27.4	45	2	S43149	ig upsilon chain -
43	26	27.4	48	2	C70864	hypothetical prote
44	26	27.4	48	2	AC1538	hypothetical prote
45	26	27.4	49	2	D70091	hypothetical prote
46	26	27.4	50	2	G97151	hypothetical prote
47	25.5	26.8	26	2	A44036	collagen alpha 1(X
48	25	26.3	21	2	D42762	proteasome endopep
49	25	26.3	23	2	S72535	probable acr-2 reg
50	25	26.3	33	2	H72332	hypothetical prote

## ALIGNMENTS

RESULT 1  
S03353  
plastocyanin - Microcystis aeruginosa (fragment)  
C:Species: Microcystis aeruginosa  
C:Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 09-Jul-2004  
C:Accession: S03353  
R:Tan, S.; Ho, K.K.  
Biochim. Biophys. Acta 973, 111-117, 1989  
A:Title: Purification of an acidic plastocyanin from Microcystis aeruginosa.  
A:Reference number: S03353; MUID:89134784; PMID:2537099  
A:Accession: S03353  
A:Molecule type: protein  
A:Residues: 1-15 <TAN>  
A:Cross-references: UNIPROT:P10625; UNIPARC:UPI0000131BAF

Query Match 35.8%; Score 34; DB 2; Length 15;  
Best Local Similarity 72.7%; Pred. No. 49;  
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 EFTTVKSCPD 17  
|||  
DB 1 EFTTVKMGDA 11

RESULT 2  
G72312  
hypothetical protein - Thermotoga maritima (strain MSB8)  
C:Species: Thermotoga maritima  
C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
C:Accession: G72312  
R:Nelson, K.B.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hicke  
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.  
C.M.  
Nature 399, 323-329, 1999  
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se  
A:Reference number: A72200; MUID:99287316; PMID:10360571  
A:Accession: G72312  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-41 <ARN>  
A:Cross-references: UNIPROT:Q9X065; UNIPARC:UPI00000C1340; GB:AE001759; GB:AE000512; NI  
A:Experimental source: strain MSB8  
C:Genetics:  
A:Gene: TM0970

Query Match 34.7%; Score 33; DB 2; Length 41;  
Best Local Similarity 54.5%; Pred. No. 1.8e+02;

```
Matches      6;  Conservative      3;  Mismatches      2;  Indels      0;  Gaps      0;

QY      4  DVLETFYTKSC 14
      :||| | :|
Db      23 EVLETHTSQTC 33

RESULT 3
S72793
cysteine synthase (SC 4.2.99.8) B - Mycobacterium leprae
N/Alternate names: B1549_C3_238 protein; O-Acetylserine sulphydrolase B
C/Species: Mycobacterium_leprae
C/Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C/Accession: S72793
R/Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, November 1993
A/Description: Mycobacterium leprae cosmid B1549.
A/Reference number: S72582
A/Accession: S72793
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-49 <SMI>
A/Cross-references: UNIPROT:Q59529; UNIPARC:UPI00000B1374; EMBL:U00014; NID:g466903; PID
C/Genetics:
A/Gene: cysM
C/Keywords: carbon-oxygen lyase

Query Match      33.7%;  Score 32;  DB 2;  Length 49;
Best Local Similarity 33.3%;  Pred. No. 3.1e+02;
Matches      4;  Conservative      5;  Mismatches      3;  Indels      0;  Gaps      0;

QY      3  KDVLETFYTKSC 14
      ||: ||: ||:
Db      38  KDLFPSTYTRTC 49

RESULT 4
S12409
ribosomal protein S12 - wheat chloroplast (fragment)
C/Species: chloroplast Triticum aestivum (common wheat)
C/Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C/Accession: S12409
R/Gray, J.C.; Hird, S.M.; Dyer, T.A.
Plant Mol. Biol. 15, 947-950, 1990
A/Title: Nucleotide sequence of a wheat chloroplast gene encoding the proteolytic subunit
A/Reference number: S12407; MUID:91355920; PMID:2103485
A/Accession: S12409
A/Molecule type: DNA
A/Residues: 1-38 <GRA>
A/Cross-references: UNIPROT:P24066; UNIPARC:UPI000016D3FB; EMBL:X54484; NID:g12334; PIDN
C/Genetics:
A/Gene: rps12
A/Genome: chloroplast
C/Superfamily: ribosomal protein S12
C/Keywords: chloroplast; protein biosynthesis; ribosome

Query Match      32.6%;  Score 31;  DB 2;  Length 38;
Best Local Similarity 33.3%;  Pred. No. 3.6e+02;
Matches      5;  Conservative      4;  Mismatches      6;  Indels      0;  Gaps      0;

QY      1  PKQVLETFYTKSCP 15
      |:: |:: ||
Db      14  PIRNARKTAALKGCP 28

RESULT 5
AD1753
Lactococcus lactis prophage pi2 protein 41 homolog lin2569 [imported] - Listeria innocua
C/Species: Listeria innocua
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C/Accession: AD1753
R/Glaeser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Raquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duesurget, O.; Entian, K.D.; Fsihi, H.
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D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A/Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maitournam, A.; M
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A/Title: Comparative genomics of Listeria species.
A/Reference number: AB1077; MUID:21537279; PMID:11679669
A/Accession: AD1753
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-44 <GLA>
A/Cross-references: UNIPROT:Q928G6; UNIPARC:UPI00000CC9EF; GB:AL592022; PIDN:CAC97796.1.;
A/Experimental source: strain Clip11262
C/Genetics:
A/Gene: lin2569

Query Match      32.6%;  Score 31;  DB 2;  Length 44;
Best Local Similarity 53.8%;  Pred. No. 4.1e+02;
Matches      7;  Conservative      1;  Mismatches      5;  Indels      0;  Gaps      0;

QY      4  DVLETFYTKSCPD 16
      ||| |:: ||
Db      4  DDLEMMTLGSCLD 16

RESULT 6
AB0925
hypothetical protein STY3659 [imported] - Salmonella enterica subsp. enterica serovar Typh
C/Species: Salmonella enterica subsp. enterica serovar Typhi
A/Note: this species has also been called Salmonella typhi
C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C/Accession: AB0925
R/Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Conington, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A/Reference number: AB0502; MUID:21534947; PMID:11677608
A/Accession: AB0925
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-50 <PAR>
A/Cross-references: UNIPARC:UPI000005A5A3; GB:AL513382; PIDN:CAD09420.1; PID:g16504537;
C/Genetics:
A/Gene: STY3659

Query Match      32.6%;  Score 31;  DB 2;  Length 50;
Best Local Similarity 75.0%;  Pred. No. 4.6e+02;
Matches      6;  Conservative      1;  Mismatches      1;  Indels      0;  Gaps      0;

QY      1  PKQVLETF 8
      ||| ||:|
Db      33  PKKSVLKT 40

RESULT 7
AB1546
hypothetical protein CP0727 [imported] - Chlamydophila pneumoniae (strain AR39)
C/Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
C/Accession: AB1546
R/Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A/Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A/Reference number: AB1500; MUID:20150255; PMID:10684935
A/Accession: AB1546
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-50 <REA>
A/Cross-references: UNIPARC:UPI000016560C; GB:AE002231; GB:AE002161; NID:g7189633; PIDN
A/Experimental source: strain AR39, HL cells
C/Genetics:
```

A;Gene: CP0727

Query Match 31.6%; Score 30; DB 2; Length 50;  
Best Local Similarity 37.5%; Pred. No. 6.7e+02;  
Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 2 KKDVLFTFTVKSPDA 17  
||| |  
Db 23 RKDYELWFVYGSCPES 38

RESULT 8

A61309  
glycoprotein hormones alpha chain - hamster (fragment)  
N;Alternate names: chorionadotropin alpha chain; luteinizing hormone alpha chain; lut

C;Species: Cricetinae gen. sp. (hamster)

C;Date: 17-Jul-1994 #sequence\_revision 17-Jul-1994 #text\_change 09-Jul-2004

C;Accession: A61309

R;Glenn, S.D.; Nahm, H.S.; Greenwald, G.S.; Ward, D.N.

Endocrinology 111, 1263-1269, 1982

A;Title: Isolation and characterization of hamster luteinizing hormone.

A;Reference number: A61309; MUID:93003498; PMID:6889489

A;Accession: A61309

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-12 <GLE>

A;Cross-references: UNIPROT:Q7M0A7; UNIPARC:UPI00001765C7

C;Superfamily: glycoprotein hormones alpha chain

C;Keywords: glycoprotein

Query Match 30.5%; Score 29; DB 2; Length 12;  
Best Local Similarity 57.1%; Pred. No. 2.6e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 9 FTVKSCP 15  
||| |  
Db 6 FTVQGCP 12

RESULT 9

S11610  
ribosomal protein S4.eR [validated] - Halobacterium salinarum (fragment)  
N;Alternate names: ribosomal protein HS5

C;Species: Halobacterium salinarum

C;Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 05-Oct-2004

C;Accession: S11610

R;Yaguchi, M.; Visentin, L.P.; Zuker, M.; Matheson, A.T.; Roy, C.; Strom, A.R.

Zbl. Bakt. Hyg. 1. Abt. Orig. C 3, 200-208, 1982

A;Title: Amino-terminal sequences of ribosomal proteins from the 30S subunit of archaea

A;Reference number: S11609

A;Accession: S11610

A;Molecule type: protein

A;Residues: 1-32 <YAG>

A;Cross-references: UNIPROT:Q7M553; UNIPARC:UPI000017725F

A;Note: the protein is designated as ribosomal protein HS5

A;Note: the source is designated as Halobacterium cutirubrum

C;Superfamily: ribosomal protein S4

C;Keywords: protein biosynthesis; ribosome

Query Match 30.5%; Score 29; DB 2; Length 32;  
Best Local Similarity 53.8%; Pred. No. 6.4e+02;  
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 PKKDVLFTFTVKS 13  
||| |  
Db 14 FVZKRTFTFTSKS 26

RESULT 10

F95187

hypothetical protein SP1611 [imported] - Streptococcus pneumoniae (strain TIGR4)

C;Species: Streptococcus pneumoniae

C;Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 09-Jul-2004

C;Accession: F95187  
R;Tetzelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Hel  
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzap  
nson, T.; Hickey, E.K.; Holt, I.E.  
Science 293, 498-506, 2001  
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison  
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.  
A;Reference number: A95000; MUID:21357209; PMID:11463916  
A;Accession: F95187  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-34 <KUR>  
A;Cross-references: UNIPROT:Q97PJ8; UNIPARC:UPI00000518PB; GB:AE005672; PIDN:AAK75695.1  
A;Experimental source: strain TIGR4  
C;Genetics:  
A;Gene: SP1611

Query Match 30.5%; Score 29; DB 2; Length 34;  
Best Local Similarity 35.7%; Pred. No. 6.8e+02;  
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 PKKDVLFTFTVKS 14  
||| |  
Db 12 PBEDIIVTGLPKYC 25

RESULT 11

A60601

keratin, 55k, nuclear matrix - rat (fragments)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004

C;Accession: A60601

R;Alique, R.; Bastos, R.; Serratos, J.; Enrich, C.; James, P.; Pujades, C.; Bachs, O.

Exp. Cell Res. 186, 346-353, 1990

A;Title: Increase in a 55-kDa keratin-like protein in the nuclear matrix of rat liver c

A;Reference number: A60601; MUID:90127112; PMID:1688805

A;Accession: A60601

A;Molecule type: protein

A;Residues: 1-33 <ALI>

A;Cross-references: UNIPROT:Q7M0B6; UNIPARC:UPI00001774C5

C;Superfamily: cytoskeletal keratin

C;Keywords: nuclear matrix; nucleus

Query Match 29.5%; Score 28; DB 2; Length 33;  
Best Local Similarity 54.5%; Pred. No. 9.6e+02;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 KKDVLFTFTVK 12  
||| |  
Db 8 KKDVDVDEAYXXK 18

RESULT 12

I70022

kallikrein - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999

C;Accession: I70022

R;Evans, B.A.; Drinkwater, C.C.; Richards, R.I.

J. Biol. Chem. 262, 8027-8034, 1987

A;Title: Mouse glandular kallikrein genes: Structure and partial sequence analysis of t

A;Reference number: I55260; MUID:87250386; PMID:3036794

A;Accession: I70022

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-38 <RES>

A;Cross-references: UNIPARC:UPI000016CE68; GB:M18590; NID:g198528; PIDN:AAA39352.1; PID

C;Genetics:

A;Gene: KAL

Query Match 29.5%; Score 28; DB 2; Length 38;  
Best Local Similarity 38.5%; Pred. No. 1.1e+03;  
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 DVLETFVTKSCPD 16  
Db 9 ELLEDLTVRRIPN 21

## RESULT 13

T07581

hypothetical protein 42g - Japanese black pine chloroplast  
C:Species: chloroplast Pinus thunbergiana (Japanese black pine)  
C>Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 09-Jul-2004  
C:Accession: T07581  
R:Wakasugi, T.; Tsudzuki, J.; Ito, S.; Nakashima, K.; Tsudzuki, T.; Sugiura, M.  
Proc. Natl. Acad. Sci. U.S.A. 91, 9794-9798, 1994  
A:Title: Loss of all ndh genes as determined by sequencing the entire chloroplast genome  
A:Reference number: Z16030; PMID:95024047; PMID:7937893  
A:Accession: T07581  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-42 <WAK>  
A:Cross-references: UNIPROT:Q33005; UNIPARC:UPI0000093984; EMBL:D17510; NID:G529643; PII  
C:Genetics:  
A:Genome: chloroplast  
C:Keywords: chloroplast

Query Match 29.5%; Score 28; DB 2; Length 42;  
Best Local Similarity 41.7%; Pred. No. 1.2e+03;  
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 KKDVLFTFTVKS 13  
Db 24 KSCILHIYIKS 35

## RESULT 14

A34071

gag polyprotein - avian retrovirus NK24 (fragment)  
C:Species: avian retrovirus NK24  
C>Date: 21-Dec-1990 #sequence\_revision 21-Dec-1990 #text\_change 07-Feb-1997  
C:Accession: A34071  
R:Nishizawa, M.; Goto, N.; Kawai, S.  
J. Virol. 61, 3733-3740, 1987  
A:Title: An avian transforming retrovirus isolated from a nephroblastoma that carries the  
A:Reference number: A34071; PMID:88062920; PMID:2824811  
A:Accession: A34071  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-43 <NIS>  
A:Cross-references: UNIPARC:UPI000017857A  
A:Note: the authors translated the codon AAC for residue 43 as Thr  
C:Superfamily: avian retrovirus gag polyprotein  
C:Keywords: polyprotein

Query Match 29.5%; Score 28; DB 2; Length 43;  
Best Local Similarity 41.7%; Pred. No. 1.2e+03;  
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 5 VLETFVTKSCPD 16  
Db 12 IIDCFRQKSPD 23

## RESULT 15

T07537

hypothetical protein 44c - Japanese black pine chloroplast  
C:Species: chloroplast Pinus thunbergiana (Japanese black pine)  
C>Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 09-Jul-2004  
C:Accession: T07537  
R:Wakasugi, T.; Tsudzuki, J.; Ito, S.; Nakashima, K.; Tsudzuki, T.; Sugiura, M.  
Proc. Natl. Acad. Sci. U.S.A. 91, 9794-9798, 1994  
A:Title: Loss of all ndh genes as determined by sequencing the entire chloroplast genome  
A:Reference number: Z16030; PMID:95024047; PMID:7937893  
A:Accession: T07537

A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-44 <WAK>  
A:Cross-references: UNIPROT:Q32976; UNIPARC:UPI000009538A; EMBL:D17510; NID:G529643; PII  
C:Genetics:  
A:Genome: chloroplast  
C:Keywords: chloroplast

Query Match 29.5%; Score 28; DB 2; Length 44;  
Best Local Similarity 46.2%; Pred. No. 1.3e+03;  
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKQDVLETFVTKS 13  
Db 6 PKQDERTFTTSS 18

## RESULT 16

S36709

B7 protein - equine herpesvirus 4 (fragment)  
C:Species: equine herpesvirus 4  
C>Date: 09-Jun-1994 #sequence\_revision 12-May-1995 #text\_change 09-Jul-2004  
C:Accession: S36709  
R:Riggio, P.  
submitted to the EMBL Data Library, November 1989  
A:Reference number: S36709  
A:Accession: S36709  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-45 <RIG>  
A:Cross-references: UNIPROT:Q00041; UNIPARC:UPI0000126247; EMBL:X17684; NID:G312459; PII  
C:Superfamily: herpesvirus 77K alpha trans-inducing protein  
C:Keywords: transcription regulation

Query Match 29.5%; Score 28; DB 2; Length 45;  
Best Local Similarity 41.7%; Pred. No. 1.3e+03;  
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 KDVLFTFTVKSC 14  
Db 14 KNLIERRAVKGC 25

## RESULT 17

H71262

hypothetical protein TP0940 - syphilis spirochete  
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)  
C>Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 09-Jul-2004  
C:Accession: H71262  
R:Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin  
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.  
Science 281, 375-388, 1998  
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.  
A:Reference number: A71250; PMID:98332770; PMID:9665876  
A:Accession: H71262  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-46 <COL>  
A:Cross-references: UNIPROT:O83910; UNIPARC:UPI0000139845; GB:AE001262; NID:AE000520; NID

A:Experimental source: strain Nichols  
C:Genetics:  
A:Gene: TP0940

Query Match 29.5%; Score 28; DB 2; Length 46;  
Best Local Similarity 40.0%; Pred. No. 1.3e+03;  
Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18  
Db 37 FPAPGCPDTL 46

## RESULT 18

A32457  
myeloperoxidase (EC 1.11.1.7) - bovine (fragments)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 26-Oct-1989 #sequence\_revision 24-Nov-1999 #text\_change 24-Nov-1999  
C:Accession: B32457; A32457  
R;Ikeda-Saito, M.; Lee, H.C.; Adachi, K.; Eck, H.S.; Prince, R.C.; Booth, K.S.; Caughey, J. Biol. Chem. 264, 4559-4563, 1989  
A;Title: Demonstration that spleen green hemeprotein is identical to granulocyte myeloperoxidase  
A;Reference number: A32457; MUID:89174712; PMID:2538448  
A;Accession: B32457  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-26 <IKB1>  
A;Cross-references: UNIPROT:Q7M356; UNIPARC:UPI0000175203  
A;Accession: A32457  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 27-48 <IKB2>  
A;Cross-references: UNIPARC:UPI0000175204  
C:Superfamily: myeloperoxidase; myeloperoxidase homology  
C;Keywords: oxidoreductase  
F;1-26/Domain: light chain (fragment) #status experimental <CHL>  
F;27-48/Domain: heavy chain (fragment) #status experimental <CHH>

Query Match 29.5%; Score 28; DB 2; Length 48;  
Best Local Similarity 46.3%; Pred. No. 1.4e+03;  
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 PKKDVLFTFKS 13  
|:|:|:|:|:  
DB 2 PEKDEYRTIGQS 14

## RESULT 19

WISNAA  
alpha-amylase inhibitor AI-3688 - Streptomyces aureofaciens  
C:Species: Streptomyces aureofaciens  
C:Date: 17-Mar-1987 #sequence\_revision 17-Mar-1987 #text\_change 09-Jul-2004  
C:Accession: A01331  
R;Vertesy, L.; Triptier, D.  
FEBS Lett. 185, 187-190, 1985  
A;Title: Isolation and structure elucidation of an alpha-amylase inhibitor, AI-3688, from  
A;Reference number: A01331; MUID:85204394; PMID:2581812  
A;Accession: A01331  
A;Molecule type: protein  
A;Residues: 1-36 <VER>  
A;Cross-references: UNIPROT:P04082; UNIPARC:UPI000012D0A7  
A;Experimental source: FH1656, strain DSM 2790  
C:Comment: This protein is an effective inhibitor of pancreatic alpha-amylase, forming a  
does not inhibit the B. subtilis enzyme. Inhibition is pH-independent but does require  
C:Superfamily: alpha-amylase inhibitor, Streptomyces type  
C;Keywords: alpha-amylase inhibitor  
F;14-18/Region: inhibitory #status predicted  
F;9-25/Disulfide bonds: #status experimental

Query Match 28.9%; Score 27.5; DB 1; Length 36;  
Best Local Similarity 28.0%; Pred. No. 1.1e+03;  
Matches 7; Conservative 3; Mismatches 8; Indels 7; Gaps 1;

QY 1 PKKDVLFTF-----TVKSCPDAI 18  
|:|:|:|:|:  
DB 5 PAPDCVESFQSWRYTDVRNGCSDAV 29

## RESULT 20

C39558  
matricotin A - elapid snake (Maticora bivirgata) (fragment)  
C:Species: Maticora bivirgata  
C:Date: 14-Feb-1992 #sequence\_revision 14-Feb-1992 #text\_change 09-Jul-2004  
C:Accession: C39558  
R;Takasaki, C.; Yoshida, H.; Shimazu, T.; Teruuchi, T.; Toriba, M.; Tamiya, N.  
Toxicon 29, 191-200, 1991

A;Title: Studies on the venom components of the long-glanded coral snake, Maticora bivi

A;Reference number: A39558; MUID:91263097; PMID:2048137

A;Accession: C39558

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-41 <TAK>

A;Cross-references: UNIPROT:P24742; UNIPARC:UPI00001287FD

Query Match 28.9%; Score 27.5; DB 2; Length 41;  
Best Local Similarity 37.5%; Pred. No. 1.4e+03;  
Matches 6; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY 2 KKD-VLETFVKSCPD 16  
|:|:|:|:|:  
DB 26 KKDVMNLYPIRGAD 41

## RESULT 21

A60225  
pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) alpha chain - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 21-Oct-1992 #sequence\_revision 21-Oct-1992 #text\_change 31-Dec-2004  
C:Accession: A60225  
R;Lawson, R.; Aitken, A.; Yeaman, S.J.  
Biochem. Soc. Trans. 11, 298-299, 1983  
A;Title: Primary sequence of the N-terminal region of the alpha-subunit of pyruvate dehy

A;Reference number: A60225

A;Accession: A60225

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-21 <LAW>

A;Cross-references: UNIPROT:Q9N1X8; UNIPARC:UPI0000174FD1

C:Superfamily: thiamin pyrophosphate-binding domain homology

C;Keywords: oxidoreductase

Query Match 28.4%; Score 27; DB 2; Length 21;  
Best Local Similarity 57.1%; Pred. No. 9.2e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 TPTVKSC 14  
|:|:|:|:|:  
DB 6 TPEIKKC 12

## RESULT 22

S22603  
ribosomal protein L26, cytosolic - African clawed frog (fragment)  
C:Species: Xenopus laevis (African clawed frog)  
C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
C:Accession: S22603  
R;Lorenzi, F.; Francesconi, A.; Jappelli, R.; Amaldi, P.  
Nucleic Acids Res. 20, 1859-1863, 1992  
A;Title: Analysis of mRNAs under translational control during Xenopus embryogenesis: is

A;Reference number: S22601; MUID:92253404; PMID:1579486

A;Accession: S22603

A;Molecule type: mRNA

A;Residues: 1-33 <LOR>

A;Cross-references: UNIPROT:P49629; UNIPARC:UPI0000133DF0; EMBL:X64211; NID:G65086; PID

C:Superfamily: rat ribosomal protein L26

C;Keywords: cytosol; protein biosynthesis; ribosome

Query Match 28.4%; Score 27; DB 2; Length 33;  
Best Local Similarity 30.8%; Pred. No. 1.4e+03;  
Matches 4; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 3 KDVLFTFKSCPD 15  
|:|:|:|:|:  
DB 15 KELRQKYSVRSMP 27

## RESULT 23

T29808  
hypothetical protein C25A8.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C:Accession: T29808  
 R:Latreille, P.; Stellyes, L.  
 Submitted to the EMBL Data Library, June 1996  
 A:Description: The sequence of C. elegans cosmid C25A8.  
 A:Reference number: Z20689  
 A:Accession: T29808  
 A>Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-37 <LAT>  
 A:Cross-references: UNIPROT:Q18145; UNIPARC:UPI0000081748; EMBL:U61958; PIDN:ARB03181.1;  
 A:Experimental source: strain Bristol N2; clone C25A8  
 C:Genetics:  
 A:Gene: CESP:C25A8.1  
 A:Map position: 4

Query Match 28.4%; Score 27; DB 2; Length 37;  
 Best Local Similarity 83.3%; Pred. No. 1.6e+03;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVL 6  
 ||:|:|  
 Db 28 PKEDVL 33

RESULT 24  
 T03344  
 gene e23 protein - Lactococcus phage bIL170  
 C:Species: Lactococcus phage bIL170  
 C>Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 09-Jul-2004  
 C:Accession: T03344  
 R:Cruciz-Le Coq, A.M.; Cesselin, B.; Commissaire, J.; Anba, J.; Kyriakidis, S.; Chopin, M  
 Submitted to the EMBL Data Library, June 1997  
 A:Description: Sequence and organization of the lactococcal isometric bIL170 phage genom  
 A:Reference number: Z14903  
 A:Accession: T03344  
 A>Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-39 <CRU>  
 A:Cross-references: UNIPROT:O80137; UNIPARC:UPI000009BB13; EMBL:AF009630; NID:G3282260;  
 C:Genetics:  
 A:Gene: e23

Query Match 28.4%; Score 27; DB 2; Length 39;  
 Best Local Similarity 33.3%; Pred. No. 1.6e+03;  
 Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 KDVLFTFTVKSC 14  
 ||:|:|:|  
 Db 2 KDTVKTLMIIAC 13

RESULT 25  
 HPB0  
 haptoglobin precursor - bovine (fragments)  
 C:Species: Bos primigenius taurus (cattle)  
 C>Date: 28-Feb-1992 #sequence\_revision 31-May-1996 #text\_change 31-Oct-1997  
 C:Accession: A40430; B40430  
 R:Morimatsu, M.; Syuto, B.; Shimada, N.; Fujinaga, T.; Yamamoto, S.; Saito, M.; Naiki, M  
 J. Biol. Chem. 266, 11833-11837, 1991  
 A>Title: Isolation and characterization of bovine haptoglobin from acute phase sera.  
 A:Reference number: A40430; MUID:91268055; PMID:1904872  
 A:Accession: A40430  
 A:Molecule type: protein  
 A:Residues: 1-25 <MOR>  
 A:Cross-references: UNIPROT:Q7M365; UNIPARC:UPI0000172B09  
 A:Accession: B40430  
 A:Molecule type: protein  
 A:Residues: 26-45 <MO2>  
 A:Cross-references: UNIPARC:UPI0000172B0A  
 C:Comment: The mature haptoglobin molecule is a dimer of heterodimers, the two chains of  
 C:Comment: Haptoglobin is a plasma glycoprotein; haptoglobin forms a complex with hemogl

C:Superfamily: haptoglobin; complement factor H repeat homology; trypsin homology  
 C:Keywords: acute phase; glycoprotein; hemoglobin binding; heterotetramer; iron transpo  
 F:1-25/Product: haptoglobin alpha chain (fragment) #status experimental <ALP>  
 F:26-45/Product: haptoglobin beta chain (fragment) #status experimental <BET>

Query Match 28.4%; Score 27; DB 1; Length 45;  
 Best Local Similarity 62.5%; Pred. No. 1.9e+03;  
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 TVKSCPD 17  
 ||:|:|  
 Db 8 TADSCPKA 15

RESULT 26  
 JS0655  
 hypothetical 5K protein (kan region) - Streptomyces griseus (strain SS-1198PR)  
 C:Species: Streptomyces griseus  
 C>Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
 C:Accession: JS0655  
 R:Fishikawa, J.; Hotta, K.  
 Gene 108, 127-132, 1991  
 A>Title: Nucleotide sequence and transcriptional start point of the kan gene encoding a  
 A:Reference number: JS0652; MUID:92104494; PMID:1761222  
 A:Accession: JS0655  
 A>Status: translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-45 <ISH>  
 A:Cross-references: UNIPROT:Q7M0K4; UNIPARC:UPI000017AE1A

Query Match 28.4%; Score 27; DB 2; Length 45;  
 Best Local Similarity 45.5%; Pred. No. 1.9e+03;  
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 7 EFTVKSQPD 17  
 ||:|:|:|  
 Db 31 EAWTRNCDA 41

RESULT 27  
 T07305  
 hypothetical protein 48d - Chlorella vulgaris chloroplast  
 C:Species: chloroplast Chlorella vulgaris  
 C>Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 21-Jul-2000  
 C:Accession: T07305  
 R:Wakasugi, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, M.; Ito, S.; Tsudzuki, J.; Nakas  
 Proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997  
 A>Title: Complete nucleotide sequence of the chloroplast genome from the green alga Chlc  
 A:Reference number: Z15985; MUID:97303241; PMID:9159184  
 A:Accession: T07305  
 A>Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-48 <WAK>  
 A:Cross-references: UNIPARC:UPI000011E47A; EMBL:AB001684; NID:G2224352; PIDN:BAA57953.1;  
 C:Genetics:  
 A:Genome: chloroplast  
 C:Keywords: chloroplast

Query Match 28.4%; Score 27; DB 2; Length 48;  
 Best Local Similarity 36.4%; Pred. No. 2e+03;  
 Matches 4; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 3 KDVLFTFTVKS 13  
 ||:|:|:|  
 Db 27 KPILKTFSLN 37

RESULT 28  
 AB1181  
 hypothetical protein lmo0850 [imported] - Listeria monocytogenes (strain EGD-e)  
 C:Species: Listeria monocytogenes  
 C>Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004  
 C:Accession: AB1181

R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloechle, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. Science 294, 849-852, 2001

A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Makok, C.; Schluster, T.; Simoes, N.; Tierrez, A.; Varquez-Boland, J.A.; Voss, H.; Wehlend, A.; Title: Comparative genomics of *Listeria species*.

A; Reference number: AB1077; UID:21537279; PMID:11679669

A; Accession: AB1181

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-48 <GLA>

A; Cross-references: UNIPROT:Q8Y8P6; UNIPARC:UPI000000CF10E; GB:NC\_003210; PIDN:CAC989828.1

A; Experimental source: strain EGD-e

C; Genetics:

A; Gene: lmo0850

Query Match 28.4%; Score 27; DB 2; Length 48;  
Best Local Similarity 26.7%; Pred. No. 2e+03;  
Matches 4; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 2 KDVLFTFTVKSPD 16  
::: : : : :  
Db 28 RKDIWKSVSSEKAMPN 42

RESULT 29

D70253 conserved hypothetical protein BBX18 - Lyme disease spirochete plasmid K/lp36

C; Species: Borrelia burgdorferi (Lyme disease spirochete)

C; Date: 13-Feb-1998 #sequence\_revision 13-Feb-1998 #text\_change 09-Jul-2004

C; Accession: D70253

R; Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Nature 390, 580-586, 1997

A; Authors: Smith, H.O.; Venter, J.C.

A; Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.

A; Reference number: A70100; UID:98065943; PMID:9403685

A; Accession: D70253

A; Status: preliminary; nucleic acid sequence not shown; translation not shown

A; Molecule type: DNA

A; Residues: 1-30 <KL>

A; Cross-references: UNIPROT:O50822; UNIPARC:UPI00000568B0; GB:AE000788; NID:g2690123; PI

A; Experimental source: strain B31

C; Genetics:

A; Genome: plasmid

Query Match 27.9%; Score 26.5; DB 2; Length 30;  
Best Local Similarity 38.5%; Pred. No. 1.5e+03;  
Matches 5; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

Qy 3 KDVL-ETFTVSKC 14  
||: : | :|  
Db 14 KDLMHKIFIKNIC 26

RESULT 30

S65371 tRNA-guanine transglycosylase, 32 K chain - bovine (fragments)

C; Species: Bos primigenius taurus (cattle)

C; Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004

C; Accession: S65371

R; Slany, R.K.; Mueller, S.O.  
Eur. J. Biochem. 230, 221-228, 1995

A; Title: tRNA-guanine transglycosylase from bovine liver. Purification of the enzyme to

A; Reference number: S65370; UID:95324527; PMID:7601103

A; Accession: S65371

A; Status: preliminary

A; Molecule type: protein

A; Residues: 1-13; 14-34 <SLA>

A; Cross-references: UNIPROT:Q9TR63; UNIPARC:UPI0000086AF4; UNIPARC:UPI0000017C580

A; Note: 15-Thr, 15-Gln, 15-Gly were also found



```
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: C85939
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-27 <STO>
A;Cross-references: UNIPROT:Q8X3L8; UNIPARC:UPI00000D0EF5; GB:AE005174; NID:gl2517358; F
A;Experimental source: strain O157:H7, substrain EDL333
A;Genetics:
A;Gene: Z4183

Query Match 27.4%; Score 26; DB 2; Length 27;
Best Local Similarity 30.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 3 KDVLFTFTVK 12
DB 13 QDLLESYAIR 22

RESULT 34
A60914
pheromone-binding protein 1 - gypsy moth (fragment)
C;Species: Lymantria dispar (gypsy moth)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: A60914
R;Vogt, R.G.; Koehne, A.C.; Dubnau, J.T.; Prestwich, G.D.
J. Neurosci. 9, 3332-3346, 1989
A;Title: Expression of pheromone binding proteins during antennal development in the gyp
A;Reference number: A60914; MUID:90011285; PMID:2795166
A;Accession: A60914
A;Molecule type: protein
A;Residues: 1-30 <VOG>
A;Cross-references: UNIPROT:P34176; UNIPARC:UPI000017956F
C;Superfamily: tobacco hornworm pheromone-binding protein
C;Keywords: olfaction

Query Match 27.4%; Score 26; DB 2; Length 30;
Best Local Similarity 25.0%; Pred. No. 1.9e+03;
Matches 7; Conservative 7; Mismatches 2; Indels 12; Gaps 2;

QY 3 KDVLFTFTV-----KSC-----PDAI 18
DB 2 KEVMQMTINFAPKPEACKQELNVPDV 29

RESULT 35
C82312
hypothetical protein VC0536 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: C82312
R;Heldelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardon, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, B
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: C82312
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-33 <HEI>
A;Cross-references: UNIPROT:Q9KUI5; UNIPARC:UPI00000C2D09; GB:AE004139; GB:AE003852; NID
A;Experimental source: serogroup O1, strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC0536
A;Map position: 1

Query Match 27.4%; Score 26; DB 2; Length 33;
Best Local Similarity 54.5%; Pred. No. 2e+03;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 LETFTVKSCPD 16
|:|:|:|:|:|:|
```

```
Db 23 LKTVTENSKPD 33

RESULT 36
S29726
lignin peroxidase (EC 1.11.1.1-) 10 - white-rot fungus (Trametes versicolor) (fragment)
C;Species: Trametes versicolor (white-rot fungus)
C;Date: 19-Mar-1997 #sequence_revision 17-Jul-1998 #text_change 12-Jul-2004
C;Accession: S29726
R;Johansson, T.; Welinder, K.G.; Nyman, P.O.
Arch. Biochem. Biophys. 300, 57-62, 1993
A;Title: Isozymes of lignin peroxidase and manganese(II) peroxidase from the white-rot f
ions.
A;Reference number: S29724; MUID:93143365; PMID:8424691
A;Accession: S29726
A;Molecule type: protein
A;Residues: 1-35 <JOH>
A;Cross-references: UNIPROT:Q9URA2; UNIPARC:UPI00000696DB
A;Experimental source: strain PRL 572
C;Function:
A;Description: probably required for degradation of lignin and certain xenobiotics
C;Superfamily: peroxidase
C;Keywords: extracellular protein; heme; oxidoreductase

Query Match 27.4%; Score 26; DB 2; Length 35;
Best Local Similarity 50.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 13 SCPDAI 18
DB 2 TCPDGV 7

RESULT 37
S29728
lignin peroxidase (EC 1.11.1.1-) 12 - white-rot fungus (Trametes versicolor) (fragment)
C;Species: Trametes versicolor (white-rot fungus)
C;Date: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 12-Jul-2004
C;Accession: S29728
R;Johansson, T.; Welinder, K.G.; Nyman, P.O.
Arch. Biochem. Biophys. 300, 57-62, 1993
A;Title: Isozymes of lignin peroxidase and manganese(II) peroxidase from the white-rot f
ions.
A;Reference number: S29724; MUID:93143365; PMID:8424691
A;Accession: S29728
A;Molecule type: protein
A;Residues: 1-35 <JOH>
A;Cross-references: UNIPROT:Q9UQY7; UNIPARC:UPI0000069C2A
A;Experimental source: strain PRL 572
C;Function:
A;Description: involved in degradation of lignin and certain xenobiotics
C;Superfamily: peroxidase
C;Keywords: extracellular protein; heme; oxidoreductase

Query Match 27.4%; Score 26; DB 2; Length 35;
Best Local Similarity 50.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 13 SCPDAI 18
DB 2 ACPDGV 7

RESULT 38
S29729
manganese(II) peroxidase (EC 1.11.1.1-) 1 - white-rot fungus (Trametes versicolor) (fragm
C;Species: Trametes versicolor (white-rot fungus)
C;Date: 19-Mar-1997 #sequence_revision 17-Jul-1998 #text_change 12-Jul-2004
C;Accession: S29729
R;Johansson, T.; Welinder, K.G.; Nyman, P.O.
Arch. Biochem. Biophys. 300, 57-62, 1993
A;Title: Isozymes of lignin peroxidase and manganese(II) peroxidase from the white-rot b
ions.
```



A;Reference number: S29724; MUID:93143365; PMID:8424691  
A;Accession: S29729  
A;Molecule type: protein  
A;Residues: 1-35 <JOH>  
A;Cross-references: UNIPROT:Q9URAI; UNIPARC:UPI0000065C1D  
A;Experimental source: strain PRL 572  
C;Superfamily: peroxidase  
C;Keywords: extracellular protein; heme; manganese; oxidoreductase

Query Match 27.4%; Score 26; DB 2; Length 35;  
Best Local Similarity 50.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 13 SCPDAI 18  
:|:|:|:  
Db 2 ACPDGV 7

## RESULT 39

S29731  
manganese(II) peroxidase (RC 1.11.1.1-) 5 - white-rot fungus (Trametes versicolor) (fragment)  
C;Species: Trametes versicolor (white-rot fungus)  
C;Date: 19-Mar-1997 #sequence\_revision 17-Jul-1998 #text\_change 12-Jul-2004  
C;Accession: S29731  
R;Johansson, T.; Welinder, K.G.; Nyman, P.O.  
Arch. Biochem. Biophys. 300, 57-62, 1993  
A;Title: Isozymes of lignin peroxidase and manganese(II) peroxidase from the white-rot fungus.

A;Reference number: S29724; MUID:93143365; PMID:8424691  
A;Accession: S29731  
A;Molecule type: protein  
A;Residues: 1-35 <JOH>  
A;Cross-references: UNIPROT:Q9UR99; UNIPARC:UPI000006ADBA  
A;Experimental source: strain PRL 572  
C;Superfamily: peroxidase  
C;Keywords: extracellular protein; heme; manganese; oxidoreductase

Query Match 27.4%; Score 26; DB 2; Length 35;  
Best Local Similarity 50.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 13 SCPDAI 18  
:|:|:|:  
Db 2 ACPDGV 7

## RESULT 40

S70092  
hypothetical protein (orf36) - Amycolatopsis methanolica  
C;Species: Amycolatopsis methanolica  
C;Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 07-May-1999  
C;Accession: S70092  
R;Vrijbloed, J.W.; Jelinkova, M.; Hessel, G.I.; Dijkhuizen, L.  
Mol. Microbiol. 18, 21-31, 1995  
A;Title: Identification of the minimal replicon of plasmid pMEA300 of the methylotrophic bacterium Amycolatopsis methanolica  
A;Reference number: S70087; MUID:96154938; PMID:8596458  
A;Accession: S70092  
A;Status: Preliminary  
A;Molecule type: DNA  
A;Residues: 1-36 <VRI>  
A;Cross-references: UNIPARC:UPI000017AD65; EMBL:L36679

Query Match 27.4%; Score 26; DB 2; Length 36;  
Best Local Similarity 56.7%; Pred. No. 2.2e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 VKSCPD 16  
:|:|:|:  
Db 13 VATCPD 18

Search completed: January 20, 2006, 17:34:27  
Job time : 6.66667 secs

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OM protein - protein search, using sw model

Run on: January 20, 2006, 17:22:44 ; Search time 39.1111 Seconds  
(without alignments)  
324.703 Million cell updates/sec

Title: US-10-619-323-6

Perfect score: 95  
Sequence: 1 PKXVLETTVKSCPDAL 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 90886

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 50 summaries

Database : Uniprot\_05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	38.9	39	2	Q4RAQ9_TETNG
2	36	37.9	43	2	Q87JQ4_VIBPA
3	34	35.8	15	1	PLAS_MICAE
4	34	35.8	18	2	Q9XJQ5_9CAUD
5	34	35.8	46	2	Q9NYL8_HUMAN
6	33	34.7	18	2	Q63506_RAT
7	33	34.7	32	2	Q4XWD9_PLACH
8	33	34.7	37	2	Q84TL9_BRARP
9	33	34.7	41	2	Q8BX0_SHEON
10	33	34.7	41	2	Q9X065_THEMEA
11	32.5	34.2	22	2	Q6VQ25_9NEOP
12	32	33.7	38	2	Q4LDM8_9PICO
13	32	33.7	43	2	Q4XGQ9_PLACH
14	32	33.7	49	2	Q59529_MYCLE
15	31.5	33.2	35	2	Q8ZXK8_PYRAE
16	31	32.6	16	2	Q9PRY2_PETWA
17	31	32.6	29	2	Q71992_9RETR
18	31	32.6	33	2	Q65517_MANSAM
19	31	32.6	35	2	Q8LXAB_MUSAC
20	31	32.6	41	2	Q8VVR6_STAAU
21	31	32.6	44	2	Q8U2U2_PYRPU
22	31	32.6	44	2	Q785Q7_NEUCR
23	31	32.6	44	2	Q928G6_LISIN
24	31	32.6	44	2	Q8G001_BRUSU
25	31	32.6	48	2	Q81213_BACAN
26	31	32.6	48	2	Q4RC18_TETNG
27	31	32.6	48	2	Q4RNV7_TETNG
28	31	32.6	50	2	Q82374_SALTI
29	30.5	32.1	40	2	Q4YRD6_PLABE
30	30	31.6	16	2	Q47605_ECOLI
31	30	31.6	20	2	Q62435_MOUSE

32	30	31.6	30	2	Q86487_RVVF	Q86487 rift valley
33	30	31.6	30	2	Q86488_RVVF	Q86488 rift valley
34	30	31.6	30	2	Q86489_RVVF	Q86489 rift valley
35	30	31.6	30	2	Q86490_RVVF	Q86490 rift valley
36	30	31.6	30	2	Q86491_RVVF	Q86491 rift valley
37	30	31.6	30	2	Q86492_RVVF	Q86492 rift valley
38	30	31.6	30	2	Q86493_RVVF	Q86493 rift valley
39	30	31.6	30	2	Q04247_RVVF	Q04247 rift valley
40	30	31.6	30	2	Q4JFJ3_RVVF	Q4JFJ3 rift valley
41	30	31.6	30	2	Q4JFJ4_RVVF	Q4JFJ4 rift valley
42	30	31.6	30	2	Q4JFJ5_RVVF	Q4JFJ5 rift valley
43	30	31.6	30	2	Q4JFJ6_RVVF	Q4JFJ6 rift valley
44	30	31.6	30	2	Q4JFJ7_RVVF	Q4JFJ7 rift valley
45	30	31.6	30	2	Q4JFJ8_RVVF	Q4JFJ8 rift valley
46	30	31.6	30	2	Q4JFJ9_RVVF	Q4JFJ9 rift valley
47	30	31.6	30	2	Q4JFK0_RVVF	Q4JFK0 rift valley
48	30	31.6	30	2	Q4JFK1_RVVF	Q4JFK1 rift valley
49	30	31.6	30	2	Q4JFK2_RVVF	Q4JFK2 rift valley
50	30	31.6	30	2	Q4JFK3_RVVF	Q4JFK3 rift valley

#### ALIGNMENTS

#### RESULT 1

Q4RAQ9\_TETNG ID Q4RAQ9\_TETNG PRELIMINARY; PRT; 39 AA.  
AC Q4RAQ9\_TETNG PRELIMINARY; PRT; 39 AA.  
DT 13-SEP-2005 (TREMBlrel. 31, Created)  
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)  
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)  
DE Chromosome undetermined SCAF23077, whole genome shotgun sequence.  
DE (Fragment).  
GN ORFNames-GSTENG00037463001;  
OS Tetraodon nigroviridis (Green puffer).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
OC Tetraodontidae; Tetraodontidae; Tetraodon.  
OX NCBI\_TaxID=99883;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,  
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
RA Nicaud C., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,  
RA Biemont C., Skalli Z., Cattolico L., Foulain J., De Berardinis V.,  
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,  
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,  
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,  
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
RA Laudet F., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.,  
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
the early vertebrate proto-karyotype.";  
RL Nature 431:946-957(2004).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Genoscope; Whitehead Institute Centre for Genome Research;  
RG Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
preliminary data.  
DR EMBL; CAAE01023077; CAG14524.1; -; Genomic\_DNA.  
FR NON TER 1  
SQ SEQUENCE 39 AA; 4099 MW; 897972726CB0CCFE CRC64;

Query Match 38.9%; Score 37; DB 2; Length 39;  
Best Local Similarity 66.7%; Pred.No. 1.8e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 10 TVKSCPDAL 18

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Db      |||:| | |
      30 TVNCFPVA 38

RESULT 2
Q87JQ4 VIBPA
ID Q87JQ4_VIBPA PRELIMINARY; PRT; 43 AA.
AC Q87JQ4;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Hypothetical protein VPA0194.
GN OrderedLocNames-VPA0194;
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
NCBI_TaxID=670;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=RIMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae.";
RL Lancet 361:743-749 (2003).
DR EMBL; BA000032; BAC61537.1; -; Genomic DNA.
SQ Complete proteome; Hypothetical protein.
KW SEQUENCE 43 AA; 4813 MW; B65EBB8D43C1E79A CRC64;

Query Match 37.9%; Score 36; DB 2; Length 43;
Best Local Similarity 42.9%; Pred. No. 2.9e+02;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 5 VLETFVKSCPDAI 18
      | : | | : | |
      21 VFDLFTIKRPNAL 34

RESULT 3
PLAS MICAE
ID PLAS MICAE STANDARD; PRT; 15 AA.
AC P10825;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Plastocyanin (Fragment).
GN Name=petE;
OS Microcystis aeruginosa.
OC Bacteria; Cyanobacteria; Chroococcales; Microcystis.
OX NCBI_TaxID=1126;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=89134784; PubMed=2537099;
RA Tan S., Ho K.-K.;
RT "Purification of an acidic plastocyanin from Microcystis aeruginosa.";
RL Biochim. Biophys. Acta 973:111-117(1989).
CC -!- FUNCTION: Participates in electron transfer between P700 and the
CC cytochrome b6-f complex in photosystem I.
CC -!- SIMILARITY: Contains 1 plastocyanin-like domain.
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CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
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CC PIR; S03353; S03353.
DR HAMAP; MF_00566; -; 1.
DR InterPro; IPR000923; BlueCu 1.
DR PROSITE; PS00196; COPPER BLUE; PARTIAL.
KW Copper; Direct protein sequencing; Electron transport; Metal-binding;
```

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KW Transport. 15
FT NON_TER 15
SQ SEQUENCE 15 AA; 1555 MW; 32B6D46G2F44F969 CRC64;

Query Match 35.8%; Score 34; DB 1; Length 15;
Best Local Similarity 72.7%; Pred. No. 2.1e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 EFTTVKSCPD 17
      ||| | | |
      1 EFTTVKMGDA 11

RESULT 4
Q9XJQ5 9CAUD
ID Q9XJQ5_9CAUD PRELIMINARY; PRT; 18 AA.
AC Q9XJQ5;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE NiH protein.
GN Name=niH;
OS Bacteriophage 21.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=10743;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20092464; PubMed=10628842; DOI=10.1007/s004380051122;
RA Karch H., Schmidt H., Janetzki-Mittmann C., Scheef J., Kroege M.;
RT "Shiga toxins even when different are encoded at identical positions
RT in the genomes of related temperate bacteriophages.";
RL Mol. Gen. Genet. 262:600-607(1999).
DR EMBL; AJ237660; CAB39992.1; -; Genomic DNA.
SQ SEQUENCE 18 AA; 1975 MW; 2A8A468527FDBB8 CRC64;

Query Match 35.8%; Score 34; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 TFTVKSCPD 16
      ||| | |
      2 TFSVKTIPT 10

RESULT 5
Q9NYL8 HUMAN
ID Q9NYL8_HUMAN PRELIMINARY; PRT; 46 AA.
AC Q9NYL8;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TRENBLrel. 15, Last annotation update)
DE Ran binding protein 2 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA McCarthy N.F., Lindeman R.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF237700; AAF64155.1; -; mRNA.
FT NON_TER 1
FT NON_TER 46
SQ SEQUENCE 46 AA; 5051 MW; 5CF49EED493DDEBB CRC64;

Query Match 35.8%; Score 34; DB 2; Length 46;
Best Local Similarity 63.6%; Pred. No. 6.8e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 KDVLFTFTVKS 13
      | : | | | |
      17 KEVVFANKS 27
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RESULT 6
Q63506 RAT PRELIMINARY; PRT; 18 AA.
AC Q63506;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Rat asialoglycoprotein receptor RHL1 (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=87257885; PubMed=3600647;
RA McPhaul M., Berg P.;
RT Identification and characterization of cDNA clones encoding two
RT homologous proteins that are part of the asialoglycoprotein
RT receptor.
RL Mol. Cell. Biol. 7:1841-1847(1987).
DR EMBL; M16349; AAA42039.1; -; mRNA.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 1988 MW; 43474B8AB145735C CRC64;

Query Match 34.7%; Score 33; DB 2; Length 18;
Best Local Similarity 75.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 VKSCPDAL 18
DB 6 VQSCPSAI 13

RESULT 7
Q4XWD9 PLACH
ID Q4XWD9 PLACH PRELIMINARY; PRT; 32 AA.
AC Q4XWD9;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PC105305.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriaman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrrell B., Turner C.M.K., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses."
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAJ01002657; CAH78772.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 1 1
SQ SEQUENCE 32 AA; 4013 MW; 2906341BFEEFBB6E CRC64;

Query Match 34.7%; Score 33; DB 2; Length 32;
Best Local Similarity 85.7%; Pred. No. 6.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 9 FTVKSCP 15
DB 15 FFVKSCP 21

RESULT 8
Q84TL9 BRARP
ID Q84TL9 BRARP PRELIMINARY; PRT; 37 AA.
AC Q84TL9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transcription factor CRC (Fragment).
OS Brassica rapa subsp. pekinensis (Chinese cabbage) (Celery cabbage).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=51351;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Leaf;
RA Jang H., Hux Y.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY220357; AAO63101.1; -; mRNA.
DR InterPro; IPR006780; YABBY.
DR Pfam; PF04690; YABBY; 1.
FT NON_TER 1 1
FT NON_TER 37 37
SQ SEQUENCE 37 AA; 3937 MW; D87BDE9C33BA34CB CRC64;

Query Match 34.7%; Score 33; DB 2; Length 37;
Best Local Similarity 58.3%; Pred. No. 8e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 PKQVLETFVK 12
DB 3 PLKRLDITVK 14

RESULT 9
Q8E8X0 SHEON
ID Q8E8X0 SHEON PRELIMINARY; PRT; 41 AA.
AC Q8E8X0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein SO4531.
GN OrderedLocustNames=SO4531;
OS Shewanella oneidensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Shewanellaceae; Shewanella.
OX NCBI_TaxID=70863;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=NR-1;
RX MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;
RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA Read T.D., Eisen J.A., Seshadri R., Ward N.L., Methe B.A.,
RA Clayton R.A., Meyer T., Tsapin A., Scott J., Bean M.J.,
RA Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,
RA Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A.,
RA White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Impraim M.,
RA Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J.,
RA Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,
RA Venter J.C., Neilson K.H., Fraser C.M.;
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis."
RL Nat. Biotechnol. 20:1118-1123(2002).
DR EMBL; AR015885; AAN57494.1; -; Genomic_DNA.
DR TIGR; SO4531; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 41 AA; 4596 MW; 3F6B72512EE9CA13 CRC64;
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RX PubMed:15210977; DOI=10.1073/pnas.0306243101;  
 RA Flanagan N.S., Tobler A., Davison A., Pybus O.G., Kapan D.D.,  
 RA Planas S., Linares M., Heckel D., McWilliam W.O.;  
 RT "Historical demography of Mullerian mimicry in the neotropical  
 RT Heliconius butterflies."; *Proc. Natl. Acad. Sci. U.S.A.* 101:9704-9709 (2004)  
 RL

RA Hall N.M., Kallus M., Kaine G.D., Carlton O.M., Kool J.W.A.,  
RA Berlman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,  
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,  
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,  
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,  
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.,  
RT "A comprehensive survey of the Plasmodium life cycle by genomic,  
transcriptomic, and proteomic analyses.",  
RL Science 307:82-86(2005).

CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; CAJ01006357; CAH83908.1; -; Genomic\_DNA.  
KW Hypothetical protein.  
FT NON\_TER 1  
SQ SEQUENCE 43 AA; 4914 MW; 6A0EBAB7BC302A1E CRC64;

Query Match 33.7%; Score 32; DB 2; Length 43;  
Best Local Similarity 35.3%; Pred. No. 1.4e+03;  
Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 2 KKDVLFTFTVKSCPDAI 18  
||:|:|:|:|:|:|  
DB 8 KKIIEKFEHLRCFCDOI 24

RESULT 14  
Q59529 MYCLE PRELIMINARY; PRT; 49 AA.  
AC Q59529;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE CySM (EC 4.2.99.8).  
OS Mycobacterium leprae.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.  
OX NCBI\_TaxID=1769;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Smith D.R.;  
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Robison K.;  
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U00014; AAA50898.1; -; Genomic\_DNA.  
DR PIR; S72793; S72793.  
DR GO; GO:0016829; F-lyase activity; IEA.  
KW Lyase.

SQ SEQUENCE 49 AA; 5575 MW; 8B5B3B41CA813D5E CRC64;

Query Match 33.7%; Score 32; DB 2; Length 49;  
Best Local Similarity 33.3%; Pred. No. 1.6e+03;  
Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 3 KDVLEFTFTVKSC 14  
||:|:|:|:|:|  
DB 38 KDLFPSTVTRTC 49

RESULT 15  
Q82WX8 PYRAE PRELIMINARY; PRT; 35 AA.  
AC Q82WX8;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE PAREP2a.  
GN OrderedLocusNames=PAE1570;  
OS Pyrobaculum aerophilum.  
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;  
OC Thermoproteaceae; Pyrobaculum.  
OX NCBI\_TaxID=13773;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=IN2 / ATCC 51768 / DSM 7523;  
RX MEDLINE=21664397; PubMed=11792859; DOI=10.1073/pnas.241636498;  
RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,  
RA Miller J.H.;  
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum  
aerophilum.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).  
DR EMBL; AR009828; AAL63571.1; -; Genomic\_DNA.  
KW Complete proteome.  
SQ SEQUENCE 35 AA; 4009 MW; 6E27A3D94168BF24 CRC64;

Query Match 33.2%; Score 31.5; DB 2; Length 35;  
Best Local Similarity 41.2%; Pred. No. 1.3e+03;  
Matches 7; Conservative 3; Mismatches 2; Indels 5; Gaps 1;

QY 6 LETFTVKSC-----PDA 17  
:|:|:|:|:|:|:|  
DB 1 METLSVKRCRRVKLFEA 17

RESULT 16  
Q9PRY2 PETMA PRELIMINARY; PRT; 16 AA.  
AC Q9PRY2;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DE Lectin 30 kDa subunit (fragment).  
OS Petromyzon marinus (Sea lamprey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;  
OC Petromyzontiformes; Petromyzontidae; Petromyzon.  
OX NCBI\_TaxID=7757;  
RN [1]  
RP PROTEIN SEQUENCE.  
RX MEDLINE=94249896; PubMed=8192354;  
RA Schluter S.F., Schroeder J., Wang E., Marchalonis J.J.;  
RT "Recognition molecules and immunoglobulin domains in invertebrates.";  
RL Ann. N. Y. Acad. Sci. 712:74-81(1994).  
SQ SEQUENCE 16 AA; 1728 MW; 3BBF03DD4185F446 CRC64;

Query Match 32.6%; Score 31; DB 2; Length 16;  
Best Local Similarity 83.3%; Pred. No. 7.1e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 KSCPPDA 17  
|:|:|:|:|  
DB 5 KGCPDA 10

RESULT 17  
O71992 9RETR PRELIMINARY; PRT; 29 AA.  
AC O71992;  
DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Reverse transcriptase (fragment).  
OS Human endogenous retrovirus.  
OC Viruses; Retroviridae; Retroviridae.  
OX NCBI\_TaxID=11827;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Rose T., Schultz E.R., Henikoff J.G., Pietrokovski S., McCallum C.M.,  
RA Henikoff S.;  
RT "Consensus-degenerate hybrid oligonucleotide primers for amplification  
of distantly-related sequences.";  
RL Nucleic Acids Res. 0:0-0(1998).  
DR EMBL; AF050505; AAC05560.1; -; Genomic DNA.  
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.  
KW RNA-directed DNA polymerase.  
FT NON\_TER 1  
FT NON\_TER 29  
SQ SEQUENCE 29 AA; 3303 MW; CD65212FE4DB04AB CRC64;

Query Match 32.6%; Score 31; DB 2; Length 29;  
Best Local Similarity 71.4%; Pred. No. 1.3e+03;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCP 15

```
Db 17 FTCKKCP 23

RESULT 18
Q65SI7 MANSF
ID Q65SI7_MANSF PRELIMINARY; PRT; 33 AA.
AC Q65SI7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=MS1466;
OS Mannheimia succiniciproducens (strain MBEL55E).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Mannheimia.
OX NCBI_TaxID=221988;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15378067; DOI=10.1038/nbt1010;
RA Hong S.H., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K.,
RA Kim C.H., Jeong H., Hur C.G., Kim J.J.;
RT "The genome sequence of the capnophilic rumen bacterium Mannheimia
RT succiniciproducens.";
RL Nat. Biotechnol. 22:1275-1281(2004).
DR EMBL; AB015827; AAU38073.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 33 AA; 3808 MW; 4CF423D666243384 CRC64;

Query Match 32.6%; Score 31; DB 2; Length 33;
Best Local Similarity 46.7%; Pred. No. 1.5e+03;
Matches 7; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

QY 2 KKDVLFTFTV--KSC 14
|||:|:|:|
Db 17 KKPILKSYLVWEKSC 31

RESULT 19
Q8LKA8 MUSAC
ID Q8LKA8_MUSAC PRELIMINARY; PRT; 35 AA.
AC Q8LKA8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Osmotin-like protein (Fragment).
OS Musa acuminata (Banana).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Musaceae;
OC Musa.
OX NCBI_TaxID=4641;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Regav I., Gepstein S., Khayat E.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF516691; AM69297.1; -; mRNA.
DR HSSP; PJ3679; IDUS.
DR InterPro; IPR001938; Thaumatin.
DR Pfam; PF00314; Thaumatin; 1.
DR ProDom; PD001321; Thaumatin; 1.
FT NON_TER 1
FT NON_TER 35
SQ SEQUENCE 35 AA; 3964 MW; 414338178F1747B2 CRC64;

Query Match 32.6%; Score 31; DB 2; Length 35;
Best Local Similarity 55.6%; Pred. No. 1.6e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPD 17
|:|:|:|
Db 15 FFRKNCPPD 23

RESULT 20
Q8VVR6 STAAU
ID Q8VVR6_STAAU PRELIMINARY; PRT; 41 AA.
AC Q8VVR6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE ORF31.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21562640; PubMed=11705958;
DOI=10.1128/IAI.69.12.7760-7771.2001;
RA Yamaguchi T., Hayashi T., Takami H., Ohnisi M., Murata T.,
RA Nakayama K., Asakawa K., Ohara M., Komatezawa H., Sugai M.;
RT "Complete nucleotide sequence of a Staphylococcus aureus exfoliative
RT toxin B plasmid and identification of a novel ADP-ribosyltransferase,
RT EDIN-C.";
RL Infect. Immun. 69:7760-7771(2001).
DR EMBL; AP003088; BAB78429.1; -; Genomic_DNA.
KW Plasmid.
SQ SEQUENCE 41 AA; 4558 MW; CFE1AAB2C0389744 CRC64;

Query Match 32.6%; Score 31; DB 2; Length 41;
Best Local Similarity 31.2%; Pred. No. 1.9e+03;
Matches 5; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 PKQVLETFVTVKSCPD 16
|||:|:|:|
Db 3 PHKNIVEALNCIALPD 18

RESULT 21
Q8U2U2 PYRFU
ID Q8U2U2_PYRFU PRELIMINARY; PRT; 44 AA.
AC Q8U2U2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein PF0737.
GN OrderedLocusNames=PF0737;
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VC1 / DSM 3638 / ATCC 43587 / JCM 8422;
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT "The complete sequence of the Pyrococcus furiosus genome.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE010192; AAL80861.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 44 AA; 5284 MW; 479C3074528E272E CRC64;

Query Match 32.6%; Score 31; DB 2; Length 44;
Best Local Similarity 58.3%; Pred. No. 2.1e+03;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 PKQVLETFVTVK 12
|||:|:|:|
Db 2 PKSPSLVTLTK 13

RESULT 22
Q7S6Q7 NEUCR
ID Q7S6Q7_NEUCR PRELIMINARY; PRT; 44 AA.
AC Q7S6Q7;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
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DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DE 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DN Predicted protein.
GN Name=NCU05533.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels P., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Tanakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamysseilis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Siller S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -|- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AABX01000322; EAA31259.1; -; Genomic DNA.
SQ SEQUENCE 44 AA; 5283 MW; 5D58B345C3059404 CRC64;

Query Match 32.6%; Score 31; DB 2; Length 44;
Best Local Similarity 39.9%; Pred. No. 2.1e+03;
Matches 7; Conservative 4; Mismatches 5; Indels 2; Gaps 1;

QY 1 PKKDLVLTFTVK--SCPD 16
| : : | : : |
| : : | : : |
Db 2 PEKKLTFTVRRMTAPD 19

RESULT 23
Q928G6 LISIN
ID Q928G6 LISIN PRELIMINARY; PRT; 44 AA.
AC Q928G6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Lin2569 protein.
GN OrderedLocusNames=lin2569;
OS Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CLIP 11262 / Serovar 6a;
RX MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;
RA Glaser P., Frangeul L., Buchrieser C., Ruenik K., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussauguet O.,
RA Etian K.-D., Faihi H., Garcia-del Portillo P., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Krefz J., Kuhn M., Kunst F., Kurapat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordieck G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluster T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
DR EMBL; AL596172; GCA7796.1; -; Genomic DNA.
DR PIR; AD1753; AD1753.

DR Listalist; LIN2569; -.
KW Complete proteome.
SQ SEQUENCE 44 AA; 5094 MW; BB580562E5D52418 CRC64;

Query Match 32.6%; Score 31; DB 2; Length 44;
Best Local Similarity 53.8%; Pred. No. 2.1e+03;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 DVLETFVTKSCPD 16
| : : | : : |
| : : | : : |
Db 4 DDLEMTLGSCLD 16

RESULT 24
Q8G001 BRUSU
ID Q8G001 BRUSU PRELIMINARY; PRT; 44 AA.
AC Q8G001;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=BR1316;
OS Brucella suis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29461;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=1330 / Biovar 1;
RX MEDLINE=22247741; PubMed=12271122; DOI=10.1073/pnas.192319099;
RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
RA Read T.D., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
RA Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J.A.,
RA Van Aken S.B., Riedmuller S., Tettelin H., Gill S.R., White O.,
RA Salzberg S.L., Hoover D.L., Lindler L.E., Hailing S.M., Boyle S.M.,
RA Fraser C.M.;
RT "The Brucella suis genome reveals fundamental similarities between
RT animal and plant pathogens and symbionts.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
DR EMBL; AB014291; AAN30233.1; -; Genomic DNA.
DR TIGR; BR1316; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 44 AA; 4670 MW; A38180FD364DB2FB CRC64;

Query Match 32.6%; Score 31; DB 2; Length 44;
Best Local Similarity 42.9%; Pred. No. 2.1e+03;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 5 VLETFVTKSCPD 18
| : : | : : |
| : : | : : |
Db 12 VLCAFTLSCANTV 25

RESULT 25
Q81Z13 BACAN
ID Q81Z13 BACAN PRELIMINARY; PRT; 48 AA.
AC Q81Z13; G6KXMi;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=BA0463; GBA0463;
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1392;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ames / isolate Porton;
RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
RA Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,

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RA Holtzapple B.K., Okstad O.A., Helgason E., Rillstone J., Wu M.,  
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,  
RA DeBoy R.T., Madpu R., Dougherty S.C., Durkin A.S., Haft D.H.,  
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,  
RA Benton J.L., Mahmoud Y., Jiang L., Hance I.R., Weidman J.F.,  
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,  
RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,  
RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,  
RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;  
RT "The genome sequence of *Bacillus anthracis* Ames and comparison to  
RT closely related bacteria.";  
RL Nature 423:81-86(2003).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Ames / isolate 0581;  
RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,  
RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,  
RA Fraser C.M.;  
RT "Bacillus anthracis comparative genomics";  
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AS017025; AAP24489.1; -; Genomic DNA.  
DR EMBL; AS017334; AAT29559.1; -; Genomic DNA.  
DR TIGR; BA0463; -;  
DR TIGR; GBAA0463; -;  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 48 AA; 5591 MW; B3EECD3DCA388B609 CRC64;  
Query Match 32.6%; Score 31; DB 2; Length 48;  
Best Local Similarity 85.7%; Pred. No. 2.3e+03;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 PKKQVLE 7  
Db 26 PSKQVLE 32  
RESULT 26  
Q4RC18 TETNG  
ID Q4RC18 TETNG PRELIMINARY; PRT; 48 AA.  
AC Q4RC18;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Chromosome 5 SCAF18819, whole genome shotgun sequence.  
DE (Fragment).  
GN ORFNames=GSTENG0038457001;  
OS Tetraodon nigroviridis (Green puffer).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
OC Tetraodontidae; Tetraodontidae; Tetraodon.  
OX NCBI\_TaxID=99883;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,  
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,  
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,  
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,  
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,  
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,  
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;  
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
RT the early vertebrate proto-karyotype.";  
RL Nature 431:946-957(2004).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,  
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,  
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,  
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,  
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,  
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,  
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;  
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
RT the early vertebrate proto-karyotype.";  
RL Nature 431:946-957(2004).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Genoscope; Whitehead Institute Centre for Genome Research;  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.

CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; CAAE01018819; CAG13895.1; -; Genomic DNA.  
FT NON\_TER 1 48  
FT NON\_TER 48 48  
SQ SEQUENCE 48 AA; 5561 MW; ABCB2CCE7B88813F CRC64;  
Query Match 32.6%; Score 31; DB 2; Length 48;  
Best Local Similarity 35.3%; Pred. No. 2.3e+03;  
Matches 6; Conservative 4; Mismatches 7; Indels 0; Gaps 0;  
QY 1 PKKQVLETFYKSCPD 17  
Db 13 PKASMVVXKCVKACSDS 29  
RESULT 27  
Q4RNY7 TETNG  
ID Q4RNY7 TETNG PRELIMINARY; PRT; 48 AA.  
AC Q4RNY7;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Chromosome 10 SCAF15009, whole genome shotgun sequence.  
DE ORFNames=GSTENG00031353001;  
OS Tetraodon nigroviridis (Green puffer).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
OC Tetraodontidae; Tetraodontidae; Tetraodon.  
OX NCBI\_TaxID=99883;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,  
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,  
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,  
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,  
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,  
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,  
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;  
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
RT the early vertebrate proto-karyotype.";  
RL Nature 431:946-957(2004).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Genoscope; Whitehead Institute Centre for Genome Research;  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; CAAE01015009; CAG09895.1; -; Genomic DNA.  
SQ SEQUENCE 48 AA; 5634 MW; F15FPD65C046C13B CRC64;  
Query Match 32.6%; Score 31; DB 2; Length 48;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 PKKQVLE 6  
Db 20 PKKQVLE 25  
RESULT 28  
Q8Z374 SALT  
ID Q8Z374 SALT PRELIMINARY; PRT; 50 AA.  
AC Q8Z374 Q7C6T9;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)  
DE Hypothetical protein STY3659.  
GN OrderedLocusNames=STY3659, t3401,  
OS Salmonella typhi.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Salmonella.  
OX NCBI\_TaxID=601;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=CT18;  
RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;  
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,  
RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,  
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,  
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,  
RA Feltham T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,  
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Farry C.,  
RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,  
RA Whitehead S., Barrall B.G.;  
RT "Complete genome sequence of a multiple drug resistant Salmonella  
enterica serovar Typhi CT18.";  
RL Nature 413:848-852(2001).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Ty2 / ATCC 700931;  
RX MEDLINE=22531367; PubMed=12644504;  
RX DOI=10.1128/JB.185.7.2330-2337.2003;  
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.P., Rose D.J.,  
RA Burlingand V., Kodyanni V., Schwartz D.C., Blattner F.R.;  
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2  
and CT18.";  
RT J. Bacteriol. 185:2330-2337(2003).  
RL EMBL; AL627279; CAD09420.1; -; Genomic\_DNA.  
DR EMBL; AE016845; AK070924.1; -; Genomic\_DNA.  
SQ Complete proteome; Hypothetical protein.  
SQ SEQUENCE 50 AA; 5747 MW; F6BA26E5DFB21F6E CRC64;  
  
Query Match 32.6%; Score 31; DB 2; Length 50;  
Best Local Similarity 75.0%; Pred. No. 2.4e+03;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 PKQVLET 8  
||| |||  
DB 33 PKQSVLKT 40  
  
RESULT 29  
Q4YRD6 PLABE PRELIMINARY; PRT; 40 AA.  
AC Q4YRD6;  
DT 13-SEP-2005 (TREMBlrel. 31, Created)  
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)  
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)  
DE Hypothetical protein.  
GN ORFNames=PB107303.00.0;  
OS Plasmodium berghei.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5821;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,  
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,  
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,  
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,  
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,  
RA Janse C.J., Barrall B., Turner C.M.R., Waters A.P., Sinden R.S.;  
RT "A comprehensive survey of the Plasmodium life cycle by genomic,  
transcriptomic, and proteomic analyses.";  
RT Science 307:82-86(2005).  
RL -!- CAUTION: The sequence shown here is derived from an  
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
preliminary data.

DR EMBL; CAAI01002794; CAH99421.1; -; Genomic\_DNA.  
KW Hypothetical protein.  
SQ SEQUENCE 40 AA; 4792 MW; 8F9ED2034E69675F CRC64;  
  
Query Match 32.1%; Score 30.5; DB 2; Length 40;  
Best Local Similarity 46.7%; Pred. No. 2.3e+03;  
Matches 7; Conservative 2; Mismatches 3; Indels 3; Gaps 1;  
  
QY 2 KQVLETFVVKSCPD 16  
||| : |||  
DB 17 KKHINKLFT---CPD 28  
  
RESULT 30  
Q47605 ECOLI PRELIMINARY; PRT; 16 AA.  
ID Q47605\_ECOLI PRELIMINARY;  
AC Q47605;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)  
DE C protein (Fragment).  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=91139577; PubMed=1995588;  
RA Tao T., Bourne J.C., Blumenthal R.M.;  
RT "A family of regulatory genes associated with type II restriction-  
RT modification systems.";  
RL J. Bacteriol. 173:1367-1375(1991).  
DR EMBL; M63622; AAA24561.1; -; Genomic\_DNA.  
FT NON\_TER 1  
SQ SEQUENCE 16 AA; 1853 MW; E46774511496607C CRC64;  
  
Query Match 31.6%; Score 30; DB 2; Length 16;  
Best Local Similarity 41.7%; Pred. No. 1e+03;  
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
  
QY 3 KQVLETFVVKSC 14  
||| : |||  
DB 1 KDLDFTTGNC 12  
  
RESULT 31  
Q62435 MOUSE PRELIMINARY; PRT; 20 AA.  
ID Q62435\_MOUSE PRELIMINARY;  
AC Q62435;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE Mutant formin (Fragment).  
GN Name=Fmnl; Synonyms=Fmn;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=ldtgbri mutant;  
RX MEDLINE=96394449; PubMed=8798555; DOI=10.1074/jbc.271.38.23472;  
RA Chan D.C., Leder P.;  
RT "Genetic evidence that formins function within the nucleus.";  
RL J. Biol. Chem. 271:23472-23477(1996).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=ldtgbri mutant;  
RA Chan D. C., Leder P.;  
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U60966; AAC52807.1; -; mRNA.  
MG1; MG1:101815; Fmn.

```
DR MGI; MGI:101815; Fmnl.
DR GO; GO:005515; F:protein binding; IPI.
FT NON_TER 1
SQ SEQUENCE 20 AA; 2297 MW; A548619EB899933A CRC64;

Query Match          31.6%; Score 30; DB 2; Length 20;
Best Local Similarity 53.8%; Pred. No. 1.3e+03;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KDVLFTFTVKSCP 15
   ||| ||| |||
Db 2 KDKLEEFKKGSP 14

RESULT 32
Q86487 RVFV
ID Q86487 RVFV PRELIMINARY; PRT; 30 AA.
AC Q86487;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Nonstructural glycoprotein (Fragment).
GN Name=nonstructural glycoprotein;
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=89086601; PubMed=2462795;
RA Battles J.K., Dalrymple J.M.;
RT "Genetic variation among geographic isolates of Rift Valley fever virus.";
RL Am. J. Trop. Med. Hyg. 39:617-631 (1988).
DR EMBL; M33073; AAA47428.1; -; Genomic RNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019012; C:virion; IEA.
DR InterPro; IPR010826; Phlebovirus G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 30
SQ SEQUENCE 30 AA; 3295 MW; D024A1F37F21A6AE CRC64;

Query Match          31.6%; Score 30; DB 2; Length 30;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 LETFTVKSCP 15
   |::| : ||
Db 14 LKSFDISQCP 23

RESULT 33
Q86488 RVFV
ID Q86488 RVFV PRELIMINARY; PRT; 30 AA.
AC Q86488;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Nonstructural glycoprotein (Fragment).
GN Name=nonstructural glycoprotein;
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=89086601; PubMed=2462795;
RA Battles J.K., Dalrymple J.M.;
RT "Genetic variation among geographic isolates of Rift Valley fever virus.";
RL Am. J. Trop. Med. Hyg. 39:617-631 (1988).
DR EMBL; M33076; AAA47431.1; -; Genomic RNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019012; C:virion; IEA.
DR InterPro; IPR010826; Phlebovirus_G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.

DR MGI; MGI:101815; Fmnl.
DR GO; GO:005515; F:protein binding; IPI.
FT NON_TER 1
SQ SEQUENCE 20 AA; 2297 MW; A548619EB899933A CRC64;

Query Match          31.6%; Score 30; DB 2; Length 20;
Best Local Similarity 53.8%; Pred. No. 1.3e+03;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KDVLFTFTVKSCP 15
   ||| ||| |||
Db 2 KDKLEEFKKGSP 14

RESULT 34
Q86489 RVFV
ID Q86489 RVFV PRELIMINARY; PRT; 30 AA.
AC Q86489;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Nonstructural glycoprotein (Fragment).
GN Name=nonstructural glycoprotein;
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=89086601; PubMed=2462795;
RA Battles J.K., Dalrymple J.M.;
RT "Genetic variation among geographic isolates of Rift Valley fever virus.";
RL Am. J. Trop. Med. Hyg. 39:617-631 (1988).
DR EMBL; M33077; AAA47432.1; -; Genomic RNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019012; C:virion; IEA.
DR InterPro; IPR010826; Phlebovirus G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 30
SQ SEQUENCE 30 AA; 3297 MW; 8017A1F36AFB96AC CRC64;

Query Match          31.6%; Score 30; DB 2; Length 30;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 LETFTVKSCP 15
   |::| : ||
Db 14 LKSFDISQCP 23

RESULT 35
Q86490 RVFV
ID Q86490 RVFV PRELIMINARY; PRT; 30 AA.
AC Q86490;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Nonstructural glycoprotein (Fragment).
GN Name=nonstructural glycoprotein;
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=89086601; PubMed=2462795;
RA Battles J.K., Dalrymple J.M.;
RT "Genetic variation among geographic isolates of Rift Valley fever virus.";
RL Am. J. Trop. Med. Hyg. 39:617-631 (1988).
DR EMBL; M33078; AAA47433.1; -; Genomic RNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019012; C:virion; IEA.
DR InterPro; IPR010826; Phlebovirus G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
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FT NON_TER 30 30
SQ SEQUENCE 30 AA; 3269 MW; 933693F37F21A6AC CRC64;

Query Match 31.6%; Score 30; DB 2; Length 30;
Best Local Similarity 40.0%; Pred.No. 2e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 LETFTVKSCP 15
   |::|:|
Db 14 LKSFDISQCP 23

RESULT 36
Q86491 RVFV PRELIMINARY; PRT; 30 AA.
AC Q86491;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Nonstructural glycoprotein (Fragment).
GN Name:nonstructural glycoprotein;
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=89086601; PubMed=2462795;
RA Battles J.K., Dalrymple J.M.;
RT "Genetic variation among geographic isolates of Rift Valley fever virus.";
RL Am. J. Trop. Med. Hyg. 39:617-631(1988).
DR EMBL; M33080; AAA47435.1; -; Genomic RNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019012; C:virion; IEA.
DR InterPro; IPR010826; Phlebovirus_G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 30 30
SQ SEQUENCE 30 AA; 3304 MW; 8017B4137F21A6AC CRC64;

Query Match 31.6%; Score 30; DB 2; Length 30;
Best Local Similarity 40.0%; Pred.No. 2e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 LETFTVKSCP 15
   |::|:|
Db 14 LKSFDISQCP 23

RESULT 37
Q86492 RVFV PRELIMINARY; PRT; 30 AA.
AC Q86492;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Nonstructural glycoprotein (Fragment).
GN Name:nonstructural glycoprotein;
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=89086601; PubMed=2462795;
RA Battles J.K., Dalrymple J.M.;
RT "Genetic variation among geographic isolates of Rift Valley fever virus.";
RL Am. J. Trop. Med. Hyg. 39:617-631(1988).
DR EMBL; M33086; AAA47438.1; -; Genomic RNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019012; C:virion; IEA.
DR InterPro; IPR010826; Phlebovirus_G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 30 30
SQ SEQUENCE 30 AA; 3285 MW; 8017A1F37F21A6AC CRC64;
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SQ SEQUENCE 30 AA; 3297 MW; 8017A1F36AFB96AC CRC64;

Query Match 31.6%; Score 30; DB 2; Length 30;
Best Local Similarity 40.0%; Pred.No. 2e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 LETFTVKSCP 15
   |::|:|
Db 14 LKSFDISQCP 23

RESULT 38
Q86493 RVFV PRELIMINARY; PRT; 30 AA.
AC Q86493;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Nonstructural glycoprotein (Fragment).
GN Name:nonstructural glycoprotein;
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=89086601; PubMed=2462795;
RA Battles J.K., Dalrymple J.M.;
RT "Genetic variation among geographic isolates of Rift Valley fever virus.";
RL Am. J. Trop. Med. Hyg. 39:617-631(1988).
DR EMBL; M33095; AAA47447.1; -; Genomic RNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019012; C:virion; IEA.
DR InterPro; IPR010826; Phlebovirus_G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 30 30
SQ SEQUENCE 30 AA; 3297 MW; 8017BD2B221A6AC CRC64;

Query Match 31.6%; Score 30; DB 2; Length 30;
Best Local Similarity 40.0%; Pred.No. 2e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 LETFTVKSCP 15
   |::|:|
Db 14 LKSFDISQCP 23

RESULT 39
Q04247 RVFV PRELIMINARY; PRT; 30 AA.
AC Q04247;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Nonstructural glycoprotein (Fragment).
GN Name:nonstructural glycoprotein;
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=89086601; PubMed=2462795;
RA Battles J.K., Dalrymple J.M.;
RT "Genetic variation among geographic isolates of Rift Valley fever virus.";
RL Am. J. Trop. Med. Hyg. 39:617-631(1988).
DR EMBL; M33085; AAA47437.1; -; Genomic RNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019012; C:virion; IEA.
DR InterPro; IPR010826; Phlebovirus_G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 30 30
SQ SEQUENCE 30 AA; 3285 MW; 8017A1F37F21A6AC CRC64;
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Query Match 31.6%; Score 30; DB 2; Length 30;  
Best Local Similarity 40.0%; Pred. No. 2e+03;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 6 LETFTVKSCP 15  
|::|:|  
Db 14 LKSFDISQCP 23

RESULT 40  
Q4JFJ3 RVFV  
ID Q4JFJ3\_RVFV PRELIMINARY; PRT; 30 AA.  
AC Q4JFJ3;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DE 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Nonstructural glycoprotein (Fragment).  
GN Name=nonstructural glycoprotein;  
OS Rift valley fever virus (RVFV).  
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.  
OX NCBI\_TaxID=11588;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Zimbabwean isolate ZIM34;  
RX MEDLINE=89086601; PubMed=2462795;  
RA Batties J.K.; Dalrymple J.M.;  
RT "Genetic variation among geographic isolates of Rift Valley fever  
RT virus.";  
RL Am. J. Trop. Med. Hyg. 39:617-631(1988).  
DR EMBL; M33096; AAA47448.1; -; Genomic\_RNA.  
FT NON\_TER 30 30  
SQ SEQUENCE 30 AA; 3285 MW; 8017A1F37F21A6AC CRC64;

Query Match 31.6%; Score 30; DB 2; Length 30;  
Best Local Similarity 40.0%; Pred. No. 2e+03;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 6 LETFTVKSCP 15  
|::|:|  
Db 14 LKSFDISQCP 23

Search completed: January 20, 2006, 17:33:49  
Job time : 40.1111 secs



101	6	7.5	91	4	US-10-282-122A-48985	Sequence 48985, A	174	6	7.5	169	4	US-10-424-599-160487	Sequence 160487,
102	6	7.5	92	4	US-10-437-963-138750	Sequence 138750,	175	6	7.5	171	4	US-10-767-701-141615	Sequence 41615, A
103	6	7.5	93	4	US-10-437-963-161910	Sequence 161910,	176	6	7.5	173	4	US-10-097-111-314	Sequence 314, App
104	6	7.5	92	4	US-10-425-115-243779	Sequence 243779,	177	6	7.5	173	4	US-10-425-115-295975	Sequence 295975,
105	6	7.5	92	5	US-10-732-923-4616	Sequence 4616, App	178	6	7.5	175	5	US-10-128-558-386	Sequence 386, App
106	6	7.5	93	4	US-10-415-478A-56	Sequence 56, App	179	6	7.5	175	5	US-10-450-763-54071	Sequence 54071, A
107	6	7.5	93	5	US-10-472-928-2080	Sequence 2080, App	180	6	7.5	179	4	US-10-425-115-211486	Sequence 211486,
108	6	7.5	95	4	US-10-424-599-183489	Sequence 183489,	181	6	7.5	181	4	US-10-149-819-14	Sequence 14, Appl
109	6	7.5	96	4	US-10-425-114-44440	Sequence 44440, A	182	6	7.5	183	4	US-10-369-493-21469	Sequence 21469, A
110	6	7.5	96	4	US-10-437-963-176947	Sequence 176947,	183	6	7.5	186	5	US-10-472-928-2884	Sequence 2884, Ap
111	6	7.5	97	4	US-10-424-599-137678	Sequence 137678,	184	6	7.5	186	4	US-10-104-047-2159	Sequence 2159, Ap
112	6	7.5	97	5	US-10-947-979-30	Sequence 30, Appl	185	6	7.5	188	4	US-10-767-701-36311	Sequence 36311, A
113	6	7.5	97	5	US-10-947-979-40	Sequence 40, Appl	186	6	7.5	192	4	US-10-112-944-778	Sequence 778, App
114	6	7.5	97	5	US-10-732-923-4612	Sequence 4612, App	187	6	7.5	192	4	US-10-425-115-329363	Sequence 329363,
115	6	7.5	97	5	US-10-732-923-4613	Sequence 4613, App	188	6	7.5	194	4	US-10-437-963-117735	Sequence 117735,
116	6	7.5	97	5	US-10-732-923-4614	Sequence 4614, App	189	6	7.5	197	4	US-10-424-599-176820	Sequence 176820,
117	6	7.5	97	5	US-10-732-923-4615	Sequence 4615, App	190	6	7.5	202	4	US-10-087-192-1308	Sequence 1308, Ap
118	6	7.5	98	4	US-10-425-114-42963	Sequence 42963, A	191	6	7.5	205	4	US-10-424-599-194704	Sequence 194704,
119	6	7.5	98	4	US-10-425-114-53363	Sequence 53363, A	192	6	7.5	205	4	US-10-437-963-117602	Sequence 117602,
120	6	7.5	98	4	US-10-425-114-71946	Sequence 71946, A	193	6	7.5	207	4	US-10-724-972A-5001	Sequence 5001, Ap
121	6	7.5	98	4	US-10-425-115-336280	Sequence 336280,	194	6	7.5	208	4	US-10-767-701-42923	Sequence 42923, A
122	6	7.5	99	4	US-10-425-114-44643	Sequence 44643, A	195	6	7.5	210	4	US-10-148-641A-8	Sequence 8, Appl
123	6	7.5	100	4	US-10-425-115-212744	Sequence 212744,	196	6	7.5	210	4	US-10-767-701-62449	Sequence 62449, A
124	6	7.5	101	4	US-10-425-114-43845	Sequence 43845, A	197	6	7.5	211	4	US-10-425-114-44997	Sequence 44997, A
125	6	7.5	101	4	US-10-425-115-358309	Sequence 358309,	198	6	7.5	212	4	US-10-425-115-348394	Sequence 348394,
126	6	7.5	101	5	US-10-732-923-4620	Sequence 4620, App	199	6	7.5	217	4	US-10-334-143-64	Sequence 64, Appl
127	6	7.5	102	5	US-10-732-923-4620	Sequence 4620, App	200	6	7.5	222	3	US-09-925-301-1244	Sequence 1244, Ap
128	6	7.5	102	5	US-10-450-763-57153	Sequence 57153, A	201	6	7.5	222	4	US-10-437-963-169287	Sequence 169287,
129	6	7.5	103	4	US-10-425-114-42976	Sequence 42976, A	202	6	7.5	225	5	US-10-491-467-40	Sequence 40, Appl
130	6	7.5	103	4	US-10-425-114-46649	Sequence 46649, A	203	6	7.5	225	4	US-10-425-115-333593	Sequence 333593,
131	6	7.5	103	5	US-10-450-763-41575	Sequence 46549, A	204	6	7.5	225	4	US-10-424-599-249946	Sequence 249946,
132	6	7.5	104	4	US-10-425-114-41168	Sequence 41575, A	205	6	7.5	227	4	US-10-282-122A-61111	Sequence 61111, A
133	6	7.5	104	5	US-10-450-763-41882	Sequence 41168, A	206	6	7.5	230	4	US-10-767-701-43040	Sequence 43040, A
134	6	7.5	105	4	US-10-425-114-54962	Sequence 41882, A	207	6	7.5	233	4	US-10-282-122A-57689	Sequence 57689, A
135	6	7.5	106	4	US-10-425-115-337484	Sequence 54962, A	208	6	7.5	235	4	US-10-732-923-7021	Sequence 7021, Ap
136	6	7.5	106	5	US-10-450-763-54070	Sequence 337484,	209	6	7.5	235	5	US-10-425-115-333687	Sequence 33687,
137	6	7.5	107	4	US-10-437-963-171807	Sequence 171807,	210	6	7.5	236	4	US-10-425-115-360181	Sequence 360181,
138	6	7.5	109	4	US-10-264-049-2663	Sequence 2663, App	211	6	7.5	241	4	US-10-425-115-216864	Sequence 216864,
139	6	7.5	110	4	US-10-338-740-200	Sequence 200, App	212	6	7.5	241	6	US-11-097-143-42351	Sequence 42351, A
140	6	7.5	111	4	US-10-425-115-257857	Sequence 257857,	213	6	7.5	244	4	US-10-437-963-189035	Sequence 189035,
141	6	7.5	112	4	US-10-425-114-45629	Sequence 45629, A	214	6	7.5	245	5	US-10-732-923-4604	Sequence 4604, Ap
142	6	7.5	112	4	US-10-425-114-55059	Sequence 55059, A	215	6	7.5	246	5	US-10-501-282-5602	Sequence 5602, Ap
143	6	7.5	113	5	US-10-450-763-41571	Sequence 41571, A	216	6	7.5	247	5	US-10-437-963-114542	Sequence 114542,
144	6	7.5	116	4	US-10-437-963-110411	Sequence 110411,	217	6	7.5	250	4	US-10-408-765A-1534	Sequence 1534, Ap
145	6	7.5	118	4	US-10-282-122A-71025	Sequence 71025, A	218	6	7.5	255	4	US-10-408-765A-1843	Sequence 1843, Ap
146	6	7.5	120	5	US-10-450-763-37587	Sequence 71025, A	219	6	7.5	258	4	US-10-106-698-6371	Sequence 6371, Ap
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148	6	7.5	123	4	US-10-724-972A-5099	Sequence 5099, App	221	6	7.5	259	5	US-10-501-282-34	Sequence 34, Appl
149	6	7.5	123	4	US-10-437-963-118361	Sequence 118361,	222	6	7.5	261	3	US-09-159-469-72	Sequence 72, Appl
150	6	7.5	125	4	US-10-389-566-1697	Sequence 1697, App	223	6	7.5	261	3	US-09-798-042-72	Sequence 72, Appl
151	6	7.5	126	4	US-10-389-566-2001	Sequence 2001, App	224	6	7.5	261	3	US-09-953-108-72	Sequence 72, Appl
152	6	7.5	126	4	US-10-389-566-1742	Sequence 1742, App	225	6	7.5	265	4	US-10-270-845-1	Sequence 1, Appl
153	6	7.5	132	4	US-10-425-115-313709	Sequence 313709,	226	6	7.5	265	4	US-10-224-356-16	Sequence 16, Appl
154	6	7.5	133	4	US-10-424-599-248440	Sequence 248440,	227	6	7.5	265	4	US-10-440-366-16	Sequence 16, Appl
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156	6	7.5	139	4	US-10-425-115-268856	Sequence 268856,	229	6	7.5	274	4	US-10-302-382-10	Sequence 10, Appl
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158	6	7.5	144	4	US-10-082-828A-167	Sequence 167, App	231	6	7.5	275	4	US-10-369-493-19115	Sequence 19115, A
159	6	7.5	144	5	US-10-437-963-126470	Sequence 126470,	232	6	7.5	275	4	US-10-282-122A-72346	Sequence 72346, A
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161	6	7.5	146	4	US-11-057-807-167	Sequence 167, App	234	6	7.5	280	4	US-10-424-599-163943	Sequence 163943,
162	6	7.5	146	4	US-10-091-007-196	Sequence 196, App	235	6	7.5	281	4	US-10-767-701-23334	Sequence 23334, A
163	6	7.5	147	4	US-10-424-599-263420	Sequence 263420,	236	6	7.5	281	5	US-10-732-923-5848	Sequence 5848, Ap
164	6	7.5	148	4	US-10-424-599-147625	Sequence 147625,	237	6	7.5	282	3	US-09-815-242-5576	Sequence 5576, Ap
165	6	7.5	149	5	US-10-741-849-7294	Sequence 7294, App	238	6	7.5	285	4	US-10-156-761-7886	Sequence 7886, Ap
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171	6	7.5	161	3	US-09-953-108-106	Sequence 106, App	244	6	7.5	290	4	US-10-102-806-592	Sequence 592, App
172	6	7.5	166	3	US-09-864-408A-2368	Sequence 2368, App	245	6	7.5	292	3	US-09-815-242-12440	Sequence 12440, A
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248	6	7.5	293	4	US-10-282-122A-60768	Sequence 60768, A	321	6	7.5	387	4	US-10-356-861-140	Sequence 140, App
249	6	7.5	295	5	US-10-721-922A-50	Sequence 50, Appl	322	6	7.5	387	4	US-10-309-584-140	Sequence 140, App
250	6	7.5	296	4	US-10-425-115-19890	Sequence 19890,	323	6	7.5	387	5	US-10-897-793-140	Sequence 140, App
251	6	7.5	297	4	US-10-264-213-233	Sequence 233, App	324	6	7.5	387	5	US-10-783-557-141	Sequence 141, App
252	6	7.5	299	4	US-10-424-598-182535	Sequence 182535,	325	6	7.5	389	4	US-10-243-552-341	Sequence 341, App
253	6	7.5	303	3	US-09-903-190-107	Sequence 107, App	326	6	7.5	390	4	US-10-112-944-321	Sequence 321, App
254	6	7.5	303	3	US-09-978-360A-763	Sequence 763, App	327	6	7.5	390	4	US-10-489-906-2	Sequence 2, Appl
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256	6	7.5	303	4	US-10-408-765A-844	Sequence 844, App	329	6	7.5	391	4	US-10-437-963-193222	Sequence 193222,
257	6	7.5	303	4	US-10-408-765A-845	Sequence 845, App	330	6	7.5	394	4	US-10-156-761-10991	Sequence 10991, A
258	6	7.5	305	4	US-10-930-331-107	Sequence 107, App	331	6	7.5	394	4	US-10-363-493-261	Sequence 261, App
259	6	7.5	305	4	US-10-425-114-42718	Sequence 42718, A	332	6	7.5	397	4	US-10-282-122A-47016	Sequence 47016, A
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261	6	7.5	306	4	US-10-282-122A-62082	Sequence 62082, A	334	6	7.5	399	4	US-10-369-493-671	Sequence 671, App
262	6	7.5	306	4	US-10-425-114-40549	Sequence 40549, A	335	6	7.5	399	4	US-10-369-493-156435	Sequence 156435,
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264	6	7.5	311	5	US-10-721-922A-52	Sequence 52, Appl	337	6	7.5	403	4	US-10-369-493-10827	Sequence 10827, A
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266	6	7.5	314	5	US-10-639-194-6	Sequence 6, Appl	339	6	7.5	404	4	US-10-156-761-9220	Sequence 9220, App
267	6	7.5	316	5	US-10-639-194-2	Sequence 2, Appl	340	6	7.5	405	3	US-09-769-787-62	Sequence 62, Appl
268	6	7.5	318	5	US-10-639-194-10	Sequence 10, Appl	341	6	7.5	405	3	US-10-472-928-3640	Sequence 3640, App
269	6	7.5	319	4	US-10-174-693-323	Sequence 323, App	342	6	7.5	407	4	US-10-437-963-156447	Sequence 156447,
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272	6	7.5	322	4	US-10-321-204-36	Sequence 36, Appl	345	6	7.5	410	4	US-10-369-493-366	Sequence 366, App
273	6	7.5	324	4	US-10-432-737-52	Sequence 52, Appl	346	6	7.5	410	4	US-10-437-963-184086	Sequence 184086,
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282	6	7.5	337	4	US-10-437-963-112732	Sequence 112732,	355	6	7.5	413	3	US-09-821-803A-7	Sequence 7, Appl
283	6	7.5	339	4	US-10-781-014-380	Sequence 380, App	356	6	7.5	413	3	US-09-821-803A-8	Sequence 8, Appl
284	6	7.5	345	4	US-10-209-967-16	Sequence 16, Appl	357	6	7.5	413	4	US-10-270-845-13	Sequence 13, Appl
285	6	7.5	345	4	US-10-209-967-15	Sequence 15, Appl	358	6	7.5	413	4	US-10-270-845-14	Sequence 14, Appl
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290	6	7.5	348	5	US-10-450-763-33541	Sequence 33541, A	363	6	7.5	417	6	US-11-097-143-21408	Sequence 21408, A
291	6	7.5	349	3	US-09-738-626-5897	Sequence 5897, App	364	6	7.5	418	4	US-10-282-122A-43285	Sequence 43285, A
292	6	7.5	350	4	US-10-437-963-184178	Sequence 184178,	365	6	7.5	419	4	US-10-425-114-70713	Sequence 70713, A
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295	6	7.5	356	4	US-10-408-765A-2059	Sequence 2059, App	368	6	7.5	422	4	US-10-437-963-104858	Sequence 104858,
296	6	7.5	356	6	US-11-097-143-10752	Sequence 10752, A	369	6	7.5	424	4	US-10-369-493-10059	Sequence 10059, A
297	6	7.5	360	4	US-10-437-963-155060	Sequence 155060,	370	6	7.5	429	4	US-10-369-493-2850	Sequence 2850, App
298	6	7.5	362	5	US-10-717-665-68	Sequence 68, Appl	371	6	7.5	430	4	US-10-437-963-155712	Sequence 155712,
299	6	7.5	369	4	US-10-424-599-171094	Sequence 171094,	372	6	7.5	433	3	US-09-946-290-14	Sequence 14, Appl
300	6	7.5	369	5	US-10-732-923-2849	Sequence 2849, App	373	6	7.5	433	4	US-10-369-493-22228	Sequence 22228, A
301	6	7.5	369	5	US-10-732-923-3249	Sequence 3249, App	374	6	7.5	433	4	US-10-437-963-113586	Sequence 113586,
302	6	7.5	371	4	US-10-424-599-193125	Sequence 193125,	375	6	7.5	433	5	US-10-324-035-14	Sequence 14, Appl
303	6	7.5	372	4	US-10-108-260A-4280	Sequence 4280, App	376	6	7.5	434	4	US-10-437-963-171802	Sequence 171802,
304	6	7.5	375	4	US-10-431-544-35	Sequence 35, Appl	377	6	7.5	435	4	US-10-437-963-155371	Sequence 155371,
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306	6	7.5	375	5	US-10-830-828-61	Sequence 61, Appl	379	6	7.5	439	4	US-10-382-248-30	Sequence 30, Appl
307	6	7.5	376	5	US-10-780-507-120	Sequence 120, App	380	6	7.5	439	4	US-10-425-115-338498	Sequence 338498,
308	6	7.5	378	5	US-10-501-282-1904	Sequence 1904, App	381	6	7.5	439	4	US-10-425-115-338501	Sequence 338501,
309	6	7.5	379	4	US-10-369-493-3015	Sequence 3015, App	382	6	7.5	440	4	US-10-437-963-149358	Sequence 149358,
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311	6	7.5	381	4	US-10-203-319A-26	Sequence 26, Appl	384	6	7.5	442	4	US-10-369-493-14197	Sequence 14197, A
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313	6	7.5	382	5	US-10-732-923-4753	Sequence 4753, App	386	6	7.5	449	4	US-10-323-281-102	Sequence 102, App
314	6	7.5	384	4	US-09-815-242-10742	Sequence 10742, A	387	6	7.5	451	4	US-10-607-631-18	Sequence 18, Appl
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316	6	7.5	384	6	US-11-097-143-3378	Sequence 3378, App	389	6	7.5	453	4	US-10-369-493-11158	Sequence 11158, A
317	6	7.5	387	3	US-09-940-244-140	Sequence 140, App	390	6	7.5	454	4	US-10-471-115-12	Sequence 12, Appl
318	6	7.5	387	3	US-09-732-622A-140	Sequence 140, App	391	6	7.5	457	4	US-10-437-963-171647	Sequence 171647,
319	6	7.5	387	4	US-10-033-297-140	Sequence 140, App	392	6	7.5	459	4	US-10-369-493-11744	Sequence 11744, A

393	6	7.5	460	3	US-09-975-719-132	Sequence 132, App	466	6	7.5	538	4	US-10-245-033-50	Sequence 50, Appl
394	6	7.5	463	4	US-10-424-599-244931	Sequence 244931,	467	6	7.5	538	4	US-10-243-095-50	Sequence 50, Appl
395	6	7.5	467	4	US-10-437-963-156510	Sequence 156510,	468	6	7.5	538	4	US-10-245-185-50	Sequence 50, Appl
396	6	7.5	468	3	US-09-923-300-1661	Sequence 1661, Ap	469	6	7.5	538	4	US-10-245-427-50	Sequence 50, Appl
397	6	7.5	468	4	US-10-264-049-3018	Sequence 3018, Ap	470	6	7.5	538	4	US-10-245-473-50	Sequence 50, Appl
398	6	7.5	469	4	US-10-437-963-155757	Sequence 155757,	471	6	7.5	538	4	US-10-245-770-50	Sequence 50, Appl
399	6	7.5	470	4	US-10-437-963-139438	Sequence 139438,	472	6	7.5	538	4	US-10-245-877-50	Sequence 50, Appl
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402	6	7.5	475	5	US-10-450-763-46256	Sequence 46256, A	475	6	7.5	538	4	US-10-242-743-50	Sequence 50, Appl
403	6	7.5	478	4	US-10-369-493-15107	Sequence 15107, A	476	6	7.5	538	4	US-10-242-845-50	Sequence 50, Appl
404	6	7.5	480	4	US-10-425-114-43517	Sequence 43517, A	477	6	7.5	538	4	US-10-237-636-50	Sequence 50, Appl
405	6	7.5	480	4	US-10-437-963-139538	Sequence 139538,	478	6	7.5	538	4	US-10-238-325-50	Sequence 50, Appl
406	6	7.5	480	4	US-10-437-963-155449	Sequence 155449,	479	6	7.5	538	4	US-10-238-346-50	Sequence 50, Appl
407	6	7.5	481	4	US-10-104-047-3799	Sequence 3799, Ap	480	6	7.5	538	4	US-10-238-411-50	Sequence 50, Appl
408	6	7.5	482	4	US-10-094-749-2966	Sequence 2966, Ap	481	6	7.5	538	4	US-10-243-124-50	Sequence 50, Appl
409	6	7.5	486	4	US-10-437-963-125679	Sequence 125679,	482	6	7.5	538	4	US-10-243-425-50	Sequence 50, Appl
410	6	7.5	487	4	US-10-369-493-14476	Sequence 14476, A	483	6	7.5	538	4	US-10-243-446-50	Sequence 50, Appl
411	6	7.5	487	6	US-11-097-143-6585	Sequence 6585, Ap	484	6	7.5	538	4	US-10-245-874-50	Sequence 50, Appl
412	6	7.5	489	4	US-10-437-963-155451	Sequence 155451,	485	6	7.5	538	4	US-10-242-653-50	Sequence 50, Appl
413	6	7.5	489	4	US-10-437-963-155665	Sequence 155665,	486	6	7.5	538	4	US-10-243-167-50	Sequence 50, Appl
414	6	7.5	494	4	US-10-425-114-64720	Sequence 64720, A	487	6	7.5	538	4	US-10-243-388-50	Sequence 50, Appl
415	6	7.5	495	4	US-10-369-493-23450	Sequence 23450, A	488	6	7.5	538	4	US-10-244-947-50	Sequence 50, Appl
416	6	7.5	495	4	US-10-282-122A-70223	Sequence 70223, A	489	6	7.5	538	4	US-10-244-968-50	Sequence 50, Appl
417	6	7.5	496	4	US-10-437-963-171669	Sequence 171669,	490	6	7.5	538	4	US-10-244-990-50	Sequence 50, Appl
418	6	7.5	496	5	US-10-739-930-10234	Sequence 10234, A	491	6	7.5	538	4	US-10-245-079-50	Sequence 50, Appl
419	6	7.5	497	4	US-10-282-122A-71807	Sequence 71807, A	492	6	7.5	538	4	US-10-245-127-50	Sequence 50, Appl
420	6	7.5	497	4	US-10-282-122A-74444	Sequence 74444, A	493	6	7.5	538	4	US-10-245-207-50	Sequence 50, Appl
421	6	7.5	498	4	US-10-437-963-150223	Sequence 150223,	494	6	7.5	538	4	US-10-245-646-50	Sequence 50, Appl
422	6	7.5	500	4	US-10-282-132A-57785	Sequence 57785, A	495	6	7.5	538	4	US-10-245-695-50	Sequence 50, Appl
423	6	7.5	501	4	US-10-369-493-10711	Sequence 10711, A	496	6	7.5	538	4	US-10-245-699-50	Sequence 50, Appl
424	6	7.5	502	4	US-10-437-963-152767	Sequence 152767,	497	6	7.5	538	4	US-10-245-737-50	Sequence 50, Appl
425	6	7.5	503	4	US-10-375-657-2	Sequence 2, Appli	498	6	7.5	538	4	US-10-245-878-50	Sequence 50, Appl
426	6	7.5	506	4	US-10-094-749-2229	Sequence 2229, Ap	499	6	7.5	538	4	US-10-245-890-50	Sequence 50, Appl
427	6	7.5	507	6	US-11-097-143-24531	Sequence 24531, A	500	6	7.5	538	4	US-10-245-899-50	Sequence 50, Appl
428	6	7.5	508	2	US-08-781-986A-5241	Sequence 5241, Ap	501	6	7.5	538	4	US-10-245-900-50	Sequence 50, Appl
429	6	7.5	508	4	US-10-329-624-5241	Sequence 5241, Ap	502	6	7.5	538	4	US-10-247-058-50	Sequence 50, Appl
430	6	7.5	508	4	US-10-437-963-141593	Sequence 141593,	503	6	7.5	538	4	US-10-245-454-50	Sequence 50, Appl
431	6	7.5	508	4	US-10-437-963-149381	Sequence 149381,	504	6	7.5	538	4	US-10-237-471-50	Sequence 50, Appl
432	6	7.5	514	4	US-10-425-115-221260	Sequence 221260,	505	6	7.5	538	4	US-10-238-261-50	Sequence 50, Appl
433	6	7.5	519	4	US-10-437-963-155750	Sequence 155750,	506	6	7.5	538	4	US-10-238-324-50	Sequence 50, Appl
434	6	7.5	520	4	US-10-437-963-112331	Sequence 112331,	507	6	7.5	538	4	US-10-241-860-50	Sequence 50, Appl
435	6	7.5	521	4	US-10-060-065-34	Sequence 34, Appl	508	6	7.5	538	4	US-10-242-172-50	Sequence 50, Appl
436	6	7.5	521	4	US-10-059-585-55	Sequence 55, Appl	509	6	7.5	538	4	US-10-242-652-50	Sequence 50, Appl
437	6	7.5	521	4	US-10-341-434-111	Sequence 111, App	510	6	7.5	538	4	US-10-242-990-50	Sequence 50, Appl
438	6	7.5	523	3	US-09-983-531A-24	Sequence 24, Appl	511	6	7.5	538	4	US-10-243-023-50	Sequence 50, Appl
439	6	7.5	528	4	US-10-781-142-6	Sequence 6, Appli	512	6	7.5	538	4	US-10-243-103-50	Sequence 50, Appl
440	6	7.5	529	4	US-10-781-142-9	Sequence 9, Appli	513	6	7.5	538	4	US-10-243-276-50	Sequence 50, Appl
441	6	7.5	529	4	US-10-781-142-13	Sequence 13, Appl	514	6	7.5	538	4	US-10-243-326-50	Sequence 50, Appl
442	6	7.5	533	4	US-10-369-493-17482	Sequence 17482, A	515	6	7.5	538	4	US-10-243-364-50	Sequence 50, Appl
443	6	7.5	536	4	US-10-104-047-2780	Sequence 2780, Ap	516	6	7.5	538	4	US-10-243-494-50	Sequence 50, Appl
444	6	7.5	538	4	US-10-245-752-50	Sequence 50, Appl	517	6	7.5	538	4	US-10-244-995-50	Sequence 50, Appl
445	6	7.5	538	4	US-10-245-859-50	Sequence 50, Appl	518	6	7.5	538	4	US-10-245-230-50	Sequence 50, Appl
446	6	7.5	538	4	US-10-245-103-50	Sequence 50, Appl	519	6	7.5	538	4	US-10-245-253-50	Sequence 50, Appl
447	6	7.5	538	4	US-10-245-107-50	Sequence 50, Appl	520	6	7.5	538	4	US-10-245-479-50	Sequence 50, Appl
448	6	7.5	538	4	US-10-245-143-50	Sequence 50, Appl	521	6	7.5	538	4	US-10-245-499-50	Sequence 50, Appl
449	6	7.5	538	4	US-10-245-771-50	Sequence 50, Appl	522	6	7.5	538	4	US-10-245-772-50	Sequence 50, Appl
450	6	7.5	538	4	US-10-245-851-50	Sequence 50, Appl	523	6	7.5	538	4	US-10-245-811-50	Sequence 50, Appl
451	6	7.5	538	4	US-10-245-883-50	Sequence 50, Appl	524	6	7.5	538	4	US-10-245-812-50	Sequence 50, Appl
452	6	7.5	538	4	US-10-237-535-50	Sequence 50, Appl	525	6	7.5	538	4	US-10-245-852-50	Sequence 50, Appl
453	6	7.5	538	4	US-10-238-183-50	Sequence 50, Appl	526	6	7.5	538	4	US-10-245-875-50	Sequence 50, Appl
454	6	7.5	538	4	US-10-238-283-50	Sequence 50, Appl	527	6	7.5	538	4	US-10-245-881-50	Sequence 50, Appl
455	6	7.5	538	4	US-10-238-370-50	Sequence 50, Appl	528	6	7.5	538	4	US-10-245-911-50	Sequence 50, Appl
456	6	7.5	538	4	US-10-245-055-50	Sequence 50, Appl	529	6	7.5	538	4	US-10-245-913-50	Sequence 50, Appl
457	6	7.5	538	4	US-10-245-147-50	Sequence 50, Appl	530	6	7.5	538	4	US-10-246-080-50	Sequence 50, Appl
458	6	7.5	538	4	US-10-245-730-50	Sequence 50, Appl	531	6	7.5	538	4	US-10-246-121-50	Sequence 50, Appl
459	6	7.5	538	4	US-10-245-739-50	Sequence 50, Appl	532	6	7.5	538	4	US-10-246-305-50	Sequence 50, Appl
460	6	7.5	538	4	US-10-246-210-50	Sequence 50, Appl	533	6	7.5	538	4	US-10-246-929-50	Sequence 50, Appl
461	6	7.5	538	4	US-10-233-136-50	Sequence 50, Appl	534	6	7.5	538	4	US-10-247-036-50	Sequence 50, Appl
462	6	7.5	538	4	US-10-243-024-50	Sequence 50, Appl	535	6	7.5	538	4	US-10-243-255-50	Sequence 50, Appl
463	6	7.5	538	4	US-10-243-409-50	Sequence 50, Appl	536	6	7.5	538	4	US-10-245-810-50	Sequence 50, Appl
464	6	7.5	538	4	US-10-245-621-50	Sequence 50, Appl	537	6	7.5	538	4	US-10-245-910-50	Sequence 50, Appl
465	6	7.5	538	4	US-10-245-880-50	Sequence 50, Appl	538	6	7.5	538	4	US-10-246-098-50	Sequence 50, Appl

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540	6	7.5	4	US-10-242-074-50	Sequence 50, Appl	613	6	7.5	3	US-09-822-827-818	Sequence 818, App
541	6	7.5	4	US-10-242-505-50	Sequence 50, Appl	614	6	7.5	3	US-09-895-793-818	Sequence 818, App
542	6	7.5	4	US-10-242-574-50	Sequence 50, Appl	615	6	7.5	3	US-09-895-814-818	Sequence 818, App
543	6	7.5	4	US-10-243-261-50	Sequence 50, Appl	616	6	7.5	4	US-10-012-896-818	Sequence 818, App
544	6	7.5	4	US-10-243-282-50	Sequence 50, Appl	617	6	7.5	4	US-10-144-678A-818	Sequence 818, App
545	6	7.5	4	US-10-243-402-50	Sequence 50, Appl	618	6	7.5	4	US-10-294-025-818	Sequence 818, App
546	6	7.5	4	US-10-243-431-50	Sequence 50, Appl	619	6	7.5	5	US-10-511-556-17	Sequence 17, Appl
547	6	7.5	4	US-10-245-164-50	Sequence 50, Appl	620	6	7.5	5	US-10-511-556-19	Sequence 19, Appl
548	6	7.5	4	US-10-210-951-70	Sequence 70, Appl	621	6	7.5	5	US-10-732-923-23083	Sequence 23083, A
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550	6	7.5	4	US-10-197-942-50	Sequence 50, Appl	623	6	7.5	6	US-09-983-531A-12	Sequence 12, Appl
551	6	7.5	4	US-10-211-884-70	Sequence 70, Appl	624	6	7.5	6	US-10-316-253-273	Sequence 273, App
552	6	7.5	4	US-10-238-196-50	Sequence 50, Appl	625	6	7.5	6	US-10-282-122A-70746	Sequence 70746, A
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555	6	7.5	4	US-09-815-242-11206	Sequence 11206, A	628	6	7.5	704	US-10-418-819-2	Sequence 2, Appl
556	6	7.5	4	US-10-411-253-2	Sequence 2, Appl	629	6	7.5	704	US-10-418-819-4	Sequence 4, Appl
557	6	7.5	4	US-10-282-122A-58451	Sequence 58451, A	630	6	7.5	704	US-10-418-819-8	Sequence 8, Appl
558	6	7.5	4	US-10-741-600-1473	Sequence 1473, Ap	631	6	7.5	704	US-10-418-819-10	Sequence 10, Appl
559	6	7.5	5	US-10-714-470-1	Sequence 1, Appl	632	6	7.5	706	US-10-425-115-334013	Sequence 334013, A
560	6	7.5	5	US-10-714-470-3	Sequence 3, Appl	633	6	7.5	713	US-10-058-513-35	Sequence 35, Appl
561	6	7.5	5	US-10-732-923-18404	Sequence 18404, A	634	6	7.5	715	US-09-815-242-10450	Sequence 10450, A
562	6	7.5	5	US-10-411-253-4	Sequence 4, Appl	635	6	7.5	715	US-10-369-493-23660	Sequence 23660, A
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564	6	7.5	5	US-10-282-122A-78003	Sequence 78003, A	637	6	7.5	715	US-10-282-122A-75843	Sequence 75843, A
565	6	7.5	5	US-10-732-923-18342	Sequence 18342, A	638	6	7.5	719	US-09-159-469-59	Sequence 59, Appl
566	6	7.5	4	US-10-053-248-10	Sequence 10, Appl	639	6	7.5	719	US-09-798-042-59	Sequence 59, Appl
567	6	7.5	4	US-10-364-748-2	Sequence 2, Appl	640	6	7.5	722	US-09-953-108-59	Sequence 120558, A
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571	6	7.5	6	US-11-097-143-36531	Sequence 36531, A	644	6	7.5	727	US-10-369-493-22535	Sequence 22535, A
572	6	7.5	4	US-10-788-792-187	Sequence 187, App	645	6	7.5	729	US-09-978-697-74	Sequence 74, Appl
573	6	7.5	4	US-10-389-566-643	Sequence 643, App	646	6	7.5	735	US-09-978-295A-74	Sequence 74, Appl
574	6	7.5	4	US-10-389-566-654	Sequence 654, App	647	6	7.5	735	US-09-978-688A-74	Sequence 74, Appl
575	6	7.5	4	US-10-389-566-654	Sequence 654, App	648	6	7.5	735	US-09-978-688A-74	Sequence 74, Appl
576	6	7.5	4	US-10-425-115-198892	Sequence 198892, A	649	6	7.5	735	US-09-978-192A-74	Sequence 74, Appl
577	6	7.5	5	US-10-425-115-198880	Sequence 198880, A	650	6	7.5	735	US-09-978-191A-74	Sequence 74, Appl
578	6	7.5	3	US-09-949-029-38	Sequence 38, Appl	651	6	7.5	735	US-09-978-189-74	Sequence 74, Appl
579	6	7.5	6	US-11-097-143-2331	Sequence 2331, Ap	652	6	7.5	735	US-09-978-608A-74	Sequence 74, Appl
580	6	7.5	6	US-10-424-599-232754	Sequence 232754, A	653	6	7.5	735	US-09-978-585A-74	Sequence 74, Appl
581	6	7.5	2	US-08-808-031A-28	Sequence 28, Appl	654	6	7.5	735	US-09-978-191A-74	Sequence 74, Appl
582	6	7.5	4	US-10-369-493-21186	Sequence 21186, A	655	6	7.5	735	US-09-978-403A-74	Sequence 74, Appl
583	6	7.5	5	US-10-450-763-51530	Sequence 51530, A	656	6	7.5	735	US-09-978-564A-74	Sequence 74, Appl
584	6	7.5	4	US-10-437-963-189326	Sequence 189326, A	657	6	7.5	735	US-09-999-833A-74	Sequence 74, Appl
585	6	7.5	4	US-10-437-963-147363	Sequence 147363, A	658	6	7.5	735	US-09-978-824-74	Sequence 74, Appl
586	6	7.5	5	US-10-450-763-49527	Sequence 49527, A	659	6	7.5	735	US-09-918-585A-74	Sequence 74, Appl
587	6	7.5	4	US-10-424-599-222753	Sequence 222753, A	660	6	7.5	735	US-09-999-834A-74	Sequence 74, Appl
588	6	7.5	4	US-10-425-114-44126	Sequence 44126, A	661	6	7.5	735	US-09-978-423A-74	Sequence 74, Appl
589	6	7.5	4	US-10-389-647-688	Sequence 688, App	662	6	7.5	735	US-09-978-193A-74	Sequence 74, Appl
590	6	7.5	4	US-10-437-963-139771	Sequence 139771, A	663	6	7.5	735	US-09-999-830A-74	Sequence 74, Appl
591	6	7.5	4	US-10-425-115-239971	Sequence 239971, A	664	6	7.5	735	US-09-978-757A-74	Sequence 74, Appl
592	6	7.5	4	US-10-424-599-259258	Sequence 259258, A	665	6	7.5	735	US-09-978-187B-74	Sequence 74, Appl
593	6	7.5	605	US-10-425-115-360159	Sequence 360159, A	666	6	7.5	735	US-09-978-643A-74	Sequence 74, Appl
594	6	7.5	606	US-10-437-963-148183	Sequence 148183, A	667	6	7.5	735	US-09-978-375A-74	Sequence 74, Appl
595	6	7.5	607	US-10-732-923-23200	Sequence 23200, A	668	6	7.5	735	US-09-978-544A-74	Sequence 74, Appl
596	6	7.5	4	US-10-282-122A-53029	Sequence 53029, A	669	6	7.5	735	US-09-978-802A-74	Sequence 74, Appl
597	6	7.5	616	US-10-425-115-309918	Sequence 309918, A	670	6	7.5	735	US-09-978-681A-74	Sequence 74, Appl
598	6	7.5	617	US-10-732-923-3151	Sequence 3151, Ap	671	6	7.5	735	US-09-978-194A-74	Sequence 74, Appl
599	6	7.5	619	US-10-437-963-159314	Sequence 159314, A	672	6	7.5	735	US-09-999-831A-74	Sequence 74, Appl
600	6	7.5	623	US-10-437-963-201896	Sequence 201896, A	673	6	7.5	735	US-09-978-802A-74	Sequence 74, Appl
601	6	7.5	624	US-10-425-114-71490	Sequence 71490, A	674	6	7.5	735	US-09-978-824-74	Sequence 74, Appl
602	6	7.5	624	US-10-437-963-138441	Sequence 138441, A	675	6	7.5	735	US-10-052-586-88	Sequence 88, Appl
603	6	7.5	624	US-10-425-115-226416	Sequence 226416, A	676	6	7.5	735	US-10-176-758-88	Sequence 88, Appl
604	6	7.5	633	US-10-425-114-43725	Sequence 43725, A	677	6	7.5	735	US-10-175-737-88	Sequence 88, Appl
605	6	7.5	638	US-10-437-963-189105	Sequence 189105, A	678	6	7.5	735	US-10-174-581-88	Sequence 88, Appl
606	6	7.5	639	US-10-437-963-189095	Sequence 189095, A	679	6	7.5	735		
607	6	7.5	643	US-11-097-143-10962	Sequence 10962, A	680	6	7.5	735		
608	6	7.5	645	US-10-975-045-14	Sequence 14, Appl	681	6	7.5	735		
609	6	7.5	650	US-10-282-122A-48741	Sequence 48741, A	682	6	7.5	735		
610	6	7.5	651	US-10-058-513-3	Sequence 3, Appl	683	6	7.5	735		
611	6	7.5	652	US-09-759-143-818	Sequence 818, App	684	6	7.5	735		

685	6	7.5	735	4	US-10-176-483-88	Sequence 88, Appl	758	6	7.5	735	4	US-10-176-990-88	Sequence 88, Appl
686	6	7.5	735	4	US-10-176-749-88	Sequence 88, Appl	759	6	7.5	735	4	US-10-180-541-88	Sequence 88, Appl
687	6	7.5	735	4	US-10-176-914-88	Sequence 88, Appl	760	6	7.5	735	4	US-10-180-542-88	Sequence 88, Appl
688	6	7.5	735	4	US-10-176-915-88	Sequence 88, Appl	761	6	7.5	735	4	US-10-180-548-88	Sequence 88, Appl
689	6	7.5	735	4	US-10-173-706-88	Sequence 88, Appl	762	6	7.5	735	4	US-10-180-551-88	Sequence 88, Appl
690	6	7.5	735	4	US-10-175-738-88	Sequence 88, Appl	763	6	7.5	735	4	US-10-180-998-88	Sequence 88, Appl
691	6	7.5	735	4	US-10-175-752-88	Sequence 88, Appl	764	6	7.5	735	4	US-10-180-999-88	Sequence 88, Appl
692	6	7.5	735	4	US-10-176-482-88	Sequence 88, Appl	765	6	7.5	735	4	US-10-183-013-88	Sequence 88, Appl
693	6	7.5	735	4	US-10-176-757-88	Sequence 88, Appl	766	6	7.5	735	4	US-10-184-612-88	Sequence 88, Appl
694	6	7.5	735	4	US-10-176-913-88	Sequence 88, Appl	767	6	7.5	735	4	US-10-184-616-88	Sequence 88, Appl
695	6	7.5	735	4	US-10-180-552-88	Sequence 88, Appl	768	6	7.5	735	4	US-10-184-617-88	Sequence 88, Appl
696	6	7.5	735	4	US-10-180-557-88	Sequence 88, Appl	769	6	7.5	735	4	US-10-184-622-88	Sequence 88, Appl
697	6	7.5	735	4	US-10-173-700-88	Sequence 88, Appl	770	6	7.5	735	4	US-10-184-628-88	Sequence 88, Appl
698	6	7.5	735	4	US-10-174-572-88	Sequence 88, Appl	771	6	7.5	735	4	US-10-184-629-88	Sequence 88, Appl
699	6	7.5	735	4	US-10-174-579-88	Sequence 88, Appl	772	6	7.5	735	4	US-10-184-630-88	Sequence 88, Appl
700	6	7.5	735	4	US-10-174-582-88	Sequence 88, Appl	773	6	7.5	735	4	US-10-184-631-88	Sequence 88, Appl
701	6	7.5	735	4	US-10-174-588-88	Sequence 88, Appl	774	6	7.5	735	4	US-10-184-632-88	Sequence 88, Appl
702	6	7.5	735	4	US-10-175-739-88	Sequence 88, Appl	775	6	7.5	735	4	US-10-184-636-88	Sequence 88, Appl
703	6	7.5	735	4	US-10-175-740-88	Sequence 88, Appl	776	6	7.5	735	4	US-10-184-640-88	Sequence 88, Appl
704	6	7.5	735	4	US-10-175-743-88	Sequence 88, Appl	777	6	7.5	735	4	US-10-184-650-88	Sequence 88, Appl
705	6	7.5	735	4	US-10-176-488-88	Sequence 88, Appl	778	6	7.5	735	4	US-10-184-651-88	Sequence 88, Appl
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ALIGNMENTS

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; Publication No. US20020115214A1  
; GENERAL INFORMATION:  
; APPLICANT: June, Carl H.  
; APPLICANT: Thompson, Craig B.  
; APPLICANT: Nabel, Gary J.  
; APPLICANT: Gray, Gary S.  
; APPLICANT: Rennert, Paul D.  
; TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
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; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/592,711  
; FILING DATE: 26-JAN-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/435,816  
; FILING DATE: 4-MAY-1995  
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; FILING DATE: 3-JUNE-1994  
; APPLICATION NUMBER: US 08/073,223  
; FILING DATE: 4-JUNE-1993  
; APPLICATION NUMBER: US 08/200,947  
; FILING DATE: 23-FEB-1994  
; APPLICATION NUMBER: US 07/864,805  
; FILING DATE: 7-APR-1992  
; APPLICATION NUMBER: US 08/247,505  
; FILING DATE: 23-MAY-1994  
; APPLICATION NUMBER: US 07/864,866  
; FILING DATE: 7-APR-1992

; APPLICATION NUMBER: US 08/218,155  
; FILING DATE: 25-MAR-1994  
; APPLICATION NUMBER: US 07/864,807  
; FILING DATE: 7-APR-1992  
; APPLICATION NUMBER: US 07/902,467  
; FILING DATE: 16-JUNE-1992  
; APPLICATION NUMBER: US 07/275,433  
; FILING DATE: 23-NOV-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mandragouras, Amy E.  
; REGISTRATION NUMBER: 36,207  
; REFERENCE/DOCKET NUMBER: RPI-002CP4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 227 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-592-711-6  
Query Match 100.0%; Score 80; DB 2; Length 227;  
Best Local Similarity 100.0%; Pred. No. 6.5e-75;  
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HKDEVKEVQFYKDTYNTKLTQBPQRETLKAIHYALNCCGLAGGVQFISDICPKKV 60  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 61 LETFTVKSCPDAIKEVFDNK 80  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
172 LETFTVKSCPDAIKEVFDNK 191  
RESULT 2  
US-09-183-055-6  
; Sequence 6, Application US/09183055  
; Publication No. US20020076407A1  
; GENERAL INFORMATION:  
; APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.  
; APPLICANT: Gray, Gary S., Rennert, Paul D.  
; TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: HALE AND DORR LLP  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/183,055  
; FILING DATE: 30-Oct-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/403,253  
; FILING DATE: March 10, 1995  
; APPLICATION NUMBER: US 08/253,964  
; FILING DATE: 3 JUNE 1994  
; APPLICATION NUMBER: US 08/073,223  
; FILING DATE: 4 JUNE 1993  
; APPLICATION NUMBER: US 08/200,947  
; FILING DATE: 23 FEB 1994  
; APPLICATION NUMBER: US 07/864,805  
; FILING DATE: 7 APR 1992

```

; APPLICATION NUMBER: US 08/247,505
; FILING DATE: 23 MAY 1994
; APPLICATION NUMBER: US 07/864,866
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/218,155
; FILING DATE: 25 MAR 1994
; APPLICATION NUMBER: US 07/864,807
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 07/902,467
; FILING DATE: 16 JUNE 1992
; APPLICATION NUMBER: US 07/275,433
; FILING DATE: 23 NOV 1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Superko, Colleen
; REGISTRATION NUMBER: 39,850
; REFERENCE/DOCKET NUMBER: 36119-125US8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 526-5500
; TELEFAX: (617) 526-5564
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-183-055-6

; Query Match 100.0%; Score 80; DB 3; Length 227;
; Best Local Similarity 100.0%; Pred. No. 6.5e-75;
; Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HKDEVIKEVQEFYKDTYNKLTQDPQRETLKAIHYALNCCGLAGVQFISDIPKKDV 60
DB 112 HKDEVIKEVQEFYKDTYNKLTQDPQRETLKAIHYALNCCGLAGVQFISDIPKKDV 171
QY 61 LETFTVKSCPDAIKEVFDNK 80
DB 172 LETFTVKSCPDAIKEVFDNK 191

RESULT 3
US-09-350-202-6
; Sequence 6, Application US/09350202
; Publication No. US20030099643A1
; GENERAL INFORMATION:
; APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.
; APPLICANT: Gray, Gary S., Rennert, Paul D.
; TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/350,202
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/403,253
; FILING DATE: March 10, 1995
; APPLICATION NUMBER: US 08/253,964
; FILING DATE: 3 JUNE 1994
; APPLICATION NUMBER: US 08/073,223
; FILING DATE: 4 JUNE 1993

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; APPLICATION NUMBER: US 08/200,947
; FILING DATE: 23 FEB 1994
; APPLICATION NUMBER: US 07/864,805
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/247,505
; FILING DATE: 23 MAY 1994
; APPLICATION NUMBER: US 07/864,866
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/218,155
; FILING DATE: 25 MAR 1994
; APPLICATION NUMBER: US 07/864,807
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 07/902,467
; FILING DATE: 16 JUNE 1992
; APPLICATION NUMBER: US 07/275,433
; FILING DATE: 23 NOV 1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy B.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-350-202-6

; Query Match 100.0%; Score 80; DB 3; Length 227;
; Best Local Similarity 100.0%; Pred. No. 6.5e-75;
; Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HKDEVIKEVQEFYKDTYNKLTQDPQRETLKAIHYALNCCGLAGVQFISDIPKKDV 60
DB 112 HKDEVIKEVQEFYKDTYNKLTQDPQRETLKAIHYALNCCGLAGVQFISDIPKKDV 171
QY 61 LETFTVKSCPDAIKEVFDNK 80
DB 172 LETFTVKSCPDAIKEVFDNK 191

RESULT 4
US-10-390-330-6
; Sequence 6, Application US/10390330
; Publication No. US20040001829A1
; GENERAL INFORMATION:
; APPLICANT: June, Carl H.
; APPLICANT: Thompson, Craig B.
; APPLICANT: Nabel, Gary J.
; APPLICANT: Gray, Gary S.
; APPLICANT: Rennert, Paul D.
; TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/390,330
; FILING DATE: March 17, 2003
; CLASSIFICATION:

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/435,816A
; FILING DATE: May 4, 1995
; CLASSIFICATION:
; APPLICATION NUMBER: US 08/403,253
; FILING DATE: 10 MARCH 1995
; APPLICATION NUMBER: US 08/253,964
; FILING DATE: 3 JUNE 1994
; APPLICATION NUMBER: US 08/073,223
; FILING DATE: 4 JUNE 1993
; APPLICATION NUMBER: US 08/200,947
; FILING DATE: 23 FEB 1994
; APPLICATION NUMBER: US 07/864,805
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/247,505
; FILING DATE: 23 MAY 1994
; APPLICATION NUMBER: US 07/864,866
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/218,155
; FILING DATE: 25 MAR 1994
; APPLICATION NUMBER: US 07/864,807
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 07/902,467
; FILING DATE: 16 JUNE 1992
; APPLICATION NUMBER: US 07/275,433
; FILING DATE: 23 NOV 1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-10-390-330-6

Query Match 100.0%; Score 80; DB 4; Length 227;
Best Local Similarity 100.0%; Pred. No. 6.5e-75;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVIKEVQEFYKDTYNNKLTKDPEQRETLKAHYALNCCGLAGGVQEFISDIPCCKDV 60
Db 112 HKDEVIKEVQEFYKDTYNNKLTKDPEQRETLKAHYALNCCGLAGGVQEFISDIPCCKDV 171

QY 61 LETFTVKSCPDAlKEVFDNK 80
Db 172 LETFTVKSCPDAlKEVFDNK 191

RESULT 5
US-10-473-127-1723
; Sequence 1723, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026WO1
; CURRENT APPLICATION NUMBER: US/10/473,127
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1726
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-473-127-1726

Query Match 100.0%; Score 80; DB 5; Length 227;
Best Local Similarity 100.0%; Pred. No. 6.5e-75;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVIKEVQEFYKDTYNNKLTKDPEQRETLKAHYALNCCGLAGGVQEFISDIPCCKDV 60
Db 112 HKDEVIKEVQEFYKDTYNNKLTKDPEQRETLKAHYALNCCGLAGGVQEFISDIPCCKDV 171

QY 61 LETFTVKSCPDAlKEVFDNK 80
Db 172 LETFTVKSCPDAlKEVFDNK 191

RESULT 6
US-10-473-127-1726
; Sequence 1726, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026WO1
; CURRENT APPLICATION NUMBER: US/10/473,127
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1726
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-473-127-1726

Query Match 100.0%; Score 80; DB 5; Length 227;
Best Local Similarity 100.0%; Pred. No. 6.5e-75;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVIKEVQEFYKDTYNNKLTKDPEQRETLKAHYALNCCGLAGGVQEFISDIPCCKDV 60
Db 112 HKDEVIKEVQEFYKDTYNNKLTKDPEQRETLKAHYALNCCGLAGGVQEFISDIPCCKDV 171

QY 61 LETFTVKSCPDAlKEVFDNK 80
Db 172 LETFTVKSCPDAlKEVFDNK 191

RESULT 7
US-10-156-136-39
; Sequence 39, Application US/10156136
; Publication No. US20030129696A1
; GENERAL INFORMATION:
; APPLICANT: Ni, et al.
```

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; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1723
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-473-127-1723

Query Match 100.0%; Score 80; DB 5; Length 227;
Best Local Similarity 100.0%; Pred. No. 6.5e-75;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVIKEVQEFYKDTYNNKLTKDPEQRETLKAHYALNCCGLAGGVQEFISDIPCCKDV 60
Db 112 HKDEVIKEVQEFYKDTYNNKLTKDPEQRETLKAHYALNCCGLAGGVQEFISDIPCCKDV 171

QY 61 LETFTVKSCPDAlKEVFDNK 80
Db 172 LETFTVKSCPDAlKEVFDNK 191

RESULT 6
US-10-473-127-1726
; Sequence 1726, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026WO1
; CURRENT APPLICATION NUMBER: US/10/473,127
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1726
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-473-127-1726

Query Match 100.0%; Score 80; DB 5; Length 227;
Best Local Similarity 100.0%; Pred. No. 6.5e-75;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVIKEVQEFYKDTYNNKLTKDPEQRETLKAHYALNCCGLAGGVQEFISDIPCCKDV 60
Db 112 HKDEVIKEVQEFYKDTYNNKLTKDPEQRETLKAHYALNCCGLAGGVQEFISDIPCCKDV 171

QY 61 LETFTVKSCPDAlKEVFDNK 80
Db 172 LETFTVKSCPDAlKEVFDNK 191

RESULT 7
US-10-156-136-39
; Sequence 39, Application US/10156136
; Publication No. US20030129696A1
; GENERAL INFORMATION:
; APPLICANT: Ni, et al.
```



## TITLE OF INVENTION: Polynucleotides and Polypeptides Encoding Receptors

NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESS:

ADDRESSER: Human Genome Sciences, Inc.

STREET: 9410 Key West Ave

CITY: Rockville

STATE: MD

COUNTRY: US

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/156,136

FILING DATE: 29-May-2002

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/010,146

FILING DATE: &lt;Unknown&gt;

APPLICATION NUMBER: WO US98/00959

FILING DATE: 21-JAN-1998

ATTORNEY/AGENT INFORMATION:

NAME: A. Anders Brookes

REGISTRATION NUMBER: 36,373

REFERENCE/DOCKET NUMBER: PF354PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 301-309-8504

TELEFAX: 301-309-8439

INFORMATION FOR SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS:

LENGTH: 228 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 39:

US-10-156-136-39

Query Match 100.0%; Score 80; DB 4; Length 228;  
Best Local Similarity 100.0%; Pred. No. 6.5e-75;  
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVIKEVQEFYKDTYNKLTQDEPQRETLKAHYALNCCGLAGGVQFISDIPCKDV 60  
|||||  
Db 113 HKDEVIKEVQEFYKDTYNKLTQDEPQRETLKAHYALNCCGLAGGVQFISDIPCKDV 172

QY 61 LETFTVKSCPDAIKEVFNK 80  
|||||  
Db 173 LETFTVKSCPDAIKEVFNK 192

## RESULT 8

US-10-331-496A-41

Sequence 41, Application US/10331496A

Publication No. US20030228305A1

GENERAL INFORMATION:

APPLICANT: FRANTZ, GRETCHEN

APPLICANT: HILLAN, KENNETH J.

APPLICANT: PHILLIPS, HEIDI S.

APPLICANT: POLAKIS, PAUL

APPLICANT: SMITH, VICTORIA

APPLICANT: SPENCER, SUSAN D.

APPLICANT: WILLIAMS, P. MICKEY

APPLICANT: WU, THOMAS D.

APPLICANT: ZHANG, ZEMIN

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND

TREATMENT OF TUMOR

FILE REFERENCE: P5014R1-PCT

CURRENT APPLICATION NUMBER: US/10/331,496A

CURRENT FILING DATE: 2002-12-30

PRIOR APPLICATION NUMBER: US 60/345,444  
PRIOR FILING DATE: 2002-01-02  
PRIOR APPLICATION NUMBER: US 60/351,885  
PRIOR FILING DATE: 2002-01-25  
PRIOR APPLICATION NUMBER: US 60/360,066  
PRIOR FILING DATE: 2002-02-25  
PRIOR APPLICATION NUMBER: US 60/362,004  
PRIOR FILING DATE: 2002-03-05  
PRIOR APPLICATION NUMBER: US 60/366,869  
PRIOR FILING DATE: 2002-03-20  
PRIOR APPLICATION NUMBER: US 60/366,284  
PRIOR FILING DATE: 2002-03-21  
PRIOR APPLICATION NUMBER: US 60/368,679  
PRIOR FILING DATE: 2002-03-28  
PRIOR APPLICATION NUMBER: US 60/404,809  
PRIOR FILING DATE: 2002-08-19  
PRIOR APPLICATION NUMBER: US 60/405,645  
PRIOR FILING DATE: 2002-08-21  
NUMBER OF SEQ ID NOS: 95  
SEQ ID NO 41  
LENGTH: 228  
TYPE: PRT  
ORGANISM: Homo sapien  
US-10-331-496A-41

Query Match 100.0%; Score 80; DB 4; Length 228;  
Best Local Similarity 100.0%; Pred. No. 6.5e-75;  
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVIKEVQEFYKDTYNKLTQDEPQRETLKAHYALNCCGLAGGVQFISDIPCKDV 60  
|||||  
Db 113 HKDEVIKEVQEFYKDTYNKLTQDEPQRETLKAHYALNCCGLAGGVQFISDIPCKDV 172

QY 61 LETFTVKSCPDAIKEVFNK 80  
|||||  
Db 173 LETFTVKSCPDAIKEVFNK 192

## RESULT 9

US-10-619-323-1

Sequence 1, Application US/10619323

Publication No. US20040136985A1

GENERAL INFORMATION:

APPLICANT: Jennings, Lisa K.

APPLICANT: Longhurst, Celia M.

APPLICANT: Cook, George A.

APPLICANT: Bao, Jianxiong

APPLICANT: Zhang, Chunxiang

APPLICANT: White, Melanie M.

APPLICANT: Crossno, Jr., Joseph T.

APPLICANT: Lu, Yi

TITLE OF INVENTION: METHODS OF MODIFYING BEHAVIOR OF CD9-EXPRESSING CELLS

FILE REFERENCE: 20609/241

CURRENT APPLICATION NUMBER: US/10/619,323

CURRENT FILING DATE: 2003-07-14

PRIOR APPLICATION NUMBER: 60/395,864

PRIOR FILING DATE: 2002-07-12

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 228

TYPE: PRT

ORGANISM: Homosapien

US-10-619-323-1

Query Match 100.0%; Score 80; DB 4; Length 228;  
Best Local Similarity 100.0%; Pred. No. 6.5e-75;  
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVIKEVQEFYKDTYNKLTQDEPQRETLKAHYALNCCGLAGGVQFISDIPCKDV 60  
|||||  
Db 113 HKDEVIKEVQEFYKDTYNKLTQDEPQRETLKAHYALNCCGLAGGVQFISDIPCKDV 172

Qy 61 LETFTVKSCPDAlKEVFDNK 80  
|||||  
Db 173 LETFTVKSCPDAlKEVFDNK 192

## RESULT 10

US-10-794-899-97  
; Sequence 97, Application US/10794899  
; Publication No. US20040146516A1  
; GENERAL INFORMATION:  
; APPLICANT: Utah Ventures  
; TITLE OF INVENTION: Lumen-Exposed Molecules and Methods Targeted Delivery  
; FILE REFERENCE: 27110-715  
; CURRENT APPLICATION NUMBER: US/10/794,899  
; CURRENT FILING DATE: 2004-03-05  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 97  
; LENGTH: 228  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-794-899-97

Query Match 100.0%; Score 80; DB 4; Length 228;  
Best Local Similarity 100.0%; Pred. No. 6.5e-75;  
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKDEVKEVQEFYKDTYNTKLTQDEPQRETLKAIHYALNCCGLAGGVQFISDIPCKDV 60  
|||||  
Db 113 HKDEVKEVQEFYKDTYNTKLTQDEPQRETLKAIHYALNCCGLAGGVQFISDIPCKDV 172

Qy 61 LETFTVKSCPDAlKEVFDNK 80  
|||||  
Db 173 LETFTVKSCPDAlKEVFDNK 192

## RESULT 11

US-10-473-127-1714  
; Sequence 1714, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1714  
; LENGTH: 228  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1714

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Best Local Similarity 100.0%; Pred. No. 6.5e-75;  
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKDEVKEVQEFYKDTYNTKLTQDEPQRETLKAIHYALNCCGLAGGVQFISDIPCKDV 60  
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Db 113 HKDEVKEVQEFYKDTYNTKLTQDEPQRETLKAIHYALNCCGLAGGVQFISDIPCKDV 172

Qy 61 LETFTVKSCPDAlKEVFDNK 80  
|||||  
Db 173 LETFTVKSCPDAlKEVFDNK 192

RESULT 12

US-10-473-127-1715  
; Sequence 1715, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1715  
; LENGTH: 228  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1715

Query Match 100.0%; Score 80; DB 5; Length 228;  
Best Local Similarity 100.0%; Pred. No. 6.5e-75;  
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKDEVKEVQEFYKDTYNTKLTQDEPQRETLKAIHYALNCCGLAGGVQFISDIPCKDV 60  
|||||  
Db 113 HKDEVKEVQEFYKDTYNTKLTQDEPQRETLKAIHYALNCCGLAGGVQFISDIPCKDV 172

Qy 61 LETFTVKSCPDAlKEVFDNK 80  
|||||  
Db 173 LETFTVKSCPDAlKEVFDNK 192

## RESULT 13

US-10-473-127-1716  
; Sequence 1716, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 1716
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1716

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Best Local Similarity 100.0%; Pred. No. 6.5e-75;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 113 HKDEVKEVQBFYKDTYNKLTQDEPQRETLKAIHYALNCCGLAGGVEQFISDPCPKDV 172

QY 61 LETFTVKSCPDALKEVFDNK 80
Db 173 LETFTVKSCPDALKEVFDNK 192
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RESULT 14
US-10-473-127-1718
; Sequence 1718, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1718
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1718
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Best Local Similarity 100.0%; Pred. No. 6.5e-75;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVKEVQBFYKDTYNKLTQDEPQRETLKAIHYALNCCGLAGGVEQFISDPCPKDV 60
Db 113 HKDEVKEVQBFYKDTYNKLTQDEPQRETLKAIHYALNCCGLAGGVEQFISDPCPKDV 172

QY 61 LETFTVKSCPDALKEVFDNK 80
Db 173 LETFTVKSCPDALKEVFDNK 192
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RESULT 15
US-10-473-127-1719
; Sequence 1719, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
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; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1719
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1719

Query Match      100.0%; Score 80; DB 5; Length 228;
Best Local Similarity 100.0%; Pred. No. 6.5e-75;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVKEVQBFYKDTYNKLTQDEPQRETLKAIHYALNCCGLAGGVEQFISDPCPKDV 60
Db 113 HKDEVKEVQBFYKDTYNKLTQDEPQRETLKAIHYALNCCGLAGGVEQFISDPCPKDV 172

QY 61 LETFTVKSCPDALKEVFDNK 80
Db 173 LETFTVKSCPDALKEVFDNK 192

Search completed: January 20, 2006, 17:47:42
Job time : 99.3846 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2006, 17:42:32 ; Search time 8.46154 Seconds  
(without alignments)  
95.811 Million cell updates/sec

Title: US-10-619-323-1\_COPY\_113\_192

Perfect score: 80

Sequence: 1 HXDEVIKEVQEPYKDTYNKL.....LFTFTVKSCPDAKEVFONK 80

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 70606 seqs, 10133881 residues

Word size : 0

Total number of hits satisfying chosen parameters: 70606

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Published Applications AA\_New.\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
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- 3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US05\_NEW\_PUB.pep.\*
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- 7: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	80	100.0	228	6	US-10-821-234-1266
2	6	7.5	20	7	US-11-022-562-157
3	6	7.5	20	7	US-11-022-562-158
4	6	7.5	31	7	US-11-145-035-45
5	6	7.5	122	6	US-10-467-657-606
6	6	7.5	259	6	US-10-467-657-2734
7	6	7.5	274	6	US-10-883-512-108
8	6	7.5	303	5	US-09-978-360A-763
9	6	7.5	316	6	US-10-510-386-244
10	6	7.5	405	6	US-10-873-528-62
11	6	7.5	408	6	US-10-467-657-8004
12	6	7.5	409	6	US-10-978-927-1
13	6	7.5	521	7	US-11-109-156-34
14	6	7.5	528	6	US-10-978-927-6
15	6	7.5	529	6	US-10-821-234-1520
16	6	7.5	529	6	US-10-978-927-9
17	6	7.5	529	6	US-10-978-927-13
18	6	7.5	549	6	US-10-995-561-909
19	6	7.5	549	7	US-11-194-246-431
20	6	7.5	572	7	US-11-052-554A-129
21	6	7.5	645	6	US-10-821-234-1409
22	6	7.5	745	6	US-10-995-561-659
23	6	7.5	745	7	US-11-109-156-14
24	6	7.5	879	7	US-11-022-562-340
25	6	7.5	909	7	US-11-186-284-2

6	7.5	913	6	US-10-821-234-1040	Sequence 1040, Ap
6	7.5	1012	6	US-10-995-561-908	Sequence 908, App
6	7.5	1213	7	US-11-074-176-256	Sequence 256, App
6	7.5	1244	7	US-11-052-554A-130	Sequence 130, App
6	7.5	1381	7	US-11-052-554A-138	Sequence 138, App
6	7.5	4384	6	US-10-821-234-1120	Sequence 1120, Ap
5	6.2	10	6	US-10-859-643-185	Sequence 185, App
5	6.2	10	7	US-11-097-864-185	Sequence 185, App
5	6.2	10	7	US-11-097-912-185	Sequence 185, App
5	6.2	19	6	US-10-880-238-119	Sequence 119, App
5	6.2	20	6	US-10-485-788A-630	Sequence 630, App
5	6.2	20	7	US-11-133-465A-6	Sequence 6, Appli
5	6.2	36	5	US-09-978-360A-549	Sequence 549, App
5	6.2	37	6	US-10-957-351-6	Sequence 6, Appli
5	6.2	65	5	US-09-978-360A-764	Sequence 764, App
5	6.2	66	6	US-10-467-657-3594	Sequence 3594, Ap
5	6.2	66	6	US-10-467-657-6436	Sequence 6436, Ap
5	6.2	66	6	US-10-467-657-8428	Sequence 8428, Ap
5	6.2	91	7	US-11-046-786-1	Sequence 1, Appli
5	6.2	95	6	US-10-485-788A-788	Sequence 788, App
5	6.2	95	7	US-11-053-076-170	Sequence 170, App
5	6.2	96	6	US-10-467-657-4498	Sequence 4498, Ap
5	6.2	106	7	US-11-074-176-288	Sequence 288, App
5	6.2	107	6	US-10-793-626-1586	Sequence 1586, Ap
5	6.2	111	5	US-09-978-360A-799	Sequence 799, App
5	6.2	112	5	US-09-978-360A-507	Sequence 507, App
5	6.2	121	7	US-11-074-176-86	Sequence 86, Appli
5	6.2	129	6	US-10-485-517-304	Sequence 304, App
5	6.2	129	6	US-10-485-517-365	Sequence 365, App
5	6.2	134	6	US-10-793-626-1382	Sequence 1382, Ap
5	6.2	141	6	US-10-467-657-7286	Sequence 7286, Ap
5	6.2	143	7	US-11-120-308-56	Sequence 56, Appl
5	6.2	144	6	US-11-194-246-420	Sequence 420, App
5	6.2	155	6	US-10-793-626-3088	Sequence 3088, Ap
5	6.2	156	6	US-10-793-626-1222	Sequence 1222, Ap
5	6.2	165	7	US-11-052-554A-191	Sequence 191, App
5	6.2	170	7	US-11-069-642-12	Sequence 12, Appl
5	6.2	174	6	US-10-485-517-225	Sequence 225, App
5	6.2	175	6	US-10-873-528-97	Sequence 97, Appl
5	6.2	175	7	US-11-133-465A-1	Sequence 1, Appli
5	6.2	182	6	US-10-821-234-1114	Sequence 1114, Ap
5	6.2	185	6	US-10-967-277A-10	Sequence 10, Appl
5	6.2	190	7	US-11-069-601-13	Sequence 13, Appl
5	6.2	193	7	US-11-052-554A-76	Sequence 76, Appl
5	6.2	193	7	US-11-052-554A-196	Sequence 196, App
5	6.2	196	7	US-11-065-943-51	Sequence 51, Appl
5	6.2	201	6	US-10-793-626-312	Sequence 312, App
5	6.2	201	6	US-10-793-626-2176	Sequence 2176, Ap
5	6.2	203	6	US-10-467-657-3482	Sequence 3482, Ap
5	6.2	204	7	US-11-080-991-8	Sequence 8, Appli
5	6.2	207	7	US-11-022-562-222	Sequence 222, App
5	6.2	210	6	US-10-454-437-302	Sequence 302, App
5	6.2	211	5	US-09-978-360A-534	Sequence 534, App
5	6.2	211	6	US-10-965-972-1	Sequence 1, Appli
5	6.2	211	7	US-11-186-284-22	Sequence 22, Appl
5	6.2	214	7	US-11-096-051-16	Sequence 16, Appl
5	6.2	215	6	US-10-873-528-13	Sequence 13, Appl
5	6.2	226	6	US-10-878-556A-106	Sequence 106, App
5	6.2	226	7	US-11-052-554A-11	Sequence 11, Appl
5	6.2	230	6	US-10-884-730-372	Sequence 372, App
5	6.2	230	6	US-10-884-730-375	Sequence 375, App
5	6.2	230	6	US-10-884-730-377	Sequence 377, App
5	6.2	233	6	US-10-793-626-416	Sequence 416, App
5	6.2	236	7	US-11-100-183-15	Sequence 15, Appl
5	6.2	238	7	US-11-052-554A-38	Sequence 38, Appl
5	6.2	238	7	US-11-052-554A-51	Sequence 51, Appl
5	6.2	238	7	US-11-052-554A-52	Sequence 52, Appl
5	6.2	240	7	US-11-100-183-17	Sequence 17, Appl
5	6.2	241	7	US-11-100-183-19	Sequence 19, Appl
5	6.2	244	7	US-11-055-822-1148	Sequence 1148, Ap
5	6.2	247	6	US-10-453-372-1200	Sequence 1200, Ap
5	6.2	249	6	US-10-485-517-157	Sequence 157, App
5	6.2	256	6	US-10-510-386-112	Sequence 112, App

99	5	6.2	257	7	US-11-135-855-42	Sequence 42, Appl	172	5	6.2	397	6	US-10-878-556A-189	Sequence 189, App
100	5	6.2	259	6	US-10-793-626-2958	Sequence 2958, Ap	173	5	6.2	397	6	US-10-995-561-928	Sequence 928, App
101	5	6.2	259	7	US-11-118-853-1	Sequence 1, Appli	174	5	6.2	397	6	US-10-995-561-929	Sequence 929, App
102	5	6.2	260	7	US-11-055-822-436	Sequence 436, App	175	5	6.2	399	7	US-11-065-943-53	Sequence 53, Appl
103	5	6.2	261	6	US-10-467-657-5896	Sequence 5896, Ap	176	5	6.2	400	6	US-10-453-372-140	Sequence 140, App
104	5	6.2	262	6	US-10-453-372-1192	Sequence 1192, Ap	177	5	6.2	400	6	US-10-453-372-152	Sequence 152, App
105	5	6.2	262	6	US-10-453-372-1196	Sequence 1196, Ap	178	5	6.2	401	6	US-10-821-234-881	Sequence 881, App
106	5	6.2	263	6	US-10-467-657-6188	Sequence 6188, Ap	179	5	6.2	401	6	US-10-517-939-246	Sequence 246, App
107	5	6.2	266	6	US-10-467-657-5258	Sequence 5258, Ap	180	5	6.2	405	6	US-10-821-234-1357	Sequence 1357, Ap
108	5	6.2	266	6	US-11-055-822-1138	Sequence 1138, Ap	181	5	6.2	410	6	US-10-793-626-3258	Sequence 3258, Ap
109	5	6.2	268	6	US-10-821-234-866	Sequence 866, App	182	5	6.2	410	7	US-11-159-428-10	Sequence 10, Appl
110	5	6.2	269	6	US-10-453-372-1194	Sequence 1194, Ap	183	5	6.2	415	7	US-11-055-822-816	Sequence 816, App
111	5	6.2	271	7	US-11-052-554A-225	Sequence 225, App	184	5	6.2	416	6	US-10-641-678-73	Sequence 73, Appl
112	5	6.2	272	6	US-10-485-517-279	Sequence 279, App	185	5	6.2	420	6	US-10-131-826A-260	Sequence 260, App
113	5	6.2	273	6	US-10-793-626-84	Sequence 84, Appl	186	5	6.2	423	6	US-10-467-962B-85	Sequence 85, Appl
114	5	6.2	276	6	US-10-821-234-1501	Sequence 1501, Ap	187	5	6.2	426	6	US-10-525-710-28	Sequence 28, Appl
115	5	6.2	279	6	US-10-793-626-2998	Sequence 2998, Ap	188	5	6.2	430	7	US-11-055-822-412	Sequence 412, App
116	5	6.2	280	6	US-10-873-528-49	Sequence 49, Appl	189	5	6.2	431	6	US-10-949-720-410	Sequence 410, App
117	5	6.2	287	6	US-10-467-657-5866	Sequence 5866, Ap	190	5	6.2	433	7	US-11-070-080-12	Sequence 12, Appl
118	5	6.2	288	6	US-10-508-263-72	Sequence 72, Appl	191	5	6.2	437	7	US-11-194-246-324	Sequence 324, App
119	5	6.2	294	6	US-10-467-657-4688	Sequence 4688, Ap	192	5	6.2	441	7	US-11-196-475-120	Sequence 120, App
120	5	6.2	295	6	US-10-793-626-2998	Sequence 2998, Ap	193	5	6.2	442	6	US-11-055-822-814	Sequence 814, App
121	5	6.2	296	7	US-11-196-475-22	Sequence 22, Appl	194	5	6.2	444	6	US-10-467-657-2414	Sequence 2414, Ap
122	5	6.2	296	7	US-11-037-243-85	Sequence 85, Appl	195	5	6.2	445	6	US-10-454-437-312	Sequence 312, App
123	5	6.2	296	7	US-11-156-084-285	Sequence 285, App	196	5	6.2	445	7	US-11-082-389-376	Sequence 376, App
124	5	6.2	297	6	US-10-878-556A-119	Sequence 119, App	197	5	6.2	447	6	US-10-467-657-4034	Sequence 4034, Ap
125	5	6.2	301	6	US-10-793-626-3176	Sequence 3176, Ap	198	5	6.2	447	6	US-10-467-657-7050	Sequence 7050, Ap
126	5	6.2	301	6	US-10-979-871-2	Sequence 2, Appli	199	5	6.2	450	7	US-11-087-100-20	Sequence 20, Appl
127	5	6.2	302	7	US-11-024-959-262	Sequence 262, App	200	5	6.2	450	7	US-11-087-100-28	Sequence 28, Appl
128	5	6.2	305	7	US-11-137-465-56	Sequence 56, Appl	201	5	6.2	450	7	US-11-087-084-20	Sequence 20, Appl
129	5	6.2	309	7	US-11-156-084-200	Sequence 200, App	202	5	6.2	450	7	US-11-087-084-28	Sequence 28, Appl
130	5	6.2	311	6	US-10-055-877-181	Sequence 181, App	203	5	6.2	450	7	US-11-087-085-20	Sequence 20, Appl
131	5	6.2	311	6	US-10-055-877-182	Sequence 182, App	204	5	6.2	450	7	US-11-087-085-28	Sequence 28, Appl
132	5	6.2	312	6	US-10-467-657-5318	Sequence 5318, Ap	205	5	6.2	454	7	US-11-196-475-116	Sequence 116, App
133	5	6.2	313	6	US-10-467-657-3982	Sequence 3982, Ap	206	5	6.2	458	7	US-11-124-368A-316	Sequence 316, App
134	5	6.2	313	6	US-10-467-657-8140	Sequence 8140, Ap	207	5	6.2	461	6	US-10-878-556A-162	Sequence 162, App
135	5	6.2	313	7	US-11-052-554A-247	Sequence 247, App	208	5	6.2	468	7	US-11-122-144-8	Sequence 8, Appli
136	5	6.2	320	6	US-10-467-657-424	Sequence 424, App	209	5	6.2	469	6	US-10-793-626-276	Sequence 276, App
137	5	6.2	320	7	US-11-052-554A-239	Sequence 239, App	210	5	6.2	469	6	US-10-821-234-1151	Sequence 1151, Ap
138	5	6.2	321	6	US-10-485-517-133	Sequence 133, App	211	5	6.2	474	6	US-10-467-657-5978	Sequence 5978, Ap
139	5	6.2	323	6	US-10-508-263-52	Sequence 52, Appl	212	5	6.2	474	6	US-10-467-657-7518	Sequence 7518, Ap
140	5	6.2	323	7	US-11-156-084-294	Sequence 294, App	213	5	6.2	474	7	US-11-076-733-11	Sequence 11, Appl
141	5	6.2	323	7	US-11-156-084-336	Sequence 336, App	214	5	6.2	476	7	US-11-074-176-122	Sequence 122, App
142	5	6.2	331	6	US-10-821-234-1650	Sequence 1650, App	215	5	6.2	476	7	US-11-055-822-942	Sequence 942, App
143	5	6.2	331	6	US-10-949-720-405	Sequence 405, App	216	5	6.2	476	7	US-11-055-822-962	Sequence 962, App
144	5	6.2	338	6	US-10-793-626-2868	Sequence 2868, Ap	217	5	6.2	477	6	US-10-793-626-3250	Sequence 3250, Ap
145	5	6.2	338	6	US-10-821-234-1418	Sequence 1418, Ap	218	5	6.2	480	6	US-10-878-556A-198	Sequence 198, App
146	5	6.2	338	7	US-11-186-284-109	Sequence 109, App	219	5	6.2	484	7	US-11-024-959-351	Sequence 351, App
147	5	6.2	341	6	US-10-454-437-176	Sequence 176, App	220	5	6.2	486	6	US-10-467-657-950	Sequence 950, App
148	5	6.2	341	6	US-10-454-437-244	Sequence 244, App	221	5	6.2	490	7	US-11-063-343-31	Sequence 31, Appl
149	5	6.2	348	6	US-10-793-626-2866	Sequence 2866, Ap	222	5	6.2	490	7	US-11-124-368A-223	Sequence 223, App
150	5	6.2	354	6	US-10-878-556A-164	Sequence 164, App	223	5	6.2	497	6	US-10-763-712A-24	Sequence 24, Appl
151	5	6.2	356	6	US-10-055-877-184	Sequence 184, App	224	5	6.2	497	6	US-10-763-712A-91	Sequence 91, Appl
152	5	6.2	356	6	US-10-055-877-185	Sequence 185, App	225	5	6.2	502	6	US-10-131-826A-548	Sequence 548, App
153	5	6.2	357	6	US-10-517-939-100	Sequence 100, App	226	5	6.2	502	6	US-10-689-742-148	Sequence 148, App
154	5	6.2	358	6	US-10-485-517-227	Sequence 227, App	227	5	6.2	517	6	US-10-878-556A-23	Sequence 23, Appl
155	5	6.2	360	7	US-11-052-554A-376	Sequence 376, App	228	5	6.2	519	7	US-11-093-631-10	Sequence 10, Appl
156	5	6.2	360	7	US-10-019-711-67	Sequence 67, Appl	229	5	6.2	521	6	US-10-821-234-1546	Sequence 1546, Ap
157	5	6.2	374	6	US-10-467-657-3420	Sequence 3420, Ap	230	5	6.2	522	6	US-10-949-720-425	Sequence 425, App
158	5	6.2	377	7	US-11-152-892-8	Sequence 8, Appli	231	5	6.2	523	6	US-10-641-678-45	Sequence 45, Appl
159	5	6.2	378	7	US-11-152-892-7	Sequence 7, Appli	232	5	6.2	525	7	US-11-082-389-36	Sequence 36, Appl
160	5	6.2	380	7	US-11-196-475-118	Sequence 118, App	233	5	6.2	526	6	US-10-467-657-2186	Sequence 2186, Ap
161	5	6.2	382	5	US-09-978-360A-425	Sequence 425, App	234	5	6.2	526	6	US-10-641-678-46	Sequence 46, Appl
162	5	6.2	382	6	US-10-467-657-7540	Sequence 7540, Ap	235	5	6.2	531	6	US-10-878-556A-90	Sequence 90, Appl
163	5	6.2	383	7	US-11-147-360-2	Sequence 2, Appli	236	5	6.2	531	6	US-10-453-372-132	Sequence 132, App
164	5	6.2	388	6	US-10-467-657-8788	Sequence 8788, Ap	237	5	6.2	531	7	US-11-124-368A-314	Sequence 314, App
165	5	6.2	390	6	US-10-453-372-130	Sequence 130, App	238	5	6.2	532	6	US-10-821-234-1071	Sequence 1071, Ap
166	5	6.2	390	6	US-10-453-372-134	Sequence 134, App	239	5	6.2	533	7	US-11-230-995-3	Sequence 3, Appli
167	5	6.2	393	7	US-11-196-475-114	Sequence 114, App	240	5	6.2	536	6	US-10-821-231C-1	Sequence 1, Appli
168	5	6.2	395	6	US-10-454-437-208	Sequence 208, App	241	5	6.2	536	7	US-11-124-368A-315	Sequence 315, App
169	5	6.2	395	6	US-10-454-437-210	Sequence 210, App	242	5	6.2	537	6	US-10-949-720-424	Sequence 424, App
170	5	6.2	397	6	US-10-485-517-172	Sequence 172, App	243	5	6.2	538	7	US-11-167-856-20	Sequence 20, Appl
171	5	6.2	397	6	US-10-467-657-4202	Sequence 4202, Ap	244	5	6.2	539	6	US-10-793-626-790	Sequence 790, App

245	5	6.2	541	7	US-11-118-855-26	Sequence 26, Appl	318	5	6.2	724	7	US-11-053-100-41	Sequence 41, Appl
246	5	6.2	542	7	US-11-074-176-30	Sequence 30, Appl	319	5	6.2	726	7	US-11-052-554A-127	Sequence 127, Appl
247	5	6.2	543	6	US-10-467-657-1020	Sequence 1020, Ap	320	5	6.2	746	7	US-11-053-554A-57	Sequence 57, Appl
248	5	6.2	545	7	US-11-082-389-34	Sequence 34, Appl	321	5	6.2	749	7	US-11-052-554A-148	Sequence 148, Appl
249	5	6.2	547	7	US-11-082-389-86	Sequence 86, Appl	322	5	6.2	758	7	US-11-024-959-347	Sequence 347, Appl
250	5	6.2	555	6	US-10-949-720-387	Sequence 387, Appl	323	5	6.2	767	7	US-11-052-554A-154	Sequence 154, Appl
251	5	6.2	555	6	US-10-763-712A-30	Sequence 30, Appl	324	5	6.2	771	6	US-10-949-720-389	Sequence 389, Appl
252	5	6.2	556	6	US-10-995-561-766	Sequence 766, Appl	325	5	6.2	777	6	US-10-467-657-2474	Sequence 2474, Ap
253	5	6.2	556	6	US-10-995-561-767	Sequence 767, Appl	326	5	6.2	798	7	US-11-107-028-2	Sequence 2, Appl
254	5	6.2	563	7	US-11-113-224-18	Sequence 18, Appl	327	5	6.2	812	7	US-11-010-874-1	Sequence 1, Appl
255	5	6.2	564	7	US-11-133-360-11	Sequence 11, Appl	328	5	6.2	856	6	US-10-467-657-8534	Sequence 8534, Ap
256	5	6.2	564	7	US-11-133-360-13	Sequence 13, Appl	329	5	6.2	868	6	US-10-995-561-752	Sequence 752, Appl
257	5	6.2	564	7	US-11-133-360-15	Sequence 15, Appl	330	5	6.2	871	6	US-10-859-643-765	Sequence 765, Appl
258	5	6.2	564	7	US-11-133-360-17	Sequence 17, Appl	331	5	6.2	871	7	US-11-097-864-765	Sequence 765, Appl
259	5	6.2	564	7	US-11-133-360-11	Sequence 11, Appl	332	5	6.2	871	7	US-11-097-912-765	Sequence 765, Appl
260	5	6.2	564	7	US-11-133-346-13	Sequence 13, Appl	333	5	6.2	874	7	US-11-053-100-42	Sequence 42, Appl
261	5	6.2	564	7	US-11-133-346-15	Sequence 15, Appl	334	5	6.2	875	6	US-10-859-643-743	Sequence 743, Appl
262	5	6.2	564	7	US-11-133-346-17	Sequence 17, Appl	335	5	6.2	875	6	US-10-859-643-745	Sequence 745, Appl
263	5	6.2	568	6	US-10-793-626-2482	Sequence 2482, Ap	336	5	6.2	875	6	US-10-859-643-747	Sequence 747, Appl
264	5	6.2	570	6	US-10-949-720-386	Sequence 386, Appl	337	5	6.2	875	6	US-10-859-643-748	Sequence 748, Appl
265	5	6.2	570	6	US-10-949-720-412	Sequence 412, Appl	338	5	6.2	875	6	US-10-859-643-748	Sequence 748, Appl
266	5	6.2	572	6	US-10-454-437-68	Sequence 68, Appl	339	5	6.2	875	6	US-11-097-864-751	Sequence 751, Appl
267	5	6.2	574	7	US-11-053-100-40	Sequence 40, Appl	340	5	6.2	875	7	US-11-097-864-745	Sequence 745, Appl
268	5	6.2	577	7	US-11-074-176-184	Sequence 184, Appl	341	5	6.2	875	7	US-11-097-864-747	Sequence 747, Appl
269	5	6.2	578	7	US-11-037-243-100	Sequence 100, Appl	342	5	6.2	875	7	US-11-097-864-748	Sequence 748, Appl
270	5	6.2	579	6	US-10-821-234-1352	Sequence 1352, Ap	343	5	6.2	875	7	US-11-097-912-743	Sequence 743, Appl
271	5	6.2	580	6	US-10-453-372-138	Sequence 138, Appl	344	5	6.2	875	7	US-11-097-912-743	Sequence 743, Appl
272	5	6.2	580	6	US-10-453-372-144	Sequence 144, Appl	345	5	6.2	875	7	US-11-097-912-745	Sequence 745, Appl
273	5	6.2	584	6	US-10-454-437-66	Sequence 66, Appl	346	5	6.2	875	7	US-11-097-912-747	Sequence 747, Appl
274	5	6.2	585	6	US-10-821-234-875	Sequence 875, Appl	347	5	6.2	875	7	US-11-097-912-748	Sequence 748, Appl
275	5	6.2	587	6	US-10-453-372-964	Sequence 964, Appl	348	5	6.2	885	6	US-11-097-912-751	Sequence 751, Appl
276	5	6.2	588	7	US-11-196-475-122	Sequence 122, Appl	349	5	6.2	885	6	US-10-793-626-1660	Sequence 1660, Ap
277	5	6.2	591	6	US-10-453-372-952	Sequence 952, Appl	350	5	6.2	906	7	US-11-124-635-4	Sequence 4, Appl
278	5	6.2	591	6	US-10-453-372-956	Sequence 956, Appl	351	5	6.2	907	7	US-11-103-957-82	Sequence 82, Appl
279	5	6.2	594	6	US-10-467-657-3952	Sequence 3952, Ap	352	5	6.2	932	7	US-11-017-550-65	Sequence 65, Appl
280	5	6.2	594	6	US-10-467-657-6376	Sequence 6376, Ap	353	5	6.2	934	7	US-11-077-386-17	Sequence 17, Appl
281	5	6.2	596	6	US-10-453-372-954	Sequence 954, Appl	354	5	6.2	959	6	US-10-453-372-1074	Sequence 1074, Ap
282	5	6.2	604	6	US-10-467-657-2280	Sequence 2280, Ap	355	5	6.2	964	7	US-11-137-465-58	Sequence 58, Appl
283	5	6.2	612	7	US-11-186-284-136	Sequence 136, Appl	356	5	6.2	965	7	US-11-113-424-2	Sequence 2, Appl
284	5	6.2	614	7	US-11-165-576-2	Sequence 2, Appl	357	5	6.2	965	7	US-11-147-047-51	Sequence 51, Appl
285	5	6.2	618	6	US-10-821-234-1481	Sequence 1481, Ap	358	5	6.2	980	7	US-11-064-246-10	Sequence 10, Appl
286	5	6.2	620	6	US-10-131-826A-324	Sequence 324, Appl	359	5	6.2	980	6	US-10-949-720-395	Sequence 395, Appl
287	5	6.2	620	7	US-11-186-284-134	Sequence 134, Appl	360	5	6.2	990	6	US-10-821-234-1201	Sequence 1201, Ap
288	5	6.2	621	6	US-10-821-234-1376	Sequence 1376, Ap	361	5	6.2	1015	6	US-10-467-657-180	Sequence 180, Appl
289	5	6.2	622	7	US-11-021-441-35	Sequence 35, Appl	362	5	6.2	1015	6	US-10-467-657-3764	Sequence 3764, Ap
290	5	6.2	622	7	US-11-147-360-4	Sequence 4, Appl	363	5	6.2	1021	6	US-10-453-372-1076	Sequence 1076, Ap
291	5	6.2	622	7	US-11-155-288-17	Sequence 17, Appl	364	5	6.2	1025	6	US-10-453-372-1068	Sequence 1068, Ap
292	5	6.2	630	7	US-11-155-288-18	Sequence 18, Appl	365	5	6.2	1025	6	US-10-453-372-1070	Sequence 1070, Ap
293	5	6.2	633	6	US-10-453-372-1072	Sequence 1072, Ap	366	5	6.2	1063	6	US-11-120-308-186	Sequence 186, Appl
294	5	6.2	633	6	US-10-453-372-1078	Sequence 1078, Ap	367	5	6.2	1063	6	US-10-453-372-1066	Sequence 1066, Ap
295	5	6.2	636	6	US-10-763-712A-29	Sequence 29, Appl	368	5	6.2	1068	7	US-11-191-374-45	Sequence 45, Appl
296	5	6.2	636	6	US-10-763-712A-93	Sequence 93, Appl	369	5	6.2	1068	7	US-11-191-375-45	Sequence 45, Appl
297	5	6.2	642	6	US-10-453-372-962	Sequence 962, Appl	370	5	6.2	1068	7	US-11-191-588-45	Sequence 45, Appl
298	5	6.2	646	6	US-10-453-372-958	Sequence 958, Appl	371	5	6.2	1084	6	US-10-964-313-2	Sequence 2, Appl
299	5	6.2	646	6	US-10-453-372-960	Sequence 960, Appl	372	5	6.2	1124	7	US-11-195-197-9	Sequence 9, Appl
300	5	6.2	648	6	US-10-501-039-6	Sequence 6, Appl	373	5	6.2	1126	7	US-11-075-185-3	Sequence 3, Appl
301	5	6.2	648	6	US-10-793-626-568	Sequence 568, Appl	374	5	6.2	1145	6	US-10-793-626-1432	Sequence 1432, Ap
302	5	6.2	650	6	US-10-453-372-966	Sequence 966, Appl	375	5	6.2	1147	6	US-10-615-668-5	Sequence 5, Appl
303	5	6.2	664	7	US-11-080-991-40	Sequence 40, Appl	376	5	6.2	1167	7	US-11-052-554A-121	Sequence 121, Appl
304	5	6.2	667	7	US-11-156-163-4	Sequence 4, Appl	377	5	6.2	1174	7	US-11-053-100-43	Sequence 43, Appl
305	5	6.2	668	6	US-10-453-372-950	Sequence 950, Appl	378	5	6.2	1174	6	US-10-858-730-72	Sequence 72, Appl
306	5	6.2	668	6	US-10-453-372-968	Sequence 968, Appl	379	5	6.2	1206	6	US-10-858-730-73	Sequence 73, Appl
307	5	6.2	668	6	US-10-453-372-970	Sequence 970, Appl	380	5	6.2	1206	6	US-10-467-657-72	Sequence 72, Appl
308	5	6.2	675	6	US-10-467-657-4004	Sequence 4004, Ap	381	5	6.2	1206	6	US-10-467-657-3892	Sequence 3892, Ap
309	5	6.2	677	6	US-10-131-826A-230	Sequence 230, Appl	382	5	6.2	1215	6	US-10-964-313-6	Sequence 6, Appl
310	5	6.2	683	7	US-11-103-957-84	Sequence 84, Appl	383	5	6.2	1216	6	US-10-873-528-12	Sequence 12, Appl
311	5	6.2	684	6	US-10-793-626-2098	Sequence 2098, Ap	384	5	6.2	1259	6	US-10-467-657-5510	Sequence 5510, Ap
312	5	6.2	690	7	US-11-052-554A-232	Sequence 232, Appl	385	5	6.2	1308	7	US-11-113-202-16	Sequence 16, Appl
313	5	6.2	697	7	US-11-082-389-362	Sequence 362, Appl	386	5	6.2	1313	7	US-11-091-668-4	Sequence 4, Appl
314	5	6.2	703	6	US-10-467-657-7158	Sequence 7158, Ap	387	5	6.2	1323	6	US-10-517-939-312	Sequence 312, Appl
315	5	6.2	710	7	US-11-151-601-23	Sequence 23, Appl	388	5	6.2	1327	7	US-11-019-711-70	Sequence 70, Appl
316	5	6.2	712	7	US-11-037-243-69	Sequence 69, Appl	389	5	6.2	1342	7	US-11-115-639-2	Sequence 2, Appl
317	5	6.2	716	7	US-11-150-845-16	Sequence 16, Appl	390	5	6.2	1342	7	US-11-115-639-3	Sequence 3, Appl

391	5	6.2	1342	7	US-11-115-639-4	Sequence 4, Appli	464	4	5.0	8	7	US-11-045-024-3091	Sequence 3091, Ap
392	5	6.2	1342	7	US-11-115-639-5	Sequence 5, Appli	465	4	5.0	8	7	US-11-045-024-9415	Sequence 9415, Ap
393	5	6.2	1342	7	US-11-115-639-6	Sequence 6, Appli	466	4	5.0	8	7	US-11-045-024-10717	Sequence 10717, A
394	5	6.2	1390	6	US-10-951-351-1	Sequence 1, Appli	467	4	5.0	8	7	US-11-045-024-11485	Sequence 11485, A
395	5	6.2	1417	7	US-11-052-554A-8	Sequence 8, Appli	468	4	5.0	8	7	US-11-045-024-12493	Sequence 12493, A
396	5	6.2	1538	7	US-11-052-554A-146	Sequence 146, App	469	4	5.0	9	6	US-10-491-096-29	Sequence 29, Appl
397	5	6.2	1562	7	US-11-051-554A-211	Sequence 211, App	470	4	5.0	9	6	US-10-859-643-284	Sequence 284, App
398	5	6.2	1590	6	US-10-055-877-146	Sequence 146, App	471	4	5.0	9	6	US-10-859-643-662	Sequence 662, App
399	5	6.2	1681	7	US-11-019-711-20	Sequence 20, Appl	472	4	5.0	9	7	US-11-044-051-111	Sequence 111, App
400	5	6.2	1697	7	US-11-019-711-68	Sequence 68, Appl	473	4	5.0	9	7	US-11-073-112-14	Sequence 14, Appl
401	5	6.2	1723	7	US-11-019-711-18	Sequence 18, Appl	474	4	5.0	9	7	US-11-097-864-284	Sequence 284, App
402	5	6.2	1730	7	US-11-192-967-4	Sequence 4, Appli	475	4	5.0	9	7	US-11-097-864-662	Sequence 662, App
403	5	6.2	1730	7	US-11-193-715-4	Sequence 4, Appli	476	4	5.0	9	7	US-11-097-912-284	Sequence 284, App
404	5	6.2	1766	7	US-11-075-185-10	Sequence 10, Appl	477	4	5.0	9	7	US-11-097-912-662	Sequence 662, App
405	5	6.2	1786	7	US-11-196-400-3	Sequence 3, Appli	478	4	5.0	9	7	US-11-045-024-8133	Sequence 8133, Ap
406	5	6.2	1966	7	US-11-126-313-32	Sequence 32, Appl	479	4	5.0	9	7	US-11-045-024-8136	Sequence 8136, Ap
407	5	6.2	1976	7	US-11-069-834-52	Sequence 52, Appl	480	4	5.0	9	7	US-11-033-039-785	Sequence 785, App
408	5	6.2	1976	7	US-11-069-834-54	Sequence 54, Appl	481	4	5.0	9	7	US-11-033-039-809	Sequence 809, App
409	5	6.2	1992	7	US-11-013-759-3	Sequence 3, Appli	482	4	5.0	9	7	US-11-033-039-810	Sequence 810, App
410	5	6.2	1992	7	US-11-013-759-13	Sequence 13, Appl	483	4	5.0	10	6	US-10-491-096-28	Sequence 28, Appl
411	5	6.2	2047	7	US-11-013-759-4	Sequence 4, Appli	484	4	5.0	10	6	US-10-491-096-138	Sequence 138, App
412	5	6.2	2047	7	US-11-013-759-7	Sequence 7, Appli	485	4	5.0	10	6	US-10-929-988-17	Sequence 17, Appl
413	5	6.2	2048	7	US-11-116-939-6	Sequence 6, Appli	486	4	5.0	10	6	US-10-880-238-30	Sequence 30, Appl
414	5	6.2	2053	7	US-11-013-759-9	Sequence 9, Appli	487	4	5.0	10	6	US-10-880-238-33	Sequence 33, Appl
415	5	6.2	2059	7	US-11-087-100-4	Sequence 4, Appli	488	4	5.0	10	6	US-10-859-643-76	Sequence 76, Appl
416	5	6.2	2059	7	US-11-087-084-4	Sequence 4, Appli	489	4	5.0	10	6	US-10-859-643-202	Sequence 202, App
417	5	6.2	2059	7	US-11-087-085-4	Sequence 4, Appli	490	4	5.0	10	6	US-10-859-643-305	Sequence 305, App
418	5	6.2	2197	7	US-11-075-185-8	Sequence 8, Appli	491	4	5.0	10	6	US-10-859-643-322	Sequence 322, App
419	5	6.2	2204	7	US-11-052-554A-174	Sequence 174, App	492	4	5.0	10	6	US-11-097-864-76	Sequence 76, Appl
420	5	6.2	2312	7	US-11-126-313-34	Sequence 34, Appl	493	4	5.0	10	7	US-11-097-864-205	Sequence 205, App
421	5	6.2	2333	6	US-10-453-372-170	Sequence 170, App	494	4	5.0	10	7	US-11-097-864-205	Sequence 205, App
422	5	6.2	2551	7	US-11-052-554A-368	Sequence 368, App	495	4	5.0	10	7	US-11-097-864-205	Sequence 205, App
423	5	6.2	2630	7	US-11-186-731-2	Sequence 2, Appli	496	4	5.0	10	7	US-11-097-864-309	Sequence 309, App
424	5	6.2	2647	6	US-10-821-234-1303	Sequence 1303, Ap	497	4	5.0	10	7	US-11-097-864-322	Sequence 322, App
425	5	6.2	2657	6	US-10-821-234-1262	Sequence 1262, Ap	498	4	5.0	10	7	US-11-097-912-76	Sequence 76, Appl
426	5	6.2	2662	6	US-10-453-372-114	Sequence 114, App	499	4	5.0	10	7	US-11-097-912-202	Sequence 202, App
427	5	6.2	2715	7	US-11-096-051-2	Sequence 2, Appli	500	4	5.0	10	7	US-11-097-912-309	Sequence 309, App
428	5	6.2	2715	7	US-11-113-424-51	Sequence 51, Appl	501	4	5.0	10	7	US-11-097-912-322	Sequence 322, App
429	5	6.2	2721	7	US-11-096-051-10	Sequence 10, Appl	502	4	5.0	10	7	US-11-045-024-2670	Sequence 2670, Ap
430	5	6.2	2724	6	US-10-453-372-148	Sequence 148, App	503	4	5.0	10	7	US-11-045-024-5455	Sequence 5455, Ap
431	5	6.2	2725	7	US-11-096-051-8	Sequence 8, Appli	504	4	5.0	10	7	US-11-045-024-8134	Sequence 8134, Ap
432	5	6.2	2733	6	US-10-453-372-136	Sequence 136, App	505	4	5.0	10	7	US-11-045-024-10712	Sequence 10712, A
433	5	6.2	2733	6	US-10-453-372-142	Sequence 142, App	506	4	5.0	10	7	US-11-045-024-12490	Sequence 12490, A
434	5	6.2	2733	6	US-10-453-372-146	Sequence 146, App	507	4	5.0	10	7	US-10-982-891-25	Sequence 25, Appl
435	5	6.2	2733	6	US-10-453-372-150	Sequence 150, App	508	4	5.0	11	6	US-10-859-643-763	Sequence 763, App
436	5	6.2	2733	6	US-10-453-372-154	Sequence 154, App	509	4	5.0	11	6	US-11-097-864-763	Sequence 763, App
437	5	6.2	2759	6	US-10-453-372-168	Sequence 168, App	510	4	5.0	11	7	US-11-097-912-763	Sequence 763, App
438	5	6.2	2765	6	US-10-453-372-116	Sequence 116, App	511	4	5.0	11	7	US-11-097-912-763	Sequence 763, App
439	5	6.2	2769	7	US-11-113-424-14	Sequence 14, Appl	512	4	5.0	11	7	US-11-045-024-2687	Sequence 2687, Ap
440	5	6.2	2828	7	US-11-080-991-54	Sequence 54, Appl	513	4	5.0	11	7	US-11-045-024-8280	Sequence 8280, Ap
441	5	6.2	2828	7	US-11-186-284-49	Sequence 49, Appl	514	4	5.0	11	7	US-11-045-024-14491	Sequence 14491, A
442	5	6.2	3003	6	US-10-453-372-1080	Sequence 1080, Ap	515	4	5.0	11	7	US-11-189-321-9	Sequence 9, Appli
443	5	6.2	3056	7	US-11-109-156-20	Sequence 20, Appl	516	4	5.0	11	7	US-11-116-144-226	Sequence 226, App
444	5	6.2	3073	7	US-11-143-980-50	Sequence 50, Appl	517	4	5.0	11	7	US-11-116-144-227	Sequence 227, App
445	5	6.2	3353	7	US-11-037-243-64	Sequence 64, Appl	518	4	5.0	12	6	US-10-982-891-30	Sequence 30, Appl
446	5	6.2	3361	6	US-10-453-372-1082	Sequence 1082, Ap	519	4	5.0	12	6	US-10-632-150-82	Sequence 82, Appl
447	5	6.2	3507	7	US-11-075-185-7	Sequence 7, Appli	520	4	5.0	12	6	US-10-893-584-111	Sequence 111, App
448	5	6.2	3623	6	US-10-995-561-593	Sequence 593, App	521	4	5.0	12	7	US-11-073-457-82	Sequence 82, Appl
449	5	6.2	3674	7	US-11-000-463-454	Sequence 454, App	522	4	5.0	12	7	US-11-073-457-82	Sequence 82, Appl
450	5	6.2	3689	7	US-11-075-185-4	Sequence 4, Appli	523	4	5.0	12	7	US-11-098-763-31	Sequence 31, Appl
451	5	6.2	3803	6	US-10-995-561-773	Sequence 773, App	524	4	5.0	12	7	US-11-043-693-7	Sequence 7, Appli
452	5	6.2	3960	6	US-10-995-561-771	Sequence 771, App	525	4	5.0	12	7	US-11-127-877-540	Sequence 540, App
453	5	6.2	4374	7	US-11-128-572-2	Sequence 2, Appli	526	4	5.0	12	7	US-11-033-039-483	Sequence 483, App
454	5	6.2	5335	6	US-10-995-561-777	Sequence 777, App	527	4	5.0	12	7	US-11-033-039-522	Sequence 522, App
455	5	6.2	5406	6	US-10-995-561-774	Sequence 774, App	528	4	5.0	13	6	US-10-503-575-80	Sequence 80, Appl
456	5	6.2	5415	6	US-10-995-561-779	Sequence 779, App	529	4	5.0	13	6	US-10-716-189-8	Sequence 8, Appli
457	5	6.2	5464	6	US-10-995-561-775	Sequence 775, App	530	4	5.0	13	6	US-10-511-559-882	Sequence 882, App
458	5	6.2	5712	7	US-11-143-980-47	Sequence 47, Appl	531	4	5.0	13	6	US-10-511-559-883	Sequence 883, App
459	5	6.2	7102	7	US-11-143-980-48	Sequence 48, Appl	532	4	5.0	13	6	US-10-511-559-884	Sequence 884, App
460	5	6.2	7968	7	US-11-186-731-5	Sequence 5, Appli	533	4	5.0	13	6	US-10-511-559-903	Sequence 903, App
461	5	6.2	7968	7	US-11-143-980-49	Sequence 49, Appl	534	4	5.0	13	6	US-10-511-559-904	Sequence 904, App
462	4	5.0	7	6	US-10-753-537-7	Sequence 7, Appli	535	4	5.0	13	6	US-10-511-559-905	Sequence 905, App
463	4	5.0	7	7	US-11-039-268-7	Sequence 7, Appli	536	4	5.0	13	6	US-10-511-559-906	Sequence 906, App



537	4	5.0	13	6	US-10-467-657-9104	Sequence 9104, Ap	610	4	5.0	22	7	US-11-107-029-23	Sequence 23, Appl
538	4	5.0	13	6	US-10-889-197-3	Sequence 3, Appli	611	4	5.0	22	7	US-11-107-029-27	Sequence 27, Appl
539	4	5.0	13	7	US-11-064-774A-136	Sequence 136, App	612	4	5.0	23	7	US-11-107-029-25	Sequence 25, Appl
540	4	5.0	13	7	US-11-033-039-800	Sequence 800, App	613	4	5.0	24	5	US-09-978-360A-474	Sequence 474, App
541	4	5.0	13	7	US-11-033-039-821	Sequence 821, App	614	4	5.0	24	5	US-10-957-887B-122	Sequence 122, App
542	4	5.0	13	7	US-11-041-893-77	Sequence 77, Appl	615	4	5.0	29	6	US-11-089-601-10	Sequence 10, Appl
543	4	5.0	14	7	US-11-045-024-14251	Sequence 14251, A	616	4	5.0	29	7	US-11-188-281-10	Sequence 10, Appl
544	4	5.0	14	7	US-11-033-039-1444	Sequence 1444, Ap	617	4	5.0	30	7	US-11-033-039-679	Sequence 679, App
545	4	5.0	14	7	US-11-033-039-1450	Sequence 1450, Ap	618	4	5.0	31	7	US-11-106-932-12	Sequence 12, Appl
546	4	5.0	15	7	US-11-106-932-72	Sequence 72, Appl	619	4	5.0	32	6	US-10-467-657-1306	Sequence 1306, Ap
547	4	5.0	15	7	US-11-107-029-28	Sequence 28, Appl	620	4	5.0	32	6	US-10-746-959C-7	Sequence 7, Appli
548	4	5.0	15	7	US-11-107-029-29	Sequence 29, Appl	621	4	5.0	32	7	US-11-033-039-525	Sequence 525, App
549	4	5.0	15	7	US-11-107-029-32	Sequence 32, Appl	622	4	5.0	33	7	US-11-121-301-49	Sequence 49, Appl
550	4	5.0	15	7	US-11-033-039-1443	Sequence 1443, Ap	623	4	5.0	33	7	US-11-121-301-50	Sequence 50, Appl
551	4	5.0	15	7	US-11-041-893-5	Sequence 5, Appli	624	4	5.0	33	7	US-11-121-301-74	Sequence 74, Appl
552	4	5.0	15	7	US-11-041-893-16	Sequence 16, Appl	625	4	5.0	34	6	US-10-816-768-30	Sequence 30, Appl
553	4	5.0	15	7	US-11-041-893-210	Sequence 210, App	626	4	5.0	34	6	US-10-816-768-31	Sequence 31, Appl
554	4	5.0	15	7	US-11-051-481-52	Sequence 52, Appl	627	4	5.0	34	6	US-10-816-768-33	Sequence 33, Appl
555	4	5.0	16	6	US-10-631-558-8	Sequence 8, Appli	628	4	5.0	34	7	US-11-068-783-88	Sequence 88, Appl
556	4	5.0	16	7	US-11-017-550-78	Sequence 78, Appl	629	4	5.0	34	7	US-11-121-301-14	Sequence 14, Appl
557	4	5.0	16	7	US-11-089-764-34	Sequence 34, Appl	630	4	5.0	34	7	US-11-122-795-15	Sequence 15, Appl
558	4	5.0	16	7	US-11-089-764-35	Sequence 35, Appl	631	4	5.0	35	6	US-10-816-768-1	Sequence 1, Appli
559	4	5.0	16	7	US-11-107-029-22	Sequence 22, Appl	632	4	5.0	35	6	US-10-467-657-1036	Sequence 1036, Ap
560	4	5.0	16	7	US-11-107-029-26	Sequence 26, Appl	633	4	5.0	35	6	US-10-431-638-25	Sequence 25, Appl
561	4	5.0	16	7	US-11-033-039-1442	Sequence 1442, Ap	634	4	5.0	35	6	US-10-957-351-34	Sequence 34, Appl
562	4	5.0	17	7	US-11-033-039-1448	Sequence 1448, Ap	635	4	5.0	36	6	US-10-467-657-3056	Sequence 3056, Ap
563	4	5.0	17	7	US-11-062-186-54	Sequence 54, Appl	636	4	5.0	37	6	US-10-467-657-8849	Sequence 8849, Ap
564	4	5.0	17	7	US-11-033-039-1441	Sequence 1441, Ap	637	4	5.0	38	6	US-10-467-657-2998	Sequence 2998, Ap
565	4	5.0	17	7	US-11-033-039-1447	Sequence 1447, Ap	638	4	5.0	38	7	US-11-212-443-144	Sequence 144, App
566	4	5.0	18	7	US-11-092-496-21	Sequence 21, Appl	639	4	5.0	38	7	US-11-212-443-145	Sequence 145, App
567	4	5.0	18	7	US-11-076-164-24	Sequence 24, Appl	640	4	5.0	38	7	US-11-212-443-146	Sequence 146, App
568	4	5.0	18	7	US-11-106-415-216	Sequence 216, App	641	4	5.0	39	7	US-11-196-400-23	Sequence 23, Appl
569	4	5.0	18	7	US-11-106-415-230	Sequence 230, App	642	4	5.0	41	6	US-10-467-657-6206	Sequence 6206, Ap
570	4	5.0	18	7	US-11-106-415-254	Sequence 254, App	643	4	5.0	41	6	US-10-467-657-8759	Sequence 8759, Ap
571	4	5.0	18	7	US-11-106-415-270	Sequence 270, App	644	4	5.0	41	6	US-10-916-827-38	Sequence 38, Appl
572	4	5.0	18	7	US-11-106-415-339	Sequence 339, App	645	4	5.0	42	6	US-10-518-159-2	Sequence 2, Appli
573	4	5.0	18	7	US-11-106-415-340	Sequence 340, App	646	4	5.0	42	6	US-10-518-159-4	Sequence 4, Appli
574	4	5.0	18	7	US-11-106-415-343	Sequence 343, App	647	4	5.0	42	6	US-10-986-501-166	Sequence 166, App
575	4	5.0	18	7	US-11-106-415-344	Sequence 344, App	648	4	5.0	42	6	US-10-467-657-1478	Sequence 1478, Ap
576	4	5.0	18	7	US-11-106-415-348	Sequence 348, App	649	4	5.0	42	6	US-10-957-887B-119	Sequence 119, App
577	4	5.0	18	7	US-11-106-415-354	Sequence 354, App	650	4	5.0	42	7	US-11-090-787-1	Sequence 1, Appli
578	4	5.0	18	7	US-11-106-415-357	Sequence 357, App	651	4	5.0	42	7	US-11-090-787-2	Sequence 2, Appli
579	4	5.0	18	7	US-11-106-415-360	Sequence 360, App	652	4	5.0	42	7	US-11-090-825-1	Sequence 1, Appli
580	4	5.0	18	7	US-11-106-415-388	Sequence 388, App	653	4	5.0	42	7	US-11-090-825-2	Sequence 2, Appli
581	4	5.0	18	7	US-11-033-039-1440	Sequence 1440, Ap	654	4	5.0	43	6	US-10-952-538A-40	Sequence 40, Appl
582	4	5.0	18	7	US-11-033-039-1446	Sequence 1446, Ap	655	4	5.0	43	6	US-10-623-155-482	Sequence 482, App
583	4	5.0	19	6	US-10-503-575-125	Sequence 125, App	656	4	5.0	43	6	US-10-957-887B-28	Sequence 28, Appl
584	4	5.0	19	6	US-10-503-575-131	Sequence 131, App	657	4	5.0	43	6	US-10-957-887B-64	Sequence 64, Appl
585	4	5.0	19	6	US-10-503-575-314	Sequence 314, App	658	4	5.0	43	6	US-10-957-887B-77	Sequence 77, Appl
586	4	5.0	19	6	US-10-503-575-315	Sequence 315, App	659	4	5.0	43	6	US-10-957-887B-78	Sequence 78, Appl
587	4	5.0	19	6	US-10-503-575-317	Sequence 317, App	660	4	5.0	43	6	US-10-957-887B-79	Sequence 79, Appl
588	4	5.0	19	6	US-10-503-575-319	Sequence 319, App	661	4	5.0	43	6	US-10-957-887B-80	Sequence 80, Appl
589	4	5.0	19	6	US-10-503-575-321	Sequence 321, App	662	4	5.0	43	6	US-10-957-887B-165	Sequence 165, App
590	4	5.0	19	7	US-11-145-566-9	Sequence 9, Appli	663	4	5.0	43	6	US-10-957-887B-159	Sequence 159, App
591	4	5.0	19	7	US-11-212-443-153	Sequence 153, App	664	4	5.0	43	6	US-10-957-887B-160	Sequence 160, App
592	4	5.0	19	7	US-11-212-443-154	Sequence 154, App	665	4	5.0	43	6	US-10-957-887B-163	Sequence 163, App
593	4	5.0	19	7	US-11-212-443-155	Sequence 155, App	666	4	5.0	43	6	US-10-957-887B-164	Sequence 164, App
594	4	5.0	19	7	US-11-033-039-1439	Sequence 1439, Ap	667	4	5.0	43	6	US-10-957-887B-214	Sequence 214, App
595	4	5.0	19	7	US-11-033-039-1435	Sequence 1445, Ap	668	4	5.0	43	6	US-10-957-887B-222	Sequence 222, App
596	4	5.0	20	6	US-10-623-155-400	Sequence 400, App	669	4	5.0	43	6	US-10-957-887B-223	Sequence 223, App
597	4	5.0	20	6	US-10-623-155-401	Sequence 401, App	670	4	5.0	43	6	US-10-957-887B-224	Sequence 224, App
598	4	5.0	20	6	US-10-623-155-457	Sequence 457, App	671	4	5.0	43	6	US-10-957-887B-233	Sequence 233, App
599	4	5.0	20	6	US-10-623-155-508	Sequence 508, App	672	4	5.0	43	6	US-10-957-887B-234	Sequence 234, App
600	4	5.0	20	6	US-10-623-155-509	Sequence 509, App	673	4	5.0	43	6	US-10-957-887B-236	Sequence 236, App
601	4	5.0	20	7	US-11-106-415-290	Sequence 290, App	674	4	5.0	43	6	US-10-957-887B-237	Sequence 237, App
602	4	5.0	20	7	US-11-106-415-307	Sequence 307, App	675	4	5.0	43	6	US-10-957-887B-262	Sequence 262, App
603	4	5.0	20	7	US-11-106-415-311	Sequence 311, App	676	4	5.0	43	6	US-10-957-887B-303	Sequence 303, App
604	4	5.0	20	7	US-11-106-415-324	Sequence 324, App	677	4	5.0	43	7	US-11-108-001-4	Sequence 4, Appli
605	4	5.0	20	7	US-11-106-415-324	Sequence 324, App	678	4	5.0	44	6	US-10-957-887B-1	Sequence 1, Appli
606	4	5.0	21	6	US-10-986-501-358	Sequence 358, App	679	4	5.0	44	6	US-10-957-887B-4	Sequence 4, Appli
607	4	5.0	21	6	US-10-939-890-472	Sequence 472, App	680	4	5.0	44	6	US-10-957-887B-116	Sequence 116, App
608	4	5.0	21	6	US-10-939-890-504	Sequence 504, App	681	4	5.0	44	6	US-10-957-887B-173	Sequence 173, App
609	4	5.0	21	6	US-10-939-890-511	Sequence 511, App	682	4	5.0	44	6	US-10-957-887B-294	Sequence 294, App

683	4	5.0	45	6	US-10-986-501-170	Sequence 170, App	756	4	5.0	78	6	US-10-467-657-1764	Sequence 1764, Ap
684	4	5.0	45	6	US-10-957-887B-185	Sequence 185, App	757	4	5.0	78	6	US-10-467-657-3038	Sequence 3038, Ap
685	4	5.0	45	6	US-11-000-463-742	Sequence 742, App	758	4	5.0	78	6	US-11-082-389-170	Sequence 170, App
686	4	5.0	46	6	US-10-828-033-32	Sequence 32, Appl	759	4	5.0	80	6	US-10-986-501-200	Sequence 200, App
687	4	5.0	46	6	US-10-828-033-34	Sequence 34, Appl	760	4	5.0	80	6	US-10-467-657-5282	Sequence 5282, Ap
688	4	5.0	46	6	US-10-957-887B-33	Sequence 33, Appl	761	4	5.0	81	6	US-10-467-657-2490	Sequence 2490, Ap
689	4	5.0	46	6	US-10-957-887B-198	Sequence 198, App	762	4	5.0	81	6	US-10-467-657-5668	Sequence 5668, Ap
690	4	5.0	46	6	US-10-957-887B-275	Sequence 275, App	763	4	5.0	81	6	US-10-467-657-8338	Sequence 8338, Ap
691	4	5.0	46	6	US-10-957-887B-276	Sequence 276, App	764	4	5.0	81	6	US-10-467-657-8352	Sequence 8352, Ap
692	4	5.0	46	6	US-10-957-351-5	Sequence 5, Appl	765	4	5.0	82	6	US-11-053-076-287	Sequence 287, App
693	4	5.0	46	6	US-11-000-463-306	Sequence 306, App	766	4	5.0	83	6	US-10-467-657-7970	Sequence 7970, Ap
694	4	5.0	46	7	US-11-000-463-778	Sequence 778, App	767	4	5.0	83	7	US-11-089-426-21	Sequence 21, Appl
695	4	5.0	47	6	US-10-467-657-2348	Sequence 2348, Ap	768	4	5.0	83	7	US-11-000-463-246	Sequence 246, App
696	4	5.0	47	6	US-10-467-657-2350	Sequence 2350, Ap	769	4	5.0	85	6	US-10-986-501-129	Sequence 129, App
697	4	5.0	47	6	US-10-467-657-5500	Sequence 5500, Ap	770	4	5.0	85	6	US-10-467-657-3090	Sequence 3090, Ap
698	4	5.0	47	6	US-11-068-783-108	Sequence 108, App	771	4	5.0	85	6	US-10-485-788A-660	Sequence 660, App
699	4	5.0	47	7	US-11-000-463-414	Sequence 414, App	772	4	5.0	85	7	US-11-053-076-23	Sequence 23, Appl
700	4	5.0	47	7	US-11-000-463-886	Sequence 886, App	773	4	5.0	85	7	US-11-076-164-43	Sequence 43, Appl
701	4	5.0	48	6	US-10-467-657-6820	Sequence 6820, Ap	774	4	5.0	87	6	US-10-467-657-7678	Sequence 7678, Ap
702	4	5.0	48	6	US-10-467-657-7896	Sequence 7896, Ap	775	4	5.0	87	6	US-10-485-788A-729	Sequence 729, App
703	4	5.0	48	7	US-11-123-896-282	Sequence 282, App	776	4	5.0	87	7	US-11-053-076-99	Sequence 99, Appl
704	4	5.0	49	6	US-10-485-517-334	Sequence 334, App	777	4	5.0	88	6	US-10-467-657-5480	Sequence 5480, Ap
705	4	5.0	49	6	US-10-967-527A-15	Sequence 15, Appl	778	4	5.0	88	7	US-11-135-855-32	Sequence 32, Appl
706	4	5.0	49	6	US-10-467-657-8236	Sequence 8236, Ap	779	4	5.0	89	6	US-10-485-788A-754	Sequence 754, App
707	4	5.0	49	6	US-10-431-638-35	Sequence 35, Appl	780	4	5.0	89	6	US-10-485-788A-789	Sequence 789, App
708	4	5.0	50	6	US-10-986-501-276	Sequence 276, App	781	4	5.0	89	7	US-11-053-076-131	Sequence 131, App
709	4	5.0	50	6	US-10-982-727-63	Sequence 63, Appl	782	4	5.0	89	7	US-11-053-076-171	Sequence 171, App
710	4	5.0	50	6	US-10-982-727-64	Sequence 64, Appl	783	4	5.0	89	7	US-10-485-788A-829	Sequence 829, App
711	4	5.0	51	6	US-10-729-121-32	Sequence 32, Appl	784	4	5.0	90	6	US-10-485-788A-832	Sequence 832, App
712	4	5.0	51	6	US-10-467-657-816	Sequence 816, App	785	4	5.0	90	7	US-11-053-076-214	Sequence 214, App
713	4	5.0	51	7	US-11-000-463-286	Sequence 286, App	786	4	5.0	90	7	US-11-053-076-217	Sequence 217, App
714	4	5.0	51	7	US-11-000-463-443	Sequence 443, App	787	4	5.0	91	6	US-10-954-468-48	Sequence 48, Appl
715	4	5.0	51	7	US-11-000-463-728	Sequence 728, App	788	4	5.0	91	7	US-11-051-481-49	Sequence 49, Appl
716	4	5.0	52	6	US-10-914-165-6	Sequence 6, Appl	789	4	5.0	92	6	US-10-821-234-1505	Sequence 1505, Ap
717	4	5.0	52	7	US-11-000-463-266	Sequence 266, App	790	4	5.0	92	6	US-10-467-657-2068	Sequence 2068, Ap
718	4	5.0	52	7	US-11-000-463-738	Sequence 738, App	791	4	5.0	92	6	US-10-467-657-3456	Sequence 3456, Ap
719	4	5.0	54	6	US-10-467-657-3784	Sequence 3784, Ap	792	4	5.0	92	6	US-10-467-657-7806	Sequence 7806, Ap
720	4	5.0	54	7	US-11-000-463-712	Sequence 712, App	793	4	5.0	94	6	US-10-467-657-2090	Sequence 2090, Ap
721	4	5.0	55	5	US-09-978-360A-457	Sequence 457, App	794	4	5.0	94	6	US-10-485-788A-662	Sequence 662, App
722	4	5.0	55	6	US-10-467-657-4466	Sequence 4466, Ap	795	4	5.0	94	6	US-10-485-788A-776	Sequence 776, App
723	4	5.0	59	5	US-09-978-360A-730	Sequence 730, App	796	4	5.0	94	6	US-10-485-788A-802	Sequence 802, App
724	4	5.0	59	6	US-10-467-657-4896	Sequence 4896, Ap	797	4	5.0	94	7	US-11-053-076-25	Sequence 25, Appl
725	4	5.0	60	6	US-10-467-657-4114	Sequence 4114, Ap	798	4	5.0	94	7	US-11-053-076-158	Sequence 158, App
726	4	5.0	60	6	US-10-467-657-4940	Sequence 4940, Ap	799	4	5.0	94	7	US-11-053-076-184	Sequence 184, App
727	4	5.0	60	6	US-10-467-657-8454	Sequence 8454, Ap	800	4	5.0	94	7	US-11-055-822-828	Sequence 828, App
728	4	5.0	61	6	US-10-467-657-1506	Sequence 1506, Ap	801	4	5.0	95	6	US-10-467-657-2136	Sequence 2136, Ap
729	4	5.0	61	6	US-10-467-657-5574	Sequence 5574, Ap	802	4	5.0	95	6	US-10-467-657-2922	Sequence 2922, Ap
730	4	5.0	62	6	US-10-888-613B-86	Sequence 86, Appl	803	4	5.0	95	6	US-10-485-788A-659	Sequence 659, App
731	4	5.0	64	7	US-11-102-978-5	Sequence 5, Appl	804	4	5.0	95	6	US-10-485-788A-663	Sequence 663, App
732	4	5.0	65	6	US-10-467-657-7770	Sequence 7770, Ap	805	4	5.0	95	7	US-11-053-076-22	Sequence 22, Appl
733	4	5.0	66	6	US-10-986-501-160	Sequence 160, App	806	4	5.0	95	7	US-11-053-076-26	Sequence 26, Appl
734	4	5.0	66	6	US-10-467-657-2890	Sequence 2890, Ap	807	4	5.0	96	6	US-10-821-234-1351	Sequence 1351, Ap
735	4	5.0	67	7	US-11-068-717-13	Sequence 13, Appl	808	4	5.0	96	6	US-10-467-657-5492	Sequence 5492, Ap
736	4	5.0	67	7	US-11-074-176-302	Sequence 302, App	809	4	5.0	96	6	US-10-925-366A-222	Sequence 222, App
737	4	5.0	68	6	US-10-467-657-1436	Sequence 1436, App	810	4	5.0	96	6	US-10-485-788A-766	Sequence 766, App
738	4	5.0	68	6	US-10-467-657-3384	Sequence 3384, Ap	811	4	5.0	96	7	US-11-053-076-143	Sequence 143, App
739	4	5.0	68	6	US-10-467-657-7534	Sequence 7534, Ap	812	4	5.0	96	7	US-11-019-711-92	Sequence 92, Appl
740	4	5.0	69	6	US-10-467-657-5932	Sequence 5932, Ap	813	4	5.0	96	7	US-11-019-711-93	Sequence 93, Appl
741	4	5.0	69	7	US-11-051-481-50	Sequence 50, Appl	814	4	5.0	97	6	US-10-467-657-2016	Sequence 2016, Ap
742	4	5.0	70	6	US-10-467-657-4972	Sequence 4972, Ap	815	4	5.0	97	6	US-10-995-561-900	Sequence 900, App
743	4	5.0	70	7	US-11-021-441-116	Sequence 116, App	816	4	5.0	97	6	US-10-485-788A-676	Sequence 676, App
744	4	5.0	71	6	US-10-467-657-4162	Sequence 4162, Ap	817	4	5.0	97	6	US-10-485-788A-791	Sequence 791, App
745	4	5.0	71	7	US-11-000-463-369	Sequence 369, App	818	4	5.0	97	6	US-10-485-788A-795	Sequence 795, App
746	4	5.0	71	7	US-11-000-463-841	Sequence 841, App	819	4	5.0	97	6	US-10-485-788A-820	Sequence 820, App
747	4	5.0	72	6	US-10-467-657-2816	Sequence 2816, Ap	820	4	5.0	97	7	US-11-053-076-42	Sequence 42, Appl
748	4	5.0	72	6	US-10-528-031-2	Sequence 2, Appl	821	4	5.0	97	7	US-11-053-076-173	Sequence 173, App
749	4	5.0	73	6	US-10-467-657-8832	Sequence 8832, Ap	822	4	5.0	97	7	US-11-053-076-177	Sequence 177, App
750	4	5.0	74	6	US-10-467-657-1976	Sequence 1976, Ap	823	4	5.0	97	7	US-11-053-076-205	Sequence 205, App
751	4	5.0	75	6	US-10-986-501-139	Sequence 139, App	824	4	5.0	97	7	US-11-000-463-870	Sequence 870, App
752	4	5.0	75	6	US-10-986-501-143	Sequence 143, App	825	4	5.0	98	6	US-10-816-768-41	Sequence 41, Appl
753	4	5.0	76	7	US-11-123-896-281	Sequence 281, App	826	4	5.0	98	6	US-10-816-768-42	Sequence 42, Appl
754	4	5.0	77	7	US-11-132-142-19	Sequence 19, Appl	827	4	5.0	98	6	US-10-816-768-44	Sequence 44, Appl
755	4	5.0	78	6	US-10-986-501-357	Sequence 357, App	828	4	5.0	98	6	US-10-467-657-3490	Sequence 3490, Ap



975 4 5.0 103 7 US-11-064-774A-351 Sequence 351, App  
976 4 5.0 103 7 US-11-064-774A-357 Sequence 357, App  
977 4 5.0 103 7 US-11-064-774A-359 Sequence 359, App  
978 4 5.0 103 7 US-11-064-774A-365 Sequence 365, App  
979 4 5.0 103 7 US-11-064-774A-367 Sequence 367, App  
980 4 5.0 103 7 US-11-064-774A-373 Sequence 373, App  
981 4 5.0 103 7 US-11-064-774A-375 Sequence 375, App  
982 4 5.0 103 7 US-11-064-774A-381 Sequence 381, App  
983 4 5.0 103 7 US-11-064-774A-383 Sequence 383, App  
984 4 5.0 103 7 US-11-064-774A-389 Sequence 389, App  
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988 4 5.0 103 7 US-11-064-774A-405 Sequence 405, App  
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994 4 5.0 103 7 US-11-064-774A-429 Sequence 429, App  
995 4 5.0 103 7 US-11-064-774A-431 Sequence 431, App  
996 4 5.0 103 7 US-11-194-246-412 Sequence 412, App  
997 4 5.0 103 7 US-11-064-174-42 Sequence 42, Appl  
998 4 5.0 104 6 US-10-467-657-6588 Sequence 6588, Ap  
999 4 5.0 104 6 US-10-485-788A-835 Sequence 835, App  
1000 4 5.0 104 7 US-11-053-076-220 Sequence 220, App

## ALIGNMENTS

RESULT 1  
US-10-821-234-1266  
; Sequence 1266, Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Andarmani, Susan  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presclampsia  
; FILE REFERENCE: 821A  
; CURRENT APPLICATION NUMBER: US/10/821,234  
; CURRENT FILING DATE: 2004-04-07  
; PRIOR APPLICATION NUMBER: US 60/462,047  
; PRIOR FILING DATE: 2003-04-07  
; NUMBER OF SEQ ID NOS: 1704  
; SOFTWARE: pt\_seq\_genes Version 1.0  
; SEQ ID NO 1266  
; LENGTH: 228  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-821-234-1266  
Query Match 100.0%; Score 80; DB 6; Length 228;  
Best Local Similarity 100.0%; Pred. No. 6.6e-78;  
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HKDEVIKEVQEFYKDTYNNKLTQDEPQRETLKAIHYALNCCGLAGVQFISDICPKKDV 60  
DB 113 HKDEVIKEVQEFYKDTYNNKLTQDEPQRETLKAIHYALNCCGLAGVQFISDICPKKDV 172  
QY 61 LETFTVKSCPDAIKEVFDNK 80  
DB 173 LETFTVKSCPDAIKEVFDNK 192  
RESULT 2  
US-11-022-562-157  
; Sequence 157, Application US/11022562  
; Publication No. US20050249742A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruprecht, Ruth M.  
; APPLICANT: Shisong, Jiang  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING  
; FILE REFERENCE: DFN-043CN  
; CURRENT APPLICATION NUMBER: US/11/022,562  
; CURRENT FILING DATE: 2004-12-22  
; PRIOR APPLICATION NUMBER: PCT/US03/20322  
; PRIOR FILING DATE: 2003-06-27  
; PRIOR APPLICATION NUMBER: 60/392718  
; PRIOR FILING DATE: 2002-06-27  
; NUMBER OF SEQ ID NOS: 340  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 157  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Simian Immunodeficiency Virus  
US-11-022-562-157  
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Best Local Similarity 100.0%; Pred. No. 2.4;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 71 DAIKEV 76  
DB 12 DAIKEV 17  
RESULT 3  
US-11-022-562-158  
; Sequence 158, Application US/11022562  
; Publication No. US20050249742A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruprecht, Ruth M.  
; APPLICANT: Shisong, Jiang  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING  
; FILE REFERENCE: DFN-043CN  
; CURRENT APPLICATION NUMBER: US/11/022,562  
; CURRENT FILING DATE: 2004-12-22  
; PRIOR APPLICATION NUMBER: PCT/US03/20322  
; PRIOR FILING DATE: 2003-06-27  
; PRIOR APPLICATION NUMBER: 60/392718  
; PRIOR FILING DATE: 2002-06-27  
; NUMBER OF SEQ ID NOS: 340  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 158  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Simian Immunodeficiency Virus  
US-11-022-562-158  
Query Match 7.5%; Score 6; DB 7; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.4;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 71 DAIKEV 76  
DB 2 DAIKEV 7  
RESULT 4  
US-11-145-035-45  
; Sequence 45, Application US/11145035  
; Publication No. US20050287122A1  
; GENERAL INFORMATION:  
; APPLICANT: Bartlett et al.  
; TITLE OF INVENTION: RAV VECTORS AND METHODS  
; FILE REFERENCE: 28335/41335  
; CURRENT APPLICATION NUMBER: US/11/145,035  
; CURRENT FILING DATE: 2005-06-03  
; PRIOR APPLICATION NUMBER: US 10/038,972  
; PRIOR FILING DATE: 2002-01-04  
; PRIOR APPLICATION NUMBER: US 60/260,124

; PRIOR FILING DATE: 2001-01-05  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 45  
; LENGTH: 31  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
US-11-145-035-45

Query Match 7.5%; Score 6; DB 7; Length 31;  
Best Local Similarity 100.0%; Pred. No. 3.6;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 KDEPQR 28  
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Db 1 KDEPQR 6

RESULT 5  
US-10-467-657-606  
; Sequence 606, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SPA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: Seqwin99, version 1.04  
; SEQ ID NO 606  
; LENGTH: 122  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-606

Query Match 7.5%; Score 6; DB 6; Length 122;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 GGVEQF 50  
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Db 28 GGVEQF 33

RESULT 6  
US-10-467-657-2734  
; Sequence 2734, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SPA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: Seqwin99, version 1.04  
; SEQ ID NO 2734  
; LENGTH: 259

; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-2734

Query Match 7.5%; Score 6; DB 6; Length 259;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 GLAGGV 47  
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Db 140 GLAGGV 145

RESULT 7  
US-10-883-512-108  
; Sequence 108, Application US/10883512  
; Publication No. US20060005265A1  
; GENERAL INFORMATION:  
; APPLICANT: Bughrara, Suleiman  
; APPLICANT: Han, Zhao  
; APPLICANT: Wang, Yuxia  
; TITLE OF INVENTION: RyeGrass CBF3 Gene: Identification and Isolation  
; FILE REFERENCE: MSU-08807  
; CURRENT APPLICATION NUMBER: US/10/883,512  
; CURRENT FILING DATE: 2004-07-01  
; NUMBER OF SEQ ID NOS: 199  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 108  
; LENGTH: 274  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-10-883-512-108

Query Match 7.5%; Score 6; DB 6; Length 274;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 KKDVL 62  
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Db 184 KKDVL 189

RESULT 8  
US-09-978-360A-763

; Sequence 763, Application US/09978360A  
; Publication No. US20060009633A9  
; GENERAL INFORMATION:  
; APPLICANT: Edwards, Jean-Baptiste Dumas Milne  
; APPLICANT: Duclert, Aymeric  
; APPLICANT: Bougueleret, Lydie  
; APPLICANT: Jobert, Severin  
; APPLICANT: Clusel, Catherine  
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides  
; FILE REFERENCE: 56.US4.CIP  
; CURRENT APPLICATION NUMBER: US/09/978,360A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: US 60/066,677  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: US 60/069,957  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: US 60/074,121  
; PRIOR FILING DATE: 1998-02-09  
; PRIOR APPLICATION NUMBER: US 60/081,563  
; PRIOR FILING DATE: 1998-04-13  
; PRIOR APPLICATION NUMBER: US 60/096,116  
; PRIOR FILING DATE: 1998-08-10  
; PRIOR APPLICATION NUMBER: US 60/099,273  
; PRIOR FILING DATE: -09-04  
; PRIOR APPLICATION NUMBER: US 09/191,997  
; PRIOR FILING DATE: 1998-11-13  
; PRIOR APPLICATION NUMBER: US 09/215,435  
; PRIOR FILING DATE: 1998-12-17  
; PRIOR APPLICATION NUMBER: PCT/IB98/02122

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; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: US 09/247,155
; PRIOR FILING DATE: 1999-02-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 810
; SOFTWARE: Patent.pm
; SEQ ID NO 763
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -20...-1
US-09-978-360A-763

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Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 CGLAGG 46
Db 249 CGLAGG 254

RESULT 9
US-10-510-386-244
; Sequence 244, Application US/10510386
; Publication No. US20050244922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294.204-US
; CURRENT APPLICATION NUMBER: US/10/510,386
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 244
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-510-386-244

Query Match          7.5%; Score 6; DB 6; Length 316;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 74 KEVFDN 79
Db 302 KEVFDN 307

RESULT 10
US-10-873-528-62
; Sequence 62, Application US/10873528
; Publication No. US20050276814A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Gilbert, Christophe FG
; APPLICANT: Hansbro, Philip M
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21129W0
; CURRENT APPLICATION NUMBER: US/10/873,528
; CURRENT FILING DATE: 2004-06-23
; PRIOR APPLICATION NUMBER: US/09/769,787
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: GB 9816337.1
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/125164
; PRIOR FILING DATE: 1999-03-19
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; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 62
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-873-528-62

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Best Local Similarity 100.0%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 59 DVLETF 64
Db 178 DVLETF 183

RESULT 11
US-10-467-657-8004
; Sequence 8004, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8004
; LENGTH: 408
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8004

Query Match          7.5%; Score 6; DB 6; Length 408;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 46 GVEQFI 51
Db 228 GVEQFI 233

RESULT 12
US-10-978-927-1
; Sequence 1, Application US/10978927
; Publication No. US20060009406A1
; GENERAL INFORMATION:
; APPLICANT: Kyrkanides, Stephanos
; TITLE OF INVENTION: VECTORS HAVING BOTH ISOFORMS OF
; FILE REFERENCE: 21108.0018U2
; CURRENT APPLICATION NUMBER: US/10/978,927
; CURRENT FILING DATE: 2004-11-01
; PRIOR APPLICATION NUMBER: PCT/US03/13672
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 60/377,503
; PRIOR FILING DATE: 2002-05-02
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence./Note =
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; OTHER INFORMATION: Synthetic Construct  
US-10-978-927-1

Query Match 7.5%; Score 6; DB 6; Length 409;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 EVFDNK 80  
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Db 255 EVFDNK 260

## RESULT 13

US-11-109-156-34  
; Sequence 34, Application US/11109156  
; Publication No. US20050250144A1

; GENERAL INFORMATION:

; APPLICANT: Toshio Ota  
; APPLICANT: Takao Isogai  
; APPLICANT: Tetsuo Nishikawa  
; APPLICANT: Koji Hayashi  
; APPLICANT: Kaoru Otsuka  
; APPLICANT: Jun-Ichi Yamamoto  
; APPLICANT: Shizuko Ishii  
; APPLICANT: Tomoyasu Sugiyama  
; APPLICANT: Ai Wakamatsu  
; APPLICANT: Keiichi Nagai  
; APPLICANT: Tetsuji Otsuki  
; APPLICANT: Shin-ichi Funahashi  
; APPLICANT: Chiaki Senoo  
; APPLICANT: Jun-Ichi Nezu  
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN  
; FILE REFERENCE: 06501-099002  
; CURRENT APPLICATION NUMBER: US/11/109,156  
; CURRENT FILING DATE: 2005-04-19  
; PRIOR APPLICATION NUMBER: US/10/060,065  
; PRIOR FILING DATE: 2002-01-29  
; PRIOR APPLICATION NUMBER: PCT/JP00/05061  
; PRIOR FILING DATE: 2000-07-28  
; PRIOR APPLICATION NUMBER: US 60/159,590  
; PRIOR FILING DATE: 1999-10-18  
; PRIOR APPLICATION NUMBER: US 60/183,322  
; PRIOR FILING DATE: 2000-02-17  
; PRIOR APPLICATION NUMBER: JP 11-248036  
; PRIOR FILING DATE: 1999-07-29  
; PRIOR APPLICATION NUMBER: JP 2000-118776  
; PRIOR FILING DATE: 2000-01-11  
; PRIOR APPLICATION NUMBER: JP 2000-183767  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: JP 2000-241899  
; PRIOR FILING DATE: 2000-06-09  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 34  
; LENGTH: 521  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-109-156-34

Query Match 7.5%; Score 6; DB 7; Length 521;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 KEVFDN 79  
|||||  
Db 32 KEVFDN 37

## RESULT 14

US-10-978-927-6  
; Sequence 6, Application US/10978927  
; Publication No. US20060009406A1

; GENERAL INFORMATION:  
; APPLICANT: Kyrkanides, Stephanos  
; TITLE OF INVENTION: VECTORS HAVING BOTH ISOFORMS OF  
; FILE REFERENCE: 21108.0018U2  
; CURRENT APPLICATION NUMBER: US/10/978,927  
; CURRENT FILING DATE: 2004-11-01  
; PRIOR APPLICATION NUMBER: PCT/US03/13672  
; PRIOR FILING DATE: 2003-05-02  
; PRIOR APPLICATION NUMBER: 60/377,503  
; PRIOR FILING DATE: 2002-05-02  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 528  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:/Note =  
; OTHER INFORMATION: Synthetic Construct  
US-10-978-927-6

Query Match 7.5%; Score 6; DB 6; Length 528;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 EVFDNK 80  
|||||  
Db 374 EVFDNK 379

## RESULT 15

US-10-821-234-1520  
; Sequence 1520, Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Andarmani, Susan  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
; FILE REFERENCE: 821A  
; CURRENT APPLICATION NUMBER: US/10/821,234  
; CURRENT FILING DATE: 2004-04-07  
; PRIOR APPLICATION NUMBER: US 60/462,047  
; PRIOR FILING DATE: 2003-04-07  
; NUMBER OF SEQ ID NOS: 1704  
; SOFTWARE: pt\_seq\_genes Version 1.0  
; SEQ ID NO 1520  
; LENGTH: 529  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-821-234-1520

Query Match 7.5%; Score 6; DB 6; Length 529;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 EVFDNK 80  
|||||  
Db 375 EVFDNK 380

Search completed: January 20, 2006, 17:47:41  
Job time : 10.4615 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2006, 17:35:41 ; Search time 18.4615 Seconds  
(without alignments)  
416.939 Million cell updates/sec

Title: US-10-619-323-1\_COPY\_113\_192

Perfect score: 80

Sequence: 1 HKDEVIKEVQEFYKDYNNKL.....LEFTVKSCPDAIKEVFDNK 80

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	38	47.5	228	1 A42929	CD9 antigen - gree
3	15	18.8	226	1 S3262	CD9 antigen - rat
4	13	16.2	226	1 JX0221	CD9 antigen - bovi
5	13	16.2	226	2 I49589	antigen - mouse
6	7	8.8	100	2 T07054	cysteine proteinas
7	7	8.8	276	2 A72276	phosphate ABC tran
8	7	8.8	516	2 B64551	oligopeptide ABC t
9	7	8.8	980	2 T00045	cellohextrin phosph
10	7	8.8	1302	2 T23236	hypothetical prote
11	6	7.5	15	2 S03353	plastocyanin - Mic
12	6	7.5	57	2 H35057	MHC class II histo
13	6	7.5	60	2 H82927	hypothetical prote
14	6	7.5	66	2 PQ0469	cysteine proteinas
15	6	7.5	68	2 D64538	hypothetical prote
16	6	7.5	83	2 D56604	M protein precuro
17	6	7.5	84	2 S61082	cytochrome c6 - re
18	6	7.5	85	1 JCCPR6	cytochrome c6 - re
19	6	7.5	85	2 JCS849	nonhistone chromos
20	6	7.5	89	1 NSBQH7	nonhistone chromos
21	6	7.5	89	2 S11349	nonhistone chromos
22	6	7.5	89	2 S38666	nonhistone chromos
23	6	7.5	90	1 NSCHH7	nonhistone chromos
24	6	7.5	90	2 S03700	nonhistone chromos
25	6	7.5	90	2 S01946	nonhistone chromos
26	6	7.5	92	2 T07051	cysteine proteinas
27	6	7.5	92	2 S78005	cuticle structural
28	6	7.5	93	2 A95121	hypothetical prote
29	6	7.5	93	2 F97990	hypothetical prote

hypothetical prote  
probable minor tai  
probable minor tai  
probable minor tai  
hypothetical prote  
hypothetical prote  
cytochrome c553 -  
hypothetical prote  
hypothetical prote  
protein T16B5.6 [i  
hypothetical prote  
NADP-reducing hydr  
probable minor tai  
probable tail comp  
plastocyanin precu  
probable minor tai  
hypothetical prote  
minor tail protein  
probable tail comp  
nitric-oxide reduc  
hypothetical prote  
hypothetical prote  
conserved hypotet  
flagellar protein  
hypothetical prote  
hypothetical prote  
sensor protein chv  
hypothetical prote  
pilus assembly pro  
hypothetical prote  
ribosomal protein  
acetyltransferase,  
TATA-binding trans  
probable membrane  
hypothetical cytos  
conserved hypotet  
transcription regu  
transcription regu  
ORF13 - Agrobacter  
chemotaxis protein  
Spi20 env protein  
hypothetical prote  
oncofetal protein  
hypothetical prote  
probable phosphos  
probable transcrip  
acetoacetate decar  
hypothetical prote  
capsular polysacch  
purine nucleotide  
phosphoprotein pho  
conserved hypotet  
hypothetical prote  
probable integral  
ABC transporter (A  
minor tail protein  
coproporphyrinogen  
phosphodiesterase  
conserved hypotet  
conserved hypotet  
hypothetical prote  
conserved hypotet  
hypothetical prote  
unknown protein [i  
hypothetical prote  
endopeptidase (EC  
3alpha-hydroxyster  
probable transcrip  
hypothetical prote  
probable oxidoredu  
probable dehydroge

103	6	7.5	324	2	E91144	probable dehydroge	176	6	7.5	453	2	AG1267	ribonuclease G hom
104	6	7.5	324	2	JS0688	hypothetical 35K p	177	6	7.5	454	2	G72452	probable glucamate
105	6	7.5	325	2	A10445	probable zinc-bind	178	6	7.5	461	2	AB1649	conserved hypotnet
106	6	7.5	325	2	C36718	pyruvate dehydroge	179	6	7.5	462	2	S52528	Ura1 protein - yea
107	6	7.5	326	2	T19451	hypothetical prote	180	6	7.5	473	2	T29622	hypothetical prote
108	6	7.5	326	2	D82374	zinc-binding alcoh	181	6	7.5	474	2	F83550	serine proteinase
109	6	7.5	327	2	G83921	hypothetical prote	182	6	7.5	481	2	T01850	UTP-glucose glucos
110	6	7.5	338	2	B69439	signal-transducng	183	6	7.5	482	2	T49079	serine-type carbox
111	6	7.5	344	2	S76268	probable UDP-3-O-1	184	6	7.5	483	2	H90210	hypothetical prote
112	6	7.5	345	1	B46113	protein kinase (EC	185	6	7.5	487	2	T33192	hypothetical prote
113	6	7.5	348	2	B69790	hypothetical prote	186	6	7.5	488	2	T27532	hypothetical prote
114	6	7.5	348	2	S44628	f22b7.1 protein -	187	6	7.5	493	2	B97460	betaine aldehyde d
115	6	7.5	348	2	B69162	sulfate transport	188	6	7.5	493	2	A26278	betaine aldehyde d
116	6	7.5	355	2	T49753	related to feebly	189	6	7.5	494	2	B86671	lysine-tRNA ligase
117	6	7.5	357	2	T12464	hypothetical prote	190	6	7.5	495	2	C89778	hypothetical prote
118	6	7.5	365	2	PQ0839	envelope protein -	191	6	7.5	495	2	A75608	aldehyde dehydroge
119	6	7.5	365	2	PQ0840	envelope protein -	192	6	7.5	495	2	S55273	amine oxidase (fla
120	6	7.5	365	2	S43780	peridinin-chloroph	193	6	7.5	501	2	T31265	aldehyde dehydroge
121	6	7.5	365	2	PQ0838	envelope protein -	194	6	7.5	501	2	S66763	hypothetical prote
122	6	7.5	369	2	A95113	probable cyclin, 2	195	6	7.5	505	1	S71413	betaine-aldehyde d
123	6	7.5	371	2	T31874	hypothetical prote	196	6	7.5	521	1	A56968	phosphoprotein pho
124	6	7.5	372	2	H97277	glycosyltransferas	197	6	7.5	521	1	S35067	phosphoprotein pho
125	6	7.5	375	2	S64621	biotin synthase (E	198	6	7.5	521	2	A33257	phosphoprotein pho
126	6	7.5	375	2	T19038	hypothetical prote	199	6	7.5	521	2	A33264	phosphoprotein pho
127	6	7.5	375	2	T32251	hypothetical prote	200	6	7.5	522	1	TSBVSS	protein disulfide-
128	6	7.5	377	2	E83220	hypothetical prote	201	6	7.5	528	2	I48253	beta-N-acetylhexos
129	6	7.5	379	2	E72274	cystathionine gamm	202	6	7.5	529	1	AOHUBA	beta-N-acetylhexos
130	6	7.5	379	2	B69344	hypothetical prote	203	6	7.5	531	2	T49058	hypothetical prote
131	6	7.5	380	2	G64309	hypothetical prote	204	6	7.5	533	2	E84148	hypothetical prote
132	6	7.5	387	2	H75009	hypothetical prote	205	6	7.5	535	2	D84340	hypothetical prote
133	6	7.5	387	2	E83679	multidrug-efflux t	206	6	7.5	549	2	JC5926	secreted klotho pr
134	6	7.5	388	1	VCVGTB	coat protein - tom	207	6	7.5	549	2	S04845	ig heavy chain pre
135	6	7.5	389	2	T33340	hypothetical prote	208	6	7.5	553	2	H82189	iron-sulfur cluate
136	6	7.5	389	2	T27574	hypothetical prote	209	6	7.5	554	2	E72362	hydroxy-acid deh
137	6	7.5	392	1	H65004	hypothetical prote	210	6	7.5	557	2	AB0170	30S ribosomal prot
138	6	7.5	392	2	AG2377	phosphate-binding	211	6	7.5	561	2	T51417	protein kinase-lik
139	6	7.5	392	2	G85873	probable transport	212	6	7.5	570	2	JC5722	vacuolar protein s
140	6	7.5	392	2	F91029	probable transport	213	6	7.5	572	2	S73730	MG307 homolog H08
141	6	7.5	394	2	H84016	aryldialkylphospha	214	6	7.5	579	2	S51528	D-lactate dehydrog
142	6	7.5	395	2	G90421	hypothetical prote	215	6	7.5	584	2	S06318	endoplasmic reticu
143	6	7.5	397	2	G71031	probable DNA-direc	216	6	7.5	585	2	E97232	probable signal tr
144	6	7.5	398	2	E70113	acetyl-CoA C-acety	217	6	7.5	592	2	G35115	hypothetical prote
145	6	7.5	399	2	A75269	acetyl-CoA acetyl t	218	6	7.5	592	2	D75421	conserved hypotnet
146	6	7.5	399	2	H84108	ABC transporter BH	219	6	7.5	599	2	E83241	hypothetical prote
147	6	7.5	400	2	T35019	beta-ketoadipyl-Co	220	6	7.5	607	2	F90413	AAA family ATPase
148	6	7.5	400	2	JC2473	doc2 protein - hum	221	6	7.5	612	2	E81287	probable sugar tra
149	6	7.5	403	2	C70815	probable beta-keto	222	6	7.5	625	2	F81287	probable sugar tra
150	6	7.5	403	2	E87179	probable beta-keto	223	6	7.5	629	2	E72297	methionine-tRNA li
151	6	7.5	403	2	T16242	hypothetical prote	224	6	7.5	631	2	JC5803	ring finger protei
152	6	7.5	404	2	T35428	probable acetyl co	225	6	7.5	632	2	UC7155	brain finger prote
153	6	7.5	404	2	T35256	probable thiolase	226	6	7.5	632	2	T48316	hypothetical prote
154	6	7.5	405	2	E95205	preproteins translo	227	6	7.5	638	1	ISMSEK	protein disulfide-
155	6	7.5	409	2	C41872	groEL 3'-region hy	228	6	7.5	640	2	T45924	protein kinase-lik
156	6	7.5	411	2	AH0807	probable membrane	229	6	7.5	643	1	S32476	protein disulfide-
157	6	7.5	412	2	B88736	protein f33D4.6a [	230	6	7.5	645	1	A23723	protein disulfide-
158	6	7.5	413	2	G82422	anaerobic glycerol	231	6	7.5	646	1	S16654	RNA-directed DNA p
159	6	7.5	414	1	D42594	N-carbamyl-L-amino	232	6	7.5	660	2	T28111	hypothetical prote
160	6	7.5	417	2	I84434	Rhesus-like protei	233	6	7.5	672	2	T32557	hypothetical prote
161	6	7.5	418	2	E91037	hypothetical prote	234	6	7.5	676	2	T40772	hypothetical prote
162	6	7.5	418	2	G85881	hypothetical prote	235	6	7.5	695	2	S49163	transferrin precu
163	6	7.5	418	2	B65013	hypothetical prote	236	6	7.5	695	2	A90959	probable tail prot
164	6	7.5	420	2	T08005	flavonol 3-O-gluc	237	6	7.5	696	2	C85807	hypothetical prote
165	6	7.5	422	2	AB1154	D-tagatose-bisphos	238	6	7.5	708	2	JC4384	hypothetical prote
166	6	7.5	422	2	C82666	conserved hypotnet	239	6	7.5	708	2	S62907	gelatinase B (EC 3
167	6	7.5	428	2	D81255	histidinol dehydro	240	6	7.5	713	2	JC2522	nuclear autoantige
168	6	7.5	429	2	S75245	N-acetylmornithine	241	6	7.5	715	1	DEECFS	formate dehydrogen
169	6	7.5	429	2	G75114	hypothetical prote	242	6	7.5	715	2	JC4560	methyilmalonyl-CoA
170	6	7.5	433	2	S37790	probable serine/th	243	6	7.5	715	2	E91261	formate dehydrogen
171	6	7.5	435	2	F96939	TPR repeats contai	244	6	7.5	715	2	A86102	formate dehydrogen
172	6	7.5	438	2	G87290	major facilitator	245	6	7.5	715	2	AB1021	formate dehydrogen
173	6	7.5	439	2	C64401	hypothetical prote	246	6	7.5	720	2	T47221	replication licens
174	6	7.5	448	2	B71319	probable acetate k	247	6	7.5	724	1	QOBB15	U189 protein - hum
175	6	7.5	448	2	S39348	26S ATP/ubiquitin-	248	6	7.5	728	2	T26607	hypothetical prote

249	6	7.5	729	1	A34796	kinesin-related pr	322	6	7.5	1774	2	S13178	6-methylsalicylic
250	6	7.5	729	2	B70333	hypothetical prote	323	6	7.5	1802	2	S52611	TyB protein - Yeas
251	6	7.5	729	3	F97321	membrane export pr	324	6	7.5	1803	2	S56894	TyB protein - Yeas
252	6	7.5	734	2	AF2001	hypothetical prote	325	6	7.5	1820	2	T19430	hypothetical prote
253	6	7.5	736	2	H75460	conserved hypotet	326	6	7.5	1944	2	T40065	tRNA-splicing endo
254	6	7.5	752	2	F81203	maltose phosphoryl	327	6	7.5	2238	1	RRVUBY	genome polyprotein
255	6	7.5	752	2	C81781	probable maltose p	328	6	7.5	2326	2	T29140	hypothetical prote
256	6	7.5	756	2	S40305	multicystatin - po	329	6	7.5	2802	2	F97686	cyclic beta-(1-2)
257	6	7.5	758	2	E83884	hypothetical prote	330	6	7.5	2831	2	AI2911	beta (1->2) glucan
258	6	7.5	774	1	P31V50	RNA-directed RNA p	331	6	7.5	3110	2	AC0116	probable virulence
259	6	7.5	774	2	S13670	basic polymerase 2	332	6	7.5	3394	2	T18501	hypothetical prote
260	6	7.5	778	2	E70320	polyribonucleotide	333	6	7.5	4377	2	A55575	ankyrin 3, long sp
261	6	7.5	778	2	D85055	probable polyprote	334	6	7.5	4558	2	C82199	RTX toxin RtxA VCI
262	6	7.5	790	2	T49414	related to ahmp1 p	335	5	6.2	33	32	A61232	relaxin - orogata
263	6	7.5	821	1	T19683	hypothetical prote	336	5	6.2	39	32	A4781	pregnancy-associat
264	6	7.5	832	1	B67702	endopeptidase Clp	337	5	6.2	39	32	S23804	homeotic protein 1
265	6	7.5	853	2	A28668	hypothetical prote	338	5	6.2	39	32	S23803	homeotic protein 1
266	6	7.5	855	2	AH0853	DNA mismatch repai	339	5	6.2	40	2	C37264	E2 glycoprotein -
267	6	7.5	863	2	G96964	probable permease,	340	5	6.2	40	2	H81591	hypothetical prote
268	6	7.5	869	2	A47665	env protein gp120(	341	5	6.2	41	2	PQ0560	nonstructural prot
269	6	7.5	874	2	JC4930	S-layer protein pr	342	5	6.2	41	2	PQ0563	nonstructural prot
270	6	7.5	880	1	VCLJ52	env polyprotein pr	343	5	6.2	41	2	PQ0564	nonstructural prot
271	6	7.5	881	2	S03068	env protein - huma	344	5	6.2	41	2	PQ0562	nonstructural prot
272	6	7.5	887	2	T52488	26S proteasome reg	345	5	6.2	41	2	PQ0565	nonstructural prot
273	6	7.5	889	1	VCLJG5	env polyprotein -	346	5	6.2	46	2	C83437	hypothetical prote
274	6	7.5	899	2	T42976	hypothetical prote	347	5	6.2	49	2	T37008	hypothetical prote
275	6	7.5	904	2	T03806	hypothetical prote	348	5	6.2	55	2	B46485	Ig epsilon chain C
276	6	7.5	920	2	S53961	hypothetical prote	349	5	6.2	56	2	B89903	hypothetical prote
277	6	7.5	932	2	S65214	probable alpha/gam	350	5	6.2	57	2	G35057	MHC class II histo
278	6	7.5	940	2	H86420	probable receptor-	351	5	6.2	57	2	C35058	MHC class II histo
279	6	7.5	945	2	F83925	oxoglutarate dehyd	352	5	6.2	58	2	B43928	probable collagen
280	6	7.5	945	2	T20156	hypothetical prote	353	5	6.2	59	1	R3BPL5	integrase - Staphy
281	6	7.5	947	2	S57108	hypothetical prote	354	5	6.2	60	2	T34737	probable gas vesic
282	6	7.5	954	2	S28428	phosphoenolpyruvat	355	5	6.2	61	2	D97920	hypothetical prote
283	6	7.5	967	2	FWZAM	spheroidin precurs	356	5	6.2	63	1	H64095	carbon storage reg
284	6	7.5	1003	1	F90099	hypothetical prote	357	5	6.2	63	1	FECLC	ferredoxin [4Fe-4S
285	6	7.5	1005	2	JC5925	membrane klotho pr	358	5	6.2	63	2	C59147	conotoxin Gm5.1 pr
286	6	7.5	1012	2	A29839	RAD2 protein - yea	359	5	6.2	64	2	H91000	hypothetical prote
287	6	7.5	1031	2	F83928	hypothetical prote	360	5	6.2	64	2	B90779	hypothetical prote
288	6	7.5	1091	2	A36866	microbial collagen	361	5	6.2	65	1	A22810	small acid-soluble
289	6	7.5	1104	1	A36866	hgIC protein - Ana	362	5	6.2	66	2	B87379	ribosomal protein
290	6	7.5	1108	2	T31335	heterocyst glycoli	363	5	6.2	66	2	S14932	ribosomal protein H
291	6	7.5	1109	2	AC2475	copia-like retroel	364	5	6.2	67	2	B71666	ribosomal protein
292	6	7.5	1137	2	G84581	reverse gyrase - A	365	5	6.2	68	1	IABY3	proteinase A inhib
293	6	7.5	1146	2	B70376	copia-like retroel	366	5	6.2	68	1	QOHSNB	hypothetical prote
294	6	7.5	1166	2	C84532	protein-tyrosine-p	367	5	6.2	68	2	B84267	hypothetical prote
295	6	7.5	1175	2	S51005	hypothetical prote	368	5	6.2	68	2	C71970	hypothetical prote
296	6	7.5	1181	2	T19736	probable lipoprote	369	5	6.2	69	2	S14074	hypothetical prote
297	6	7.5	1187	1	JC3155	transferrin-like p	370	5	6.2	69	2	T48461	hypothetical prote
298	6	7.5	1189	1	JC2366	hypothetical prote	371	5	6.2	70	2	S34217	hypothetical prote
299	6	7.5	1218	2	T30447	probable helicase	372	5	6.2	70	2	T03353	acclimation protei
300	6	7.5	1228	2	S59681	probable membrane	373	5	6.2	71	2	D82686	gene e14 protein -
301	6	7.5	1235	2	C65165	hypothetical prote	374	5	6.2	71	2	D82686	hypothetical prote
302	6	7.5	1244	2	S73731	probable lipoprote	375	5	6.2	73	2	G89307	protein TolC3.2 [i
303	6	7.5	1274	2	T10729	transferrin-like p	376	5	6.2	75	1	BVECRY	tray protein - Esc
304	6	7.5	1308	2	T05178	hypothetical prote	377	5	6.2	75	2	A13305	hypothetical prote
305	6	7.5	1322	2	B71440	hypothetical prote	378	5	6.2	76	2	S65527	H+-exporting ATPas
306	6	7.5	1333	2	E84601	probable retroelem	379	5	6.2	76	2	E89472	conserved hypotet
307	6	7.5	1363	2	T47492	copia-like polypro	380	5	6.2	76	2	S69163	serine proteinase
308	6	7.5	1381	2	E70806	hypothetical glyci	381	5	6.2	76	2	S69163	hypothetical prote
309	6	7.5	1402	1	A47328	natural killer cel	382	5	6.2	77	2	H96955	CT659 hypotetical
310	6	7.5	1465	2	S31262	hypothetical prote	383	5	6.2	78	2	B86580	conserved hypotet
311	6	7.5	1467	2	PC1253	TyB protein - yeas	384	5	6.2	78	2	B75193	hypothetical prote
312	6	7.5	1468	2	S58250	DNA-directed DNA p	385	5	6.2	78	2	JC7623	proteinase A inhib
313	6	7.5	1505	2	T31418	synaptonemal compl	386	5	6.2	78	2	AB1238	B. subtilis ynef p
314	6	7.5	1507	2	B47328	natural killer cel	387	5	6.2	79	2	AG1600	B. subtilis ynef p
315	6	7.5	1513	2	S45768	mitotic spindle pr	388	5	6.2	79	2	F72354	hypothetical prote
316	6	7.5	1560	2	T02885	peroxisome prolif	389	5	6.2	79	2	B69874	hypothetical prote
317	6	7.5	1653	2	T14758	hypothetical prote	390	5	6.2	79	2	T02461	hypothetical prote
318	6	7.5	1657	2	T25421	hypothetical prote	391	5	6.2	79	2	T04983	hypothetical prote
319	6	7.5	1659	1	OKBYN2	protein kinase GCN	392	5	6.2	80	2	F75598	hypothetical prote
320	6	7.5	1663	2	T28923	hypothetical prote	393	5	6.2	81	2	S38696	class II histocomp
321	6	7.5	1706	2	I84499	zinc finger protei	394	5	6.2	81	2	T03937	reverse transcript

395	5	6.2	81	2	F75409	hypothetical prote	468	5	6.2	100	2	AD0434	probable anti-sigm
396	5	6.2	81	2	T31199	hypothetical prote	469	5	6.2	101	2	A82058	ribosomal protein
397	5	6.2	82	2	S06772	ribulose-bisphosph	470	5	6.2	101	2	A27819	anti-lipopolysacch
398	5	6.2	82	2	I61834	gene MHC DQ-beta 1	471	5	6.2	101	2	A80506	probable transcrip
399	5	6.2	82	2	I61811	gene MHC DQ-beta 1	472	5	6.2	101	2	B91275	hypothetical prote
400	5	6.2	82	2	I61810	gene MHC DQ-beta 1	473	5	6.2	101	2	B86116	hypothetical prote
401	5	6.2	82	2	I61815	gene MHC DQ-beta 1	474	5	6.2	101	2	S56419	hypothetical 10.9K
402	5	6.2	82	2	I36924	gene MHC DQ-beta 1	475	5	6.2	102	2	H71221	hypothetical prote
403	5	6.2	83	2	S38693	class II histocomp	476	5	6.2	102	2	S69741	hypothetical prote
404	5	6.2	83	2	S38690	class II histocomp	477	5	6.2	102	2	B75020	hypothetical prote
405	5	6.2	83	2	S38698	class II histocomp	478	5	6.2	102	2	C86654	hypothetical prote
406	5	6.2	83	2	S38699	class II histocomp	479	5	6.2	102	2	F71206	hypothetical prote
407	5	6.2	83	2	S38694	class II histocomp	480	5	6.2	103	2	B25913	Ig heavy chain pre
408	5	6.2	83	2	G88921	ribosomal protein	481	5	6.2	103	2	E87522	conserved hypot het
409	5	6.2	84	2	B89822	hypothetical prote	482	5	6.2	104	1	H64327	conserved hypot het
410	5	6.2	85	2	AC1066	hypothetical prote	483	5	6.2	104	2	H75140	hypothetical prote
411	5	6.2	85	2	AH1010	conserved hypot het	484	5	6.2	104	2	H82793	transposase Orfa X
412	5	6.2	85	2	S31018	gene 73 protein -	485	5	6.2	104	2	A90174	hypothetical prote
413	5	6.2	86	1	Q1BP67	gene 1.6 protein -	486	5	6.2	105	2	A97683	hypothetical prote
414	5	6.2	86	2	C83838	hypothetical prote	487	5	6.2	105	2	A12907	hypothetical prote
415	5	6.2	87	2	B32360	shiga-like toxin I	488	5	6.2	105	2	G71102	hypothetical prote
416	5	6.2	87	2	B45823	shiga-like toxin I	489	5	6.2	105	2	S76770	hypothetical prote
417	5	6.2	87	2	I83832	shiga-like toxin I	490	5	6.2	105	2	T32799	hypothetical prote
418	5	6.2	87	2	B53890	verocytotoxin B ch	491	5	6.2	106	2	S22067	hypothetical prote
419	5	6.2	87	2	I76712	variant shiga-like	492	5	6.2	106	2	F62184	hypothetical prote
420	5	6.2	87	2	B84034	PTS system, histid	493	5	6.2	106	2	S46028	hypothetical prote
421	5	6.2	87	2	A69341	cobalt transport p	494	5	6.2	106	2	AD2795	conserved hypot het
422	5	6.2	88	2	A57711	diazepam-binding i	495	5	6.2	106	2	D97574	hypothetical prote
423	5	6.2	88	2	A47760	retrovirus-related	496	5	6.2	107	2	T02814	thioredoxin TRXRp1
424	5	6.2	88	2	D64562	hypothetical prote	497	5	6.2	107	2	A27646	Ig heavy chain V r
425	5	6.2	88	2	F97888	degenerative trans	498	5	6.2	107	2	D71678	hypothetical prote
426	5	6.2	89	1	S42609	shiga-like toxin -	499	5	6.2	107	2	H86788	hypothetical prote
427	5	6.2	89	1	JN0726	Shiga-like toxin I	500	5	6.2	107	2	S51193	small zinc finger-
428	5	6.2	89	1	XVEBP9	Shiga-like toxin c	501	5	6.2	107	2	S07818	homeotic protein H
429	5	6.2	89	1	XVEBBD	Shigella toxin cha	502	5	6.2	108	1	PVNE8B	parvalbumin beta -
430	5	6.2	89	2	S58344	Shiga-like toxin I	503	5	6.2	109	1	W7ML39	E7 protein - human
431	5	6.2	89	2	F90779	Shiga toxin 2 subu	504	5	6.2	109	2	D47056	cur regulatory pro
432	5	6.2	89	2	H85640	Shiga toxin 2 subu	505	5	6.2	109	2	AF0940	conserved hypot het
433	5	6.2	89	2	E91000	Shiga toxin I subu	506	5	6.2	109	2	C97849	hypothetical prote
434	5	6.2	89	2	G85845	Shiga toxin I subu	507	5	6.2	110	2	B72496	hypothetical prote
435	5	6.2	89	2	A60279	shiga-like toxin I	508	5	6.2	110	2	A96907	hypothetical prote
436	5	6.2	89	2	I69156	shiga-like toxin I	509	5	6.2	110	2	S72390	hypothetical prote
437	5	6.2	89	2	S01033	shiga-like toxin I	510	5	6.2	112	2	E97732	ferredoxin (import
438	5	6.2	89	2	B53887	Shiga-like toxin I	511	5	6.2	112	2	A71731	ferredoxin [2Fe-2S
439	5	6.2	89	2	F97816	50S ribosomal prot	512	5	6.2	112	2	B47033	AadA2 - Pseudomona
440	5	6.2	89	2	A69513	hypothetical prote	513	5	6.2	112	2	G83169	conserved hypot het
441	5	6.2	89	2	B49754	hypothetical prote	514	5	6.2	113	1	HVMSAM	Ig heavy chain V r
442	5	6.2	89	2	T51191	small zinc finger-	515	5	6.2	113	2	G87110	50S ribosomal prot
443	5	6.2	89	2	T51192	small zinc finger-	516	5	6.2	113	2	C70927	probable ribosomal
444	5	6.2	90	2	A13583	hypothetical prote	517	5	6.2	113	2	JC2026	cell specific 10K
445	5	6.2	91	2	B82893	hypothetical prote	518	5	6.2	114	2	B97117	ribosomal protein
446	5	6.2	91	2	T42310	hypothetical prote	519	5	6.2	114	2	AC1298	ribosomal protein
447	5	6.2	92	2	G82236	glutaredoxin [semi	520	5	6.2	114	2	F83959	ribosomal protein
448	5	6.2	92	2	F69522	conserved hypot het	521	5	6.2	114	2	AC1670	ribosomal protein
449	5	6.2	92	2	B71637	hypothetical prote	522	5	6.2	114	2	A13284	hypothetical prote
450	5	6.2	93	2	A97190	hypothetical prote	523	5	6.2	114	2	A13284	guanylin precursor
451	5	6.2	93	2	A95377	hypothetical prote	524	5	6.2	115	1	A46279	hypothetical prote
452	5	6.2	94	2	I48172	glial fibrillary a	525	5	6.2	115	2	S53841	hypothetical prote
453	5	6.2	94	2	D64679	hypothetical prote	526	5	6.2	115	2	D95035	hypothetical prote
454	5	6.2	95	2	AC1040	hypothetical prote	527	5	6.2	115	2	A97911	transposase (impor
455	5	6.2	96	1	UGMS	utero globin precur	528	5	6.2	115	2	B97962	transposase (impor
456	5	6.2	96	2	A52274	phosphodiesterase	529	5	6.2	115	2	F97873	transposase (impor
457	5	6.2	96	2	A36581	polychlorinated bi	530	5	6.2	115	2	B98100	transposase (impor
458	5	6.2	97	2	T44733	hypothetical prote	531	5	6.2	115	2	T36886	hypothetical prote
459	5	6.2	97	2	B45416	hypothetical prote	532	5	6.2	116	1	A45434	ribosomal protein
460	5	6.2	98	1	B64377	conserved hypot het	533	5	6.2	116	2	S26328	Ig heavy chain V r
461	5	6.2	98	2	C86517	hypothetical prote	534	5	6.2	116	2	S78140	ribosomal protein
462	5	6.2	98	2	T22503	hypothetical prote	535	5	6.2	116	2	D89857	50S ribosomal prot
463	5	6.2	98	2	T24286	hypothetical prote	536	5	6.2	116	2	T34780	ribosomal protein
464	5	6.2	98	2	D72106	hypothetical prote	537	5	6.2	116	2	JC5188	sporulation-specif
465	5	6.2	99	1	Q8BPB7	host specificity p	538	5	6.2	116	2	G64433	hypothetical prote
466	5	6.2	99	2	B37775	phoR protein - Pse	539	5	6.2	116	2	A72272	conserved hypot het
467	5	6.2	99	2	C70941	hypothetical prote	540	5	6.2	116	2	T03489	conserved hypot het

541	5	6.2	116	2	AH1174	B. subtilis YqkP	614	5	6.2	133	2	T36401	hypothetical prote
542	5	6.2	117	2	AC2149	hypothetical prote	615	5	6.2	133	2	E82390	hypothetical prote
543	5	6.2	117	2	A72286	hypothetical prote	616	5	6.2	133	2	T49231	hypothetical prote
544	5	6.2	117	2	C90437	conserved hypothet	617	5	6.2	133	2	AE1435	PTS system, fructo
545	5	6.2	118	2	E69696	ribosomal protein	618	5	6.2	134	2	G89937	cytidine deaminase
546	5	6.2	118	2	E97289	uncharacterized co	619	5	6.2	134	2	D64381	conserved hypothet
547	5	6.2	118	2	D64347	hypothetical prote	620	5	6.2	134	2	G72465	hypothetical prote
548	5	6.2	118	2	C84181	hypothetical prote	621	5	6.2	134	2	AB2765	conserved hypothet
549	5	6.2	118	2	AH0986	phage-like lysozym	622	5	6.2	134	2	AB0784	conserved hypothet
550	5	6.2	119	2	S47942	ribosomal protein	623	5	6.2	134	2	T25527	hypothetical prote
551	5	6.2	119	2	S50634	ribosomal protein	624	5	6.2	135	2	PN0494	NAD ADP-ribosyltra
552	5	6.2	120	2	B72346	chemotaxis respons	625	5	6.2	135	2	S60977	probable membrane
553	5	6.2	120	2	F66871	hypothetical prote	626	5	6.2	135	2	S55647	hypothetical prote
554	5	6.2	120	2	JC4754	hypothetical 13.6k	627	5	6.2	135	2	D89805	hypothetical prote
555	5	6.2	120	2	G86654	transcription regu	628	5	6.2	135	2	A13164	hypothetical prote
556	5	6.2	121	1	PSGNAM	phospholipase A2 h	629	5	6.2	135	2	G96691	hypothetical prote
557	5	6.2	121	2	D86783	50S ribosomal prot	630	5	6.2	136	2	PN0529	G protein-coupled
558	5	6.2	121	2	G81121	hypothetical prote	631	5	6.2	136	2	F84234	hypothetical prote
559	5	6.2	121	2	G64315	hypothetical prote	632	5	6.2	137	2	S68429	myotoxin precursor
560	5	6.2	122	2	G69532	conserved hypothet	633	5	6.2	137	2	C70461	hypothetical prote
561	5	6.2	122	2	A41810	transcription fact	634	5	6.2	137	2	A69127	hypothetical prote
562	5	6.2	122	2	F98001	transposase [impor	635	5	6.2	137	2	F69507	c-myc binding prot
563	5	6.2	122	2	AG0221	conserved hypothet	636	5	6.2	137	2	B72720	hypothetical prote
564	5	6.2	123	1	RSRT35	ribosomal protein	637	5	6.2	138	2	D83824	transcription regu
565	5	6.2	123	2	E97918	conserved hypothet	638	5	6.2	138	2	A95133	IS630-Spn1, transp
566	5	6.2	123	2	F95047	conserved hypothet	639	5	6.2	138	2	A97032	transcription regu
567	5	6.2	123	2	H72698	hypothetical prote	640	5	6.2	139	1	MNNZ1C	nonstructural prot
568	5	6.2	123	2	A69884	cell wall protein	641	5	6.2	139	2	T36603	hypothetical prote
569	5	6.2	123	2	T00711	hypothetical prote	642	5	6.2	139	2	C83597	hypothetical prote
570	5	6.2	124	1	RSRRA	ribosomal protein	643	5	6.2	139	2	AH0372	probable exported
571	5	6.2	124	2	E70148	ribosomal protein	644	5	6.2	140	2	C97710	nucleoside-diphosp
572	5	6.2	124	2	I40348	ribosomal protein	645	5	6.2	140	2	T15738	hypothetical prote
573	5	6.2	124	2	I40350	ribosomal protein	646	5	6.2	141	2	A11105	ribosomal protein
574	5	6.2	124	2	AF3345	LSU ribosomal prot	647	5	6.2	141	2	A11467	ribosomal protein
575	5	6.2	125	2	D97595	ribosomal protein	648	5	6.2	141	2	AE1255	transcription regu
576	5	6.2	125	2	AC2817	50S ribosomal prot	649	5	6.2	141	2	T46654	transcription regu
577	5	6.2	125	2	S35629	hypothetical prote	650	5	6.2	141	2	AB1618	transcription regu
578	5	6.2	125	2	D34829	sigma lbnS protein	651	5	6.2	141	2	B82779	hypothetical prote
579	5	6.2	126	2	S42643	ubiquitin / riboso	652	5	6.2	141	2	F71176	hypothetical prote
580	5	6.2	126	2	S52255	copper resistance	653	5	6.2	143	1	FQBOGM	granulocyte-macrop
581	5	6.2	126	2	A84567	hypothetical prote	654	5	6.2	143	2	AC2693	transcription regu
582	5	6.2	127	1	I53651	hydrophilic protei	655	5	6.2	143	2	E69065	molybdopterin bios
583	5	6.2	127	2	I46269	granulocyte-macrop	656	5	6.2	143	2	S43071	hypothetical prote
584	5	6.2	127	2	H87310	ribosomal protein	657	5	6.2	143	2	T45444	hypothetical prote
585	5	6.2	127	2	A58933	ribosomal protein	658	5	6.2	143	2	D82797	phage-related repr
586	5	6.2	127	2	H90460	conserved hypothet	659	5	6.2	144	1	AE1632	granulocyte-macrop
587	5	6.2	127	2	T07301	cell division topo	660	5	6.2	144	2	JH0469	granulocyte-macrop
588	5	6.2	127	2	E83500	hypothetical prote	661	5	6.2	144	2	F64094	ribosomal protein
589	5	6.2	128	1	RGBSBI	regulatory protein	662	5	6.2	144	2	C70455	hypothetical prote
590	5	6.2	128	2	B28183	beta-lactamase rep	663	5	6.2	144	2	F75044	hypothetical prote
591	5	6.2	128	2	AE0528	conserved hypothet	664	5	6.2	144	2	AG2568	hypothetical prote
592	5	6.2	128	2	S45230	yaeh protein - Esc	665	5	6.2	144	2	T41544	hypothetical prote
593	5	6.2	128	2	G85500	probable structura	666	5	6.2	145	1	B44798	phosphotransferase
594	5	6.2	128	2	G90649	probable structura	667	5	6.2	145	2	S06307	T-cell receptor ga
595	5	6.2	128	2	H69970	conserved hypothet	668	5	6.2	145	2	B83607	hypothetical prote
596	5	6.2	128	2	F72661	hypothetical prote	669	5	6.2	145	2	D90283	hypothetical prote
597	5	6.2	128	2	I51295	vascular endotheli	670	5	6.2	146	1	C64085	hypothetical prote
598	5	6.2	129	2	B71350	probable ribosomal	671	5	6.2	146	1	T46729	citrate (pro-3S)-1
599	5	6.2	129	2	AE2508	conserved hypothet	672	5	6.2	146	1	GGZLB	bacterial hemoglob
600	5	6.2	129	2	AE0206	conserved hypothet	673	5	6.2	146	2	F75280	probable asnc-famI
601	5	6.2	130	2	T48771	hypothetical prote	674	5	6.2	146	2	G97474	transglycosylase a
602	5	6.2	130	2	S55141	hypothetical prote	675	5	6.2	146	2	G90201	conserved hypothet
603	5	6.2	130	2	AC2314	hypothetical prote	676	5	6.2	146	2	B29701	hemoglobin beta ch
604	5	6.2	131	2	S08328	Ig heavy chain V r	677	5	6.2	146	2	F83274	conserved hypothet
605	5	6.2	131	2	A81312	hypothetical prote	678	5	6.2	146	2	S60748	phaeoelotoxin synt
606	5	6.2	131	2	G82684	hypothetical prote	679	5	6.2	147	2	A70462	ribosomal protein
607	5	6.2	131	2	A11964	hypothetical prote	680	5	6.2	147	2	AD3081	hypothetical prote
608	5	6.2	132	1	PWPFEL	H+-transporting tw	681	5	6.2	147	2	D98205	hypothetical prote
609	5	6.2	132	2	AB3272	succinate dehydrog	682	5	6.2	147	2	S75758	hypothetical prote
610	5	6.2	132	2	F75510	hypothetical prote	683	5	6.2	147	2	G87278	PTS system, IIA co
611	5	6.2	132	2	G75409	hypothetical prote	684	5	6.2	147	2	D64331	hypothetical prote
612	5	6.2	132	2	B64474	hypothetical prote	685	5	6.2	148	2	A82591	conserved hypothet
613	5	6.2	133	2	JC2003	NADH ubiquinone ox	686	5	6.2	148	2	G82489	hypothetical prote

687	5	6.2	148	2	S73004	hypothetical prote	760	5	6.2	163	2	D64427	hypothetical prote
688	5	6.2	148	2	A71130	hypothetical prote	761	5	6.2	164	2	S60130	H+-exporting ATPas
689	5	6.2	148	2	AC1122	hypothetical prote	762	5	6.2	164	2	D84152	hypothetical prote
690	5	6.2	149	1	RSWXE	ribosomal protein	763	5	6.2	164	2	E97061	integrase XerD fam
691	5	6.2	149	2	A01033	translation factor	764	5	6.2	164	2	H97702	H+-transporting tw
692	5	6.2	150	2	S39980	hemoglobin II alph	765	5	6.2	165	1	A40814	H+-exporting ATPas
693	5	6.2	150	2	A87344	chemotaxis protein	766	5	6.2	165	1	RMEC18	primosomal operon
694	5	6.2	150	2	D81314	small protein B ho	767	5	6.2	165	2	S60132	H+-exporting ATPas
695	5	6.2	150	2	S48568	hypothetical prote	768	5	6.2	165	2	S61332	probable glycoprot
696	5	6.2	150	2	S36996	transposase (clone	769	5	6.2	165	2	C86135	probable glycoprot
697	5	6.2	150	2	D97188	uncharacterized pr	770	5	6.2	165	2	H91293	probable ABC sugar
698	5	6.2	150	2	G95348	nitric-oxide reduc	771	5	6.2	166	1	B35703	cofilin - chicken
699	5	6.2	150	2	AG3456	coxG protein limpo	772	5	6.2	166	2	S60131	H+-exporting ATPas
700	5	6.2	151	2	I53929	epididymal secreto	773	5	6.2	166	2	S42783	relaxin 1 precursor
701	5	6.2	151	2	I38365	epididymal secreto	774	5	6.2	166	2	S42786	relaxin 2 precursor
702	5	6.2	151	2	AE2017	cell wall-binding	775	5	6.2	166	2	A53812	cofilin, muscle -
703	5	6.2	151	2	D81713	small protein B TC	776	5	6.2	166	2	E90434	conserved hypoteth
704	5	6.2	151	2	AC2084	phosphonate metabo	777	5	6.2	166	2	A75367	heat shock protein
705	5	6.2	151	2	H97545	hypothetical prote	778	5	6.2	166	2	J70358	hypothetical prote
706	5	6.2	151	2	S65893	overoxidase - se	779	5	6.2	166	2	B81435	hypothetical prote
707	5	6.2	151	2	A83263	thiol:disulfide in	780	5	6.2	167	2	F97238	probable acetyltra
708	5	6.2	152	2	S21826	T-cell receptor be	781	5	6.2	167	2	B89970	signal transductio
709	5	6.2	152	2	AE2961	transcription regu	782	5	6.2	168	2	S36294	T-cell receptor ga
710	5	6.2	152	2	AH0368	conserved hypoteth	783	5	6.2	168	2	F96762	hypothetical prote
711	5	6.2	152	2	T33169	hypothetical prote	784	5	6.2	169	2	S73136	allophycocyanin be
712	5	6.2	152	2	H95386	protein (imported	785	5	6.2	169	2	C75595	hypothetical prote
713	5	6.2	153	2	S06503	hemoglobin I alpha	786	5	6.2	169	2	T38765	probable VBPI/PACI
714	5	6.2	153	2	F46882	ribosomal protein	787	5	6.2	169	2	D70226	hypothetical prote
715	5	6.2	153	2	AE1070	probable secreted	788	5	6.2	170	2	T11964	hypothetical prote
716	5	6.2	154	1	F65230	probable PTS syste	789	5	6.2	170	2	S18064	allophycocyanin be
717	5	6.2	154	1	A70792	hypothetical prote	790	5	6.2	170	2	I40045	peroxidase (EC 1.1
718	5	6.2	154	2	T03584	plastocyanin precu	791	5	6.2	170	2	T37792	invasion-associate
719	5	6.2	154	2	AI1051	protein-Npi-phosph	792	5	6.2	170	2	B95169	hypothetical prote
720	5	6.2	154	2	C86116	probable PTS syste	793	5	6.2	170	2	C98035	hypothetical prote
721	5	6.2	154	2	C91275	probable PTS syste	794	5	6.2	171	2	T49493	hypothetical prote
722	5	6.2	154	2	S76191	hypothetical prote	795	5	6.2	171	2	B96934	molybdopterin bios
723	5	6.2	154	2	T34818	hypothetical prote	796	5	6.2	171	2	AI0943	probable membrane
724	5	6.2	154	2	G84396	hypothetical prote	797	5	6.2	171	2	T06438	homeobox-leucine z
725	5	6.2	154	2	T36601	probable transcrip	798	5	6.2	172	2	A83628	hypothetical prote
726	5	6.2	154	2	A92627	transposase homolo	799	5	6.2	172	2	H90003	ATP synthase B cha
727	5	6.2	154	2	B71149	hypothetical prote	800	5	6.2	173	2	T26299	hypothetical prote
728	5	6.2	155	2	T41746	ribosomal protein	801	5	6.2	173	2	G64495	hypothetical prote
729	5	6.2	155	2	B86840	tmRNA-binding prot	802	5	6.2	173	2	T21815	hypothetical prote
730	5	6.2	155	2	D83098	conserved hypoteth	803	5	6.2	174	2	T12008	NADH2 dehydrogenas
731	5	6.2	155	2	AD1883	hypothetical prote	804	5	6.2	174	2	B69979	hypothetical prote
732	5	6.2	155	2	T21364	hypothetical prote	805	5	6.2	174	2	AI0038	probable chorismat
733	5	6.2	156	2	T47739	conserved hypoteth	806	5	6.2	174	2	F64413	hypothetical prote
734	5	6.2	156	2	E69196	conserved hypoteth	807	5	6.2	175	2	A49616	pancreatitis-assoc
735	5	6.2	157	2	C84271	hypothetical prote	808	5	6.2	175	2	S45905	hypothetical prote
736	5	6.2	157	2	A71137	hypothetical prote	809	5	6.2	175	2	A95058	conserved domain p
737	5	6.2	158	2	S47140	pathogenesis-relat	810	5	6.2	175	2	B97927	hypothetical prote
738	5	6.2	158	2	D70755	hypothetical prote	811	5	6.2	176	2	B70429	conserved hypoteth
739	5	6.2	158	2	E90198	hypothetical prote	812	5	6.2	176	2	C82797	hypothetical prote
740	5	6.2	159	2	C95064	conserved hypoteth	813	5	6.2	176	2	F95863	probable cytochrom
741	5	6.2	159	2	E97931	conserved hypoteth	814	5	6.2	177	2	F84782	60S ribosomal prot
742	5	6.2	159	2	T48837	hypothetical prote	815	5	6.2	177	2	C89476	hypothetical prote
743	5	6.2	159	2	A82547	hypothetical prote	816	5	6.2	177	2	T16280	hypothetical prote
744	5	6.2	160	1	C70315	2-amino-4-hydroxy-	817	5	6.2	177	2	T24466	hypothetical prote
745	5	6.2	160	2	C82875	ribosomal protein	818	5	6.2	177	2	F64645	conjugal transfer
746	5	6.2	161	1	APAIB	allophycocyanin be	819	5	6.2	177	2	B97201	hypothetical prote
747	5	6.2	161	2	B27873	allophycocyanin be	820	5	6.2	178	2	C54168	hypothetical prote
748	5	6.2	161	2	S33624	allophycocyanin be	821	5	6.2	178	2	T17520	hypothetical prote
749	5	6.2	161	2	B44462	allophycocyanin be	822	5	6.2	178	2	A64336	hypothetical prote
750	5	6.2	161	2	S73630	ribosomal protein	823	5	6.2	179	2	S36289	hypothetical prote
751	5	6.2	161	2	D82042	transcription elon	824	5	6.2	179	2	C82240	T-cell receptor ga
752	5	6.2	161	2	C36810	hypothetical prote	825	5	6.2	179	2	A33164	hypothetical prote
753	5	6.2	161	2	F69418	ISORF2 homolog ISA	826	5	6.2	179	2	C96853	hypothetical prote
754	5	6.2	162	2	C11385	allophycocyanin 1	827	5	6.2	179	2	H85429	ribosomal protein
755	5	6.2	162	2	AF1809	allophycocyanin be	828	5	6.2	179	2	T26744	hypothetical prote
756	5	6.2	162	2	T06178	ribosomal protein	829	5	6.2	180	2	E97355	hypothetical prote
757	5	6.2	162	2	T00651	hypothetical prote	830	5	6.2	180	2	H81343	molybdopterin bios
758	5	6.2	162	2	AB1842	hypothetical prote	831	5	6.2	181	1	RKRPF1	ribulose-bisphosph
759	5	6.2	163	2	T47559	60S ribosomal prot	832	5	6.2	181	1	RKRPS	ribulose-bisphosph

833	181	1	RKRVS	5	6.2	106	906	193	2	G81433	hypothetical prote
834	181	1	B44057	5	6.2	907	907	193	2	E87539	maf protein [impor
835	181	1	ERAD23	5	6.2	908	908	193	2	A85658	robable tellurium
836	181	1	F44057	5	6.2	909	909	193	2	G90797	probable tellurium
837	181	1	S37292	5	6.2	910	910	193	2	T44907	hypothetical prote
838	181	2	S37575	5	6.2	911	911	193	2	AD1221	two-component resp
839	181	2	A64393	5	6.2	912	912	193	2	AG1574	two-component resp
840	181	2	E70209	5	6.2	913	913	193	2	G64074	thymidine kinase (
841	181	2	AI0861	5	6.2	914	914	194	1	MOHUA1	myosin alkali ligh
842	181	2	B24859	5	6.2	915	915	194	2	S64075	probable ribosomal
843	182	2	T43602	5	6.2	916	916	194	2	AE1195	B. subtilis Yjbx p
844	182	2	IS9203	5	6.2	917	917	194	2	H72392	hypothetical prote
845	183	1	TLBP84	5	6.2	918	918	194	2	G83282	probable sigma-70
846	183	2	AI1821	5	6.2	919	919	194	2	JC2098	legumin type B bet
847	183	2	C81057	5	6.2	920	920	195	2	AE2145	hypothetical prote
848	183	2	S13240	5	6.2	921	921	195	2	AH2774	hypothetical prote
849	183	2	G70596	5	6.2	922	922	195	2	C70928	probable transcrip
850	183	2	AF1883	5	6.2	923	923	195	2	S32123	glycine-rich prote
851	183	2	E69029	5	6.2	924	924	196	2	C75468	gliding motility p
852	184	2	AH3581	5	6.2	925	925	196	2	B49453	transcription init
853	184	2	AF0622	5	6.2	926	926	196	2	E69042	hypoxanthine phosp
854	184	2	AE0734	5	6.2	927	927	196	2	T49023	hypothetical prote
855	184	2	G86739	5	6.2	928	928	196	2	S70957	hypothetical prote
856	185	2	S39317	5	6.2	929	929	196	2	F90572	hypothetical prote
857	185	2	S39318	5	6.2	930	930	196	2	C71053	hypothetical prote
858	185	2	JC7369	5	6.2	931	931	197	2	H64415	hypothetical prote
859	185	2	F75048	5	6.2	932	932	198	2	S61091	probable GTP-bindi
860	185	2	A64015	5	6.2	933	933	198	2	S44998	coat protein - gra
861	185	2	S77594	5	6.2	934	934	198	2	E83631	hypothetical prote
862	186	2	S04671	5	6.2	935	935	198	2	D88098	protein T06D4.5 [i
863	186	2	F69194	5	6.2	936	936	198	2	T32025	hypothetical prote
864	186	2	H91252	5	6.2	937	937	199	2	JC5126	polyU-preferential
865	186	2	G86864	5	6.2	938	938	199	2	T06871	endopeptidase Clp
866	186	2	C71601	5	6.2	939	939	199	2	C84311	hypothetical prote
867	186	2	C71093	5	6.2	940	940	199	2	AH1186	indirect negative
868	187	2	AH0877	5	6.2	941	941	199	2	T40919	probable signal re
869	187	2	G70688	5	6.2	942	942	199	2	T49450	hypothetical prote
870	187	2	F72700	5	6.2	943	943	200	2	A83566	probable bacteriop
871	188	1	G70955	5	6.2	944	944	200	2	C75303	MutY/nudix family
872	188	1	F64494	5	6.2	945	945	200	2	D96023	probable C-P (carb
873	188	2	F64496	5	6.2	946	946	201	2	H71655	endopeptidase Clp
874	188	2	A23253	5	6.2	947	947	201	2	H83086	conserved hypotet
875	188	2	AG2351	5	6.2	948	948	201	2	G69340	cobalamin biosynth
876	188	2	B82183	5	6.2	949	949	201	2	G90385	hypothetical prote
877	189	2	I57590	5	6.2	950	950	202	2	S36293	T-cell receptor ga
878	189	2	G64496	5	6.2	951	951	202	2	T08693	hypothetical prote
879	189	2	G96657	5	6.2	952	952	202	2	B87340	transcription regu
880	189	2	C64014	5	6.2	953	953	202	2	A82917	hypothetical prote
881	189	2	E90408	5	6.2	954	954	203	2	AD1326	ribosomal protein
882	189	2	D89966	5	6.2	955	955	203	2	AH1080	hypothetical prote
883	190	1	MORTA1	5	6.2	956	956	203	2	AD1080	hypothetical prote
884	190	1	VCBVC	5	6.2	957	957	204	2	C75214	hypothetical prote
885	190	2	AG0030	5	6.2	958	958	204	2	G81876	probable membrane
886	190	2	G75207	5	6.2	959	959	204	2	F81145	type IV pilus asse
887	190	2	C69844	5	6.2	960	960	204	2	F84184	hypothetical prote
888	190	2	G71672	5	6.2	961	961	204	2	G87495	hypothetical prote
889	190	2	D70027	5	6.2	962	962	205	1	B44963	nef protein - huma
890	190	2	F71242	5	6.2	963	963	205	2	C75155	methyltransferase
891	191	2	G75299	5	6.2	964	964	205	2	S35029	hypothetical prote
892	191	2	C90284	5	6.2	965	965	205	2	G84204	hypothetical prote
893	191	2	D98218	5	6.2	966	966	206	2	AB2152	transcription regu
894	191	2	AG3068	5	6.2	967	967	206	2	T26418	hypothetical prote
895	192	1	MORBLA	5	6.2	968	968	206	2	T08285	hypothetical prote
896	192	2	F70126	5	6.2	969	969	206	2	F71450	hypothetical prote
897	192	2	G83096	5	6.2	970	970	206	2	T50439	probable 60s ribos
898	192	2	S41510	5	6.2	971	971	207	1	QQLJND	nef protein - huma
899	192	2	B70352	5	6.2	972	972	207	2	AC2950	transcription regu
900	193	1	F64941	5	6.2	973	973	207	2	H75065	hypothetical prote
901	193	2	S01958	5	6.2	974	974	207	2	D90526	conserved hypotet
902	193	2	AD0725	5	6.2	975	975	207	2	F87094	conserved hypotet
903	193	2	G85791	5	6.2	976	976	208	1	MOHUSA	myosin alkali ligh
904	193	2	C90943	5	6.2	977	977	208	2	G81336	uracil phosphoribo
905	193	2	B82554	5	6.2	978	978	208	2	B86907	signal peptidase I



979 5 6.2 208 2 T34512 hypothetical prote  
980 5 6.2 209 2 E90004 uracil phosphorib  
981 5 6.2 209 2 AF726 phosphoglucomutase  
982 5 6.2 209 2 T03222 hypothetical prote  
983 5 6.2 209 2 T03422 hypothetical prote  
984 5 6.2 209 2 AH3243 conjugal transfer  
985 5 6.2 209 2 T02177 hypothetical prote  
986 5 6.2 210 1 S39662 GTP-pyrophosphokin  
987 5 6.2 210 2 S38394 alpha-actinin 2, s  
988 5 6.2 210 2 H75361 leu/phe-tRNA-prote  
989 5 6.2 210 2 T27471 hypothetical prote  
990 5 6.2 210 2 F87493 conserved hypothet  
991 5 6.2 211 1 C65080 hypothetical prote  
992 5 6.2 211 2 C97223 probable S-adenosyl  
993 5 6.2 211 2 H75079 hypothetical prote  
994 5 6.2 211 2 H91106 hypothetical prote  
995 5 6.2 211 2 C85952 hypothetical prote  
996 5 6.2 211 2 A64490 precorrin-6Y methy  
997 5 6.2 211 2 B75349 hypothetical prote  
998 5 6.2 211 2 F70103 signal peptidase I  
999 5 6.2 211 2 T47489 hypothetical prote  
1000 5 6.2 212 1 S16542 ribosomal protein

ALIGNMENTS

RESULT 1  
A40402  
CD9 antigen [validated] - human  
N:Alternate names: motility-related protein-1  
C:Species: Homo sapiens (man)  
C>Date: 06-Dec-1991 #sequence\_revision 07-Jul-1995 #text\_change 09-Jul-2004  
C:Accession: A46123; A40402; JH0555; A39029; S10564  
R:Rubinstein, E.; Benoit, P.; Billard, M.; Plessance, S.; Prenant, M.; Uzan, G.; Bouchet  
Genomics 16, 132-138, 1993  
A:Title: Organization of the human CD9 gene.  
A:Reference number: A46123; MUID:93252369; PMID:8486348  
A:Accession: A46123  
A:Molecule type: DNA  
A:Residues: 1-228 <RUB>  
A:Cross-references: UNIPROT:P21926; UNIPARC:UPI000003B45A; GB:S60489; NID:G300112; PIDN:  
A:Experimental source: leukocyte  
A>Note: sequence extracted from NCBI backbone (NCBIN:131318, NCBIN:131326, NCBIN:131328,  
R:Rianza, F.; Wolf, D.; Fox, C.F.; Kieffer, N.; Seyer, J.M.; Fried, V.A.; Coughlin, S.R.;  
J. Biol. Chem. 266, 10638-10645, 1991  
A:Title: CDNA cloning and expression of platelet p24/CD9. Evidence for a new family of m  
A:Reference number: A40402; MUID:91244846; PMID:2037603  
A:Accession: A40402  
A>Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-228 <LAN>  
A:Cross-references: UNIPARC:UPI000003B45A; GB:L34068; GB:M61880; NID:G508495; PIDN:AAAS9  
A>Note: parts of this sequence, including the amino end of the mature protein, were conf  
R:Miyake, M.; Koyama, M.; Seno, M.; Ikeyama, S.  
J. Exp. Med. 174, 1347-1354, 1991  
A:Title: Identification of the motility-related protein (MRP-1), recognized by monoclonal  
A:Reference number: JH0555; MUID:92078843; PMID:1720807  
A:Accession: JH0555  
A:Molecule type: mRNA  
A:Residues: 1-228 <MIY>  
A:Cross-references: UNIPARC:UPI000003B45A; GB:X60111; NID:G34768; PIDN:CAA42708.1; PID:G  
A:Experimental source: breast carcinoma  
A>Note: this protein has the epitope defined by cell motility-inhibiting monoclonal anti  
R:Bouchelx, C.; Benoit, P.; Frachet, P.; Billard, M.; Worthington, R.E.; Gagnon, J.; Uza  
J. Biol. Chem. 266, 117-122, 1991  
A:Title: Molecular cloning of the CD9 antigen. A new family of cell surface proteins.  
A:Reference number: A39029; MUID:91093112; PMID:1840589  
A:Accession: A39029  
A:Molecule type: mRNA  
A:Residues: 1-8, 'S', 10-66, 'A', 68-193, 195-228 <BOU>  
A:Cross-references: UNIPARC:UPI000017414B; GB:M38690  
A>Note: parts of this sequence, including the amino end of the mature protein, were conf

R:Higashihara, M.; Takahata, K.; Yatomi, Y.; Nakahara, K.; Kurokawa, K.  
FEBS Lett. 264, 270-274, 1990  
A:Title: Purification and partial characterization of CD9 antigen of human platelets.  
A:Reference number: S10564; MUID:90292223; PMID:2359073  
A:Accession: S10564  
A:Molecule type: protein  
A:Residues: 2-8, 'X', 10-21 <HIG>  
A:Cross-references: UNIPARC:UPI000017414C  
C:Genetics:  
A:Gene: GDB:CD9; MIC3  
A:Cross-references: GDB:120582; OMIM:143030  
A:Map position: 12p13-12p13  
C:Superfamily: CD9 antigen  
C:Keywords: glycoprotein; transmembrane protein  
F:2-228/Product: CD9 antigen #status experimental <MAT>  
F:2-11/Domain: intracellular #status predicted <CY1>  
F:12-35/Domain: transmembrane #status predicted <TM1>  
F:36-55/Domain: extracellular #status predicted <EX1>  
F:56-82/Domain: transmembrane #status predicted <TM2>  
F:83-86/Domain: intracellular #status predicted <CY2>  
F:87-111/Domain: transmembrane #status predicted <TM3>  
F:112-194/Domain: extracellular #status predicted <EX2>  
F:195-221/Domain: transmembrane #status predicted <TM4>  
F:222-228/Domain: intracellular #status predicted <CY3>  
F:53/Binding site: carbohydrate (Asn) #status predicted

Query Match 100.0%; Score 80; DB 1; Length 228;  
Best Local Similarity 100.0%; Pred. No. 1.7e-73;  
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HKDEVIKEVQFYKDTYNNKLTQDEPQRETILKAHYALNCCGLAGGVQFISDIPCKDV 60  
DB 113 HKDEVIKEVQFYKDTYNNKLTQDEPQRETILKAHYALNCCGLAGGVQFISDIPCKDV 172  
QY 61 LETFTVKSCPDPAIKEVFDNK 80  
DB 173 LETFTVKSCPDPAIKEVFDNK 192

RESULT 2  
A42929  
CD9 antigen - green monkey  
N:Alternate names: 27K diphtheria toxin receptor-associated protein DRAP27  
C:Species: Cercopithecus aethiops (green monkey, Grivet)  
C>Date: 01-Oct-1992 #sequence\_revision 09-Aug-1996 #text\_change 09-Jul-2004  
C:Accession: A42929  
R:Mitamura, T.; Iwamoto, R.; Umata, T.; Yomo, T.; Urabe, I.; Tsuneoka, M.; Mekada, E.  
J. Cell Biol. 118, 1389-1399, 1992  
A:Title: The 27-kD diphtheria toxin receptor-associated protein (DRAP27) from vero cells  
epitopes on toxin-sensitive cells.  
A:Reference number: A42929; MUID:92394967; PMID:1522113  
A:Accession: A42929  
A>Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-228 <MIT>  
A:Cross-references: UNIPROT:P30409; UNIPARC:UPI000016C3B8; GB:D10726; NID:G218565; PIDN:  
C:Superfamily: CD9 antigen  
C:Keywords: glycoprotein; transmembrane protein  
F:2-228/Product: CD9 antigen #status predicted <MAT>  
F:2-11/Domain: intracellular #status predicted <CY1>  
F:12-35/Domain: transmembrane #status predicted <TM1>  
F:36-55/Domain: extracellular #status predicted <EX1>  
F:56-82/Domain: transmembrane #status predicted <TM2>  
F:83-86/Domain: intracellular #status predicted <CY2>  
F:87-111/Domain: transmembrane #status predicted <TM3>  
F:112-194/Domain: extracellular #status predicted <EX2>  
F:195-221/Domain: transmembrane #status predicted <TM4>  
F:222-228/Domain: intracellular #status predicted <CY3>  
F:53/Binding site: carbohydrate (Asn) #status predicted

Query Match 47.5%; Score 38; DB 1; Length 228;  
Best Local Similarity 100.0%; Pred. No. 6.4e-31;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 1 HKDEVKEVQEFYKDTYNKLTKEPQRETLKAIHYAL 38  
|||||  
Db 113 HKDEVKEVQEFYKDTYNKLTKEPQRETLKAIHYAL 150  
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RESULT 3  
S39262  
CD9 antigen - rat  
N;Alternate names: platelet cell surface glycoprotein  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 06-Jan-1995 #sequence\_revision 09-Aug-1996 #text\_change 09-Jul-2004  
C;Accession: I56562; S39262  
R;Kaprielian, Z.; Cho, K.O.; Hadjiargyrou, M.; Patterson, P.H.  
J. Neurosci. 15, 562-573, 1995  
A;Title: CD9, a major platelet cell surface glycoprotein, is a ROCA antigen and is expressed in a variety of tissues.  
A;Reference number: I56562; MUID:95123481; PMID:7823164  
A;Accession: I56562  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-226 <RES>  
A;Cross-references: UNIPROT:P40241; UNIPARC:UPI00001708C6; EMBL:X76489; NID:g434314; PID:149589  
C;Genetics:  
A;Gene: CD9  
C;Superfamily: CD9 antigen  
C;Keywords: glycoprotein; transmembrane protein  
F;2-11/Domain: intracellular #status predicted <CY1>  
F;12-35/Domain: transmembrane #status predicted <TM1>  
F;36-53/Domain: extracellular #status predicted <EX1>  
F;54-80/Domain: transmembrane #status predicted <TM2>  
F;81-84/Domain: intracellular #status predicted <CY2>  
F;85-109/Domain: transmembrane #status predicted <TM3>  
F;110-192/Domain: extracellular #status predicted <EX2>  
F;193-219/Domain: transmembrane #status predicted <TM4>  
F;220-226/Domain: intracellular #status predicted <CY3>  
F;50/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 18.8%; Score 15; DB 1; Length 226;  
Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 AGGVEQFISDIPCK 58  
|||||  
Db 154 AGGVEQFISDIPCK 168  
|||||

RESULT 4  
JX0221  
CD9 antigen - bovine  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 09-Oct-1992 #sequence\_revision 09-Aug-1996 #text\_change 09-Jul-2004  
C;Accession: JX0221  
R;Martin-Alonso, J.M.; Hernandez, N.; Ghosh, S.; Coca-Prados, M.  
J. Biochem. 112, 63-67, 1992  
A;Title: Molecular cloning of the bovine CD9 antigen from ocular ciliary epithelial cell  
A;Reference number: JX0221; MUID:93054422; PMID:1339429  
A;Accession: JX0221  
A;Molecule type: mRNA  
A;Residues: 1-226 <MAR>  
A;Cross-references: UNIPROT:P30932; UNIPARC:UPI0000167C21; GB:M81720; NID:gi62820; PIDN:149589  
A;Experimental source: ocular ciliary epithelial cell  
C;Superfamily: CD9 antigen  
C;Keywords: glycoprotein; transmembrane protein  
F;2-226/Product: CD9 antigen #status predicted <MAT>  
F;2-11/Domain: intracellular #status predicted <CY1>  
F;12-35/Domain: transmembrane #status predicted <TM1>  
F;36-53/Domain: extracellular #status predicted <EX1>  
F;54-76/Domain: transmembrane #status predicted <TM2>  
F;77-80/Domain: intracellular #status predicted <CY2>  
F;81-109/Domain: transmembrane #status predicted <TM3>  
F;110-192/Domain: extracellular #status predicted <EX2>  
F;193-219/Domain: transmembrane #status predicted <TM4>  
F;220-226/Domain: intracellular #status predicted <CY3>

F;50/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 16.2%; Score 13; DB 1; Length 226;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 KDEPQRETLKAIH 35  
|||||  
Db 133 KDEPQRETLKAIH 145  
|||||

RESULT 5  
I49589  
antigen - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I49589  
R;Rubinstein, E.; Billard, M.; Plaisance, S.; Prenant, M.; Boucheix, C.  
Thromb. Res. 71, 377-383, 1993  
A;Title: Molecular cloning of the mouse equivalent of CD9 antigen.  
A;Reference number: I49589; MUID:94054345; PMID:8236164  
A;Accession: I49589  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-226 <RES>  
A;Cross-references: UNIPROT:P40240; UNIPARC:UPI0000003E37; GB:L08115; NID:g388911; PIDN:149589  
C;Superfamily: CD9 antigen

Query Match 16.2%; Score 13; DB 2; Length 226;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 KDEPQRETLKAIH 35  
|||||  
Db 133 KDEPQRETLKAIH 145  
|||||

RESULT 6  
T07054  
cysteine proteinase inhibitor (clone R1) - soybean (fragment)  
C;Species: Glycine max (soybean)  
C;Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 09-Jul-2004  
C;Accession: T07054  
R;Zhao, Y.; Botella, M.A.; Subramanian, L.; Niu, X.; Nielsen, S.S.; Bressan, R.A.; Hasegawa, A.; et al.  
submitted to the EMBL Data Library, March 1996  
A;Description: Wound-inducible soybean cysteine proteinase inhibitors have greater insecticidal activity than the wild-type proteinase.  
A;Reference number: Z15886  
A;Accession: T07054  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-100 <ZHA>  
A;Cross-references: UNIPROT:Q39842; UNIPARC:UPI00000A8C6C; EMBL:U51855; NID:gi1277167; PIDN:149589  
C;Superfamily: cystatin; cystatin homology  
C;Keywords: cysteine proteinase inhibitor

Query Match 8.8%; Score 7; DB 2; Length 100;  
Best Local Similarity 100.0%; Pred. No. 8.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 IKEVQEF 12  
|||||  
Db 80 IKEVQEF 86  
|||||

RESULT 7  
A72276  
phosphate ABC transporter, permease protein - Thermotoga maritima (strain MSB8)  
C;Species: Thermotoga maritima  
C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
C;Accession: A72276  
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey  
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; et al.  
C.M.

Nature 399, 323-329, 1999  
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequencing  
A;Reference number: A72200; MUID:99287316; PMID:10360571  
A;Accession: A72276  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-276 <ARN>  
A;Cross-references: UNIPROT:Q9X0Y9; UNIPARC:UPI00000D38E4; GB:AE001781; GB:AE000512; NID  
A;Experimental source: strain MSB8  
C;Genetics:  
A;Gene: TM1262  
C;Superfamily: phoW protein

Query Match 8.8%; Score 7; DB 2; Length 276;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 RETLKAI 34  
|||||  
149 RETLKAI 155

RESULT 8  
B64551  
oligopeptide ABC transporter, ATP-binding protein - Helicobacter pylori (strain 26695)  
C;Species: Helicobacter pylori  
C;Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 05-Oct-2004  
C;Accession: B64551  
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997  
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.  
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.  
A;Reference number: A64520; MUID:97394467; PMID:9252185  
A;Accession: B64551  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-516 <TOM>  
A;Cross-references: UNIPROT:Q25032; UNIPARC:UPI00000D316B; GB:AE000544; GB:AE000511; NID  
C;Keywords: ATP; nucleotide binding; P-loop  
F;17-222/Domain: ATP-binding cassette homology <ABCI>  
F;34-41/Region: nucleotide-binding motif A (P-loop)  
F;288-489/Domain: ATP-binding cassette homology <ABC2>  
F;305-312/Region: nucleotide-binding motif A (P-loop)

Query Match 8.8%; Score 7; DB 2; Length 516;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 IKEVFDN 79  
|||||  
496 IKEVFDN 502

RESULT 9  
T00045  
cellodextrin phosphorylase - Clostridium thermocellum  
C;Species: Clostridium thermocellum  
C;Date: 22-Jan-1999 #sequence\_revision 22-Jan-1999 #text\_change 09-Jul-2004  
C;Accession: T00045  
R;Kawaguchi, T.; Ikeuchi, Y.; Tsutsumi, N.; Kan, A.; Sumitani, J.; Arai, M. J. Ferment. Bioeng. 85, 144-149, 1998  
A;Title: Cloning, nucleotide sequence, and expression of the Clostridium thermocellum cellodextrin phosphorylase gene.  
A;Reference number: Z14077  
A;Accession: T00045  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-980 <KAW>  
A;Cross-references: UNIPROT:Q24780; UNIPARC:UPI00000B5BEB; EMBL:AB006822; NID:d1117395;  
A;Experimental source: ATCC 27405  
C;Genetics:  
A;Gene: cdp

Query Match 8.8%; Score 7; DB 2; Length 980;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 RETLKAI 34  
|||||  
591 RETLKAI 597

RESULT 10  
T23236  
hypothetical protein K02C4.3 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T23236  
R;Lightning, J.  
submitted to the EMBL Data Library, January 1995  
A;Reference number: Z19713  
A;Accession: T23236  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-1302 <MIL>  
A;Cross-references: UNIPROT:Q09931; UNIPARC:UPI0000137A03; EMBL:Z47811; PIDN:CAA87786.1;  
A;Experimental source: clone K02C4  
C;Genetics:  
A;Gene: CESP:K02C4.3  
A;Map position: 2  
A;Introns: 10/1; 31/3; 84/3; 279/3; 464/1; 745/1; 957/2; 978/3; 1090/2; 1201/3; 1270/3

Query Match 8.8%; Score 7; DB 2; Length 1302;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 EQFISDI 54  
|||||  
94 EQFISDI 100

RESULT 11  
S03353  
plastocyanin - Microcystis aeruginosa (fragment)  
C;Species: Microcystis aeruginosa  
C;Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 09-Jul-2004  
C;Accession: S03353  
R;Tan, S.; Ho, K.K. Biochim. Biophys. Acta 973, 111-117, 1989  
A;Title: Purification of an acidic plastocyanin from Microcystis aeruginosa.  
A;Reference number: S03353; MUID:89134784; PMID:2537099  
A;Accession: S03353  
A;Molecule type: protein  
A;Residues: 1-15 <TAN>  
A;Cross-references: UNIPROT:P10625; UNIPARC:UPI0000131BAF

Query Match 7.5%; Score 6; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 ETFTVK 67  
|||||  
1 ETFTVK 6

RESULT 12  
H35057  
MHC class II histocompatibility antigen DO-B beta chain - rhesus macaque (fragment)  
C;Species: Macaca mulatta (rhesus macaque)  
C;Date: 03-Aug-1990 #sequence\_revision 03-Aug-1990 #text\_change 31-Dec-2004  
C;Accession: H35057  
R;Gyllenstein, U.B.; Lashkari, D.; Erlich, H.A. Proc. Natl. Acad. Sci. U.S.A. 87, 1835-1839, 1990  
A;Title: Allelic diversification at the class II DOB locus of the mammalian major histocompatibility complex.  
A;Reference number: A35054; MUID:90175391; PMID:2308943

A;Accession: H35057  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 1-57 <GYL>  
A;Cross-references: UNIPROT:Q02712; UNIPROT:Q9TFP4; UNIPARC:UPI0000176FDF  
C;Superfamily: immunoglobulin homology

Query Match 7.5%; Score 6; DB 2; Length 57;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 KDVLET 63  
DB 45 KDVLET 50

RESULT 13  
H82927  
hypothetical protein UUL51 [imported] - Ureaplasma urealyticum  
C;Species: Ureaplasma urealyticum  
C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C;Accession: H82927  
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.  
submitted to GenBank, February 2000  
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min  
A;Reference number: A82870  
A;Accession: H82927  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-60 <GLA>  
A;Cross-references: UNIPARC:UPI000139389; GB:AE002115; GB:AF222894; NID:G68999102; PIDN:  
A;Experimental source: serovar 3; biovar 1  
C;Genetics:  
A;Gene: UUL51  
A;Genetic code: SGC3

Query Match 7.5%; Score 6; DB 2; Length 60;  
Best Local Similarity 100.0%; Pred. No. 59;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DEVIKE 8  
DB 50 DEVIKE 55

RESULT 14  
PQ0469  
cysteine proteinase inhibitor - potato (fragment)  
N;Alternate names: wound-induced protein  
C;Species: Solanum tuberosum (potato)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C;Accession: PQ0469; S24768  
R;Hildmann, T.; Ebnet, M.; Pena-Cortes, H.; Sanchez-Serrano, J.J.; Willmitzer, L.; Prati  
Plant Cell 4, 1157-1170, 1992  
A;Title: General roles of abscisic and jasmonic acids in gene activation as a result of  
A;Reference number: JQ1692; MUID:93005746; PMID:1392612  
A;Accession: PQ0469  
A;Molecule type: mRNA  
A;Residues: 1-66 <HIL>  
A;Cross-references: UNIPROT:Q03196; UNIPARC:UPI0000128D7E; EMBL:X67844; NID:G21440; PIDN:  
A;Experimental source: strain desirée  
C;Keywords: cysteine proteinase inhibitor  
P;18-22/region: inhibitory

Query Match 7.5%; Score 6; DB 2; Length 66;  
Best Local Similarity 100.0%; Pred. No. 64;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KEVQEP 12  
DB 53 KEVQEP 58

## RESULT 15

D64538  
hypothetical protein HP0148 - Helicobacter pylori (strain 26695)  
C;Species: Helicobacter pylori  
C;Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 09-Jul-2004  
C;Accession: D64538  
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.  
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenn  
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Matthey, L  
Nature 388, 539-547, 1997  
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C  
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.  
A;Reference number: A64520; MUID:97394467; PMID:9252185  
A;Accession: D64538  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-68 <TOM>  
A;Cross-references: UNIPROT:O24959; UNIPARC:UPI00000C07EE; GB:AE000536; GB:AE000511; NID:

Query Match 7.5%; Score 6; DB 2; Length 68;  
Best Local Similarity 100.0%; Pred. No. 66;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 TLKAIH 35  
DB 25 TLKAIH 30

Search completed: January 20, 2006, 17:44:46  
Job time : 29.4615 secs

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OM protein - protein search, using sw model

Run on: January 20, 2006, 17:34:35 ; Search time 100.769 Seconds  
(without alignments)  
560.114 Million cell updates/sec

Title: US-10-619-323-1\_COPY\_113\_192

Perfect score: 80

Sequence: 1 HKDEVIKEVQBYKYDYNKL.....LEFTFKSCPDAIKSVFONK 80

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : Uniprot\_05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	80	100.0	227	1	CD9_HUMAN
2	80	100.0	228	2	Q5J7W6_HUMAN
3	39	48.8	182	2	Q56CY1_HUMAN
4	38	47.5	227	1	CD9_CERE
5	17	21.2	225	1	CD9_FELCA
6	15	18.8	225	1	CD9_RAT
7	13	16.2	225	1	CD9_BOVIN
8	13	16.2	225	1	CD9_MOUSE
9	13	16.2	225	1	CD9_PIG
10	13	16.2	226	2	Q8MT48_PIG
11	8	10.0	298	2	Q8CSN0_STREP
12	8	10.0	298	2	Q5HPF1_STAEQ
13	8	10.0	410	2	Q5AJ90_CANAL
14	7	8.8	29	2	Q4XUQ5_PLACH
15	7	8.8	91	2	Q6LHC2_PHOPR
16	7	8.8	100	2	Q39842_SOYBN
17	7	8.8	131	2	Q5WOF4_STR11
18	7	8.8	147	2	Q92LY3_RHIME
19	7	8.8	153	2	Q7R639_GIALA
20	7	8.8	154	2	Q8ELW1_OCEIH
21	7	8.8	158	2	Q7VGL4_HELHP
22	7	8.8	171	2	Q975Y2_SULTO
23	7	8.8	196	2	Q4IJ64_GIBZE
24	7	8.8	203	2	Q90B56_HIV1
25	7	8.8	227	2	Q6NMG7_BRARE
26	7	8.8	227	2	Q4REW0_TETNG
27	7	8.8	243	2	Q5PBR2_ANAMM
28	7	8.8	250	2	Q5M501_STR12
29	7	8.8	275	2	Q624R8_CAEBR
30	7	8.8	276	2	Q9X0Y9_THEME
31	7	8.8	290	2	Q7W811_BORPA
					P21926_homo sapien
					Q5J7W6_homo sapien
					Q56CY1_homo sapien
					P30409_cercopithec
					P40239_felis silve
					P40241_rattus norv
					P30932_bos taurus
					P40240_mus muscucu
					Q8Wmq3_sus scrofa
					Q8mj48_sus scrofa
					Q8csn0_staphylococ
					Q5hpf1_staphylococ
					Q5AJ90_candida alb
					Q4XUQ5_plasmodium
					Q6LHC2_photobacter
					Q39842_glycine max
					Q5WOF4_streptococ
					Q92LY3_rhizobium m
					Q7R639_giardia lam
					Q8ELW1_oceanobacil
					Q7VGL4_helicobacte
					Q975Y2_sulfolobus
					Q4IJ64_gibberella
					Q90B56_human immu
					Q6NMG7_brachydanio
					Q4REW0_tetradon n
					Q5PBR2_anaplasma m
					Q5M501_streptococ
					Q624R8_caenorhabdi
					Q9X0Y9_thermotoga
					Q7W811_bordetella

Q7wm43 bordetella  
Q7ri86 plasmodium  
Q7rcp6 plasmodium  
Q5n5w9 synchococc  
Q93cu7 shigella bo  
Q731r4 treponema d  
Q6mqg6 bdellovibri  
Q5k5k2 bacterioph  
Q861y4 dictyosteli  
Q4fba4 candidatus  
Q65mm0 bacillus li  
Q9p95s methanosarc  
Q8ttca9 methanosarc  
Q93658 methanosarc  
P58973 methanosarc  
Q8ta73 methanosarc  
P58974 methanosarc  
Q25032 helicobacte  
Q9k5m5 anabaena ci  
Q6nz26 brachydanio  
Q8ih03 drosophila  
Q54xw5 dictyosteli  
Q82ga3 streptomyc  
Q559b2 dictyosteli  
Q6cyd6 kluyveromyc  
Q5kxy3 geobacillus  
Q95v11 drosophila  
Q6fle6 candida gla  
Q24780 clostridium  
Q93ht8 clostridium  
Q5a2l3 candida alb  
Q5a2e3 candida alb  
Q8r4d5 mus musculu  
Q8r455 rattus norv  
Q4nc75 anaeromyxob  
Q8sy6s drosophila  
Q9vn25 drosophila  
Q9u7n7 plasmodium  
Q76nl8 plasmodium  
Q09931 caenorhabdi  
Q8te31 plasmodium  
Q7ktx8 drosophila  
Q8isx3 plasmodium  
Q8ihu4 plasmodium  
P10625 microcystis  
Q93y77 atropa bell  
Q53412 bacillus su  
Q4rny7 tetradon n  
Q4rp23 tetradon n  
Q9pgz3 ureaplasma  
Q74ek4 geobacter s  
Q4flm6 candidatus  
Q03196 solanum tub  
Q7uub3 rhodopirell  
Q24959 helicobacte  
Q52950 bacillus su  
Q728a1 deaulfovibr  
Q5bqt7 schistosoma  
Q6vxz3 echinococcu  
Q6vxz4 echinococcu  
Q6dl6 erwinia car  
Q7vtu2 bordetella  
Q7w4u2 bordetella  
Q7wgb9 bordetella  
Q5p948 azoarcus sp  
Q9ypk5 encephalomy  
Q86549 bovine herp  
Q54570 streptococ  
Q8rhw9 fusobacteri  
F00111 porphyra te  
Q50t58 encephalomy  
Q5wgv9 bacillus cl  
Q6njv4 corynebacte

105	89	1	HG173 HUMAN	O00479 homo sapien	178	6	7.5	125	2	Q89J73 BRAJA	Q89j73 bradyrhizob
106	89	1	HMG17_BOVIN	P02313 bos taurus	179	6	7.5	126	2	Q8ZMG8_PVRAE	Q8zmg8 pyrobaculum
107	89	1	HMG17_CANFA	O711a6 canis famil	180	6	7.5	126	2	Q67412_9ORTO	Q67412 influenza c
108	89	1	HMG17_CHICK	P02314 galus gall	181	6	7.5	126	2	Q67413_INCNB	Q67413 influenza c
109	89	1	HMG17_GECUA	Q64ft8 gecko japon	182	6	7.5	126	2	Q67414_9ORTO	Q67414 influenza c
110	89	1	HMG17_HUMAN	P05204 homo sapien	183	6	7.5	128	2	Q9NIP7_9INSE	Q9nif7 thermobia d
111	89	1	HMG17_MOUSE	P09602 mus musculus	184	6	7.5	128	2	Q9WXM6_THEME	Q9wxm6 thermotoga
112	89	1	HMG17_PIG	P80272 sus scrofa	185	6	7.5	129	2	Q7AFY0_ECO57	Q7afy0 escherichia
113	89	1	HMG17_PONPY	Q5raa0 pongo pygma	186	6	7.5	131	2	Q5BFC1_ENENI	Q5bfc1 aspergillus
114	89	1	HMG17_RAT	P18437 rattus norv	187	6	7.5	131	2	Q8XJX2_CLOPE	Q8xjx2 clostridium
115	90	2	Q6FGI5 HUMAN	Q6fgi5 homo sapien	188	6	7.5	131	2	Q66J17_XENLA	Q66j17 xenopus lae
116	90	2	Q53R27 HUMAN	Q53r27 homo sapien	189	6	7.5	134	2	Q4FLU0_9RICK	Q4flu0 candidatus
117	90	2	Q53XL9 HUMAN	Q53xl9 homo sapien	190	6	7.5	136	2	Q6M004_WETMP	Q6m004 methanococc
118	90	2	Q5BL14 MOUSE	Q5bl14 mus musculus	191	6	7.5	136	2	Q75L69_ORYSA	Q75l69 oryza sativ
119	90	2	Q5BE57 MOUSE	Q5be57 mus musculus	192	6	7.5	137	2	Q8FIG3_ECOL6	Q8fig3 escherichia
120	90	2	Q4KLJ0 RAT	Q4klj0 rattus norv	193	6	7.5	137	2	Q8X5D5_ECO57	Q8x5d5 escherichia
121	91	2	Q91987 XENLA	Q91987 xenopus lae	194	6	7.5	138	2	Q86BP6_SCHJA	Q86ep6 schistosoma
122	91	2	Q7SYV7 XENLA	Q7syv7 xenopus lae	195	6	7.5	138	2	Q5JZX4_LACSN	Q5jzx4 lactobacill
123	92	2	Q7M478 TENMO	Q7m478 tenebrio mo	196	6	7.5	139	1	PLAS_PHOLA	PLAS1883 phormidium
124	92	2	Q8T4K7 9CEST	Q8t4k7 taenia cras	197	6	7.5	140	2	Q64328_BPN15	Q64328 bacterioph
125	92	2	Q5J2R3_9VIRU	Q5j2r3 bacterioph	198	6	7.5	140	2	Q8PRJ8_XANAC	Q8prj8 xanthomonas
126	92	2	Q39840 SOYBN	Q39840 glycine max	199	6	7.5	142	2	Q65HU6_BACLD	Q65hu6 bacillus li
127	92	2	Q5XK38 MOUSE	Q5xk38 mus musculus	200	6	7.5	142	2	Q8KQO2_ANAPH	Q8kqo2 anaplasma p
128	93	2	Q63ZT7 XENR6	Q63zt7 xenopus tro	201	6	7.5	142	2	Q4J4T6_AZOV1	Q4j4t6 azotobacter
129	93	2	Q8CYT4 STRR6	Q8cyt4 streptococc	202	6	7.5	142	2	P73568_SVNY3	P73568 synecocyst
130	93	2	Q97QZ4 STRPN	Q97qz4 streptococc	203	6	7.5	143	2	Q55DJ7_DICDI	Q55dj7 dictyosteli
131	96	2	Q38446_9VIRU	Q38446 bacterioph	204	6	7.5	144	1	VMTT_LAMB	P03735 bacterioph
132	98	2	Q647G6_ARAHY	Q647g6 arachis hyp	205	6	7.5	144	2	Q6M1B6_HUMAN	Q6mlb6 homo sapien
133	99	2	P72752 SYN3	P72752 synecocyst	206	6	7.5	144	2	Q8FEW7_ECOL6	Q8few7 escherichia
134	101	2	Q9M4Q4 MANES	Q9m4q4 manihot esc	207	6	7.5	144	2	Q8X6X1_ECO57	Q8x6x1 escherichia
135	101	2	Q7ACW6_ECO57	Q7acw6 escherichia	208	6	7.5	145	2	Q93AL4_NODSP	Q93al4 nodularia s
136	102	2	Q687F4_9VIRU	Q687f4 bacterioph	209	6	7.5	146	1	CHA3_LYMDI	P43513 lymantria d
137	102	2	Q92RP6_CASSA	Q92rp6 castanea sa	210	6	7.5	146	1	Q59Z16_CANAL	Q59z16 candida alb
138	103	2	Q9E1E0_ECO57	Q9e1e0 escherichia	211	6	7.5	149	2	Q61ML2_XENLA	Q61ml2 xenopus lae
139	103	2	Q8BX19 MACFA	Q8bx19 macaca fasc	212	6	7.5	150	2	Q9ZE16_BRAJA	Q9ze16 bradyrhizob
140	103	2	Q82726_9VIRU	Q82726 infectious	213	6	7.5	150	2	Q576W7_BRUAB	Q576w7 brucella ab
141	105	2	Q6GQRO HUMAN	Q6gqro homo sapien	214	6	7.5	150	2	Q89QB4_BRAJA	Q89qb4 bradyrhizob
142	105	2	Q50T33_ENTHI	Q50t33 entamoeba h	215	6	7.5	150	2	Q8FX41_BRUSU	Q8fx41 brucella su
143	107	2	Q6K2X1_ORYSA	Q6k2x1 oryza sativ	216	6	7.5	150	2	Q8YBA1_BRUME	Q8yba1 brucella me
144	108	2	Q5YEE3_9PROT	Q5yee3 epsilon pro	217	6	7.5	150	2	Q9D8R4_MOUSE	Q9d8r4 mus musculu
145	109	2	Q50XD9_ENTHI	Q50xd9 entamoeba h	218	6	7.5	152	2	Q52131_ECOLI	Q52131 escherichia
146	109	2	Q572K7_PHYIN	Q572k7 phytophthor	219	6	7.5	152	2	Q85639_ECOLI	Q85639 escherichia
147	110	1	CYC6_PORPU	P51200 porphyra pu	220	6	7.5	152	2	Q5WMB0_ECOLI	Q5wmb0 escherichia
148	110	1	CYC6_PORYE	Q8wkj8 porphyra ye	221	6	7.5	152	2	Q62FW3_BURMA	Q62fw3 burkholderi
149	110	2	Q9AUI9_CABEL	Q9xui9 caenorhabdi	222	6	7.5	152	2	Q7DB60_ECO57	Q7db60 escherichia
150	110	2	Q61ML3 HORSE	Q61ml3 equus cabal	223	6	7.5	154	2	Q97Z29_SULSO	Q97z29 sulfolobus
151	110	2	Q9KN87_VIBCH	Q9kn87 vibrio chol	224	6	7.5	154	2	Q7NJZ3_GLOVI	Q7njz3 gloeobacter
152	110	2	Q6D6K2_ERWCT	Q6d6k2 erwinia car	225	6	7.5	155	2	Q8A8B0_BACTN	Q8a8b0 bacteroides
153	111	2	Q5WQ72_9ZZZZ	Q5wq72 uncultured	226	6	7.5	155	2	Q5QF39_9CAUD	Q5qf39 pseudomonas
154	112	2	Q6W622_9BACT	Q6w622 uncultured	227	6	7.5	156	2	Q9LFA5_ARATH	Q9lfa5 arabidopsis
155	112	2	Q5WQ51_9ZZZZ	Q5wq51 uncultured	228	6	7.5	156	2	Q9SE07_LYCES	Q9se07 lycopersico
156	112	2	Q5WQ62_9ZZZZ	Q5wq62 uncultured	229	6	7.5	156	2	Q4LHW5_9BURK	Q4lhw5 burkholderi
157	112	2	Q5WQ66_9ZZZZ	Q5wq66 uncultured	230	6	7.5	156	2	Q8ZF92_YERPE	Q8zf92 yersinia pe
158	112	2	Q5WY22 MGEPV	Q5wy22 melanoplus	231	6	7.5	156	2	Q66BS3_YERPS	Q66bs3 yersinia ps
159	113	2	Q4TAH5_TETNG	Q4tah5 tetraodon n	232	6	7.5	156	2	Q5FBB9_9ORTO	Q5fbb9 influenza c
160	113	2	Q6G9B1_STAAR	Q6g9b1 staphylococ	233	6	7.5	156	2	Q8QZG1_9ORTO	Q8qzg1 influenza c
161	113	2	Q6G9B1_STAAR	Q6g9b1 staphylococ	234	6	7.5	156	2	Q8QZL8_9ORTO	Q8qzl8 influenza c
162	113	2	Q7HF22_STAAC	Q7hfx2 staphylococ	235	6	7.5	156	2	Q8QZL9_9ORTO	Q8qzl9 influenza c
163	113	2	Q7A5K7_STAAN	Q7a5k7 staphylococ	236	6	7.5	156	2	Q8QZM0_9ORTO	Q8qzm0 influenza c
164	113	2	Q8NWP4_STAAM	Q8nwp4 staphylococ	237	6	7.5	156	2	Q8QZM1_9ORTO	Q8qzm1 influenza c
165	113	2	Q99U38_STAAM	Q99u38 staphylococ	238	6	7.5	156	2	Q8QZM2_9ORTO	Q8qzm2 influenza c
166	114	2	Q50Y32_ENTHI	Q50y32 entamoeba h	239	6	7.5	156	2	Q8QZM3_9ORTO	Q8qzm3 influenza c
167	115	2	Q7QFQ3_ANGOA	Q7qfq9 anopheles g	240	6	7.5	156	2	Q8QZM4_9ORTO	Q8qzm4 influenza c
168	116	2	Q9UXM3_SULSO	Q9uxm3 sulfolobus	241	6	7.5	156	2	Q8QZM5_9ORTO	Q8qzm5 influenza c
169	116	2	Q5DEW6_SCHJA	Q5dev6 schistosoma	242	6	7.5	156	2	Q68CC2_9ORTO	Q68cc2 influenza c
170	117	2	Q8DW57_STRMU	Q8dw57 streptococc	243	6	7.5	156	2	Q68CC3_9ORTO	Q68cc3 influenza c
171	118	2	Q9SAC3_ARATH	Q9sac3 arabidopsis	244	6	7.5	156	2	Q68CC4_9ORTO	Q68cc4 influenza c
172	118	2	Q5HKS1_STAEO	Q5hks1 staphylococ	245	6	7.5	156	2	Q68CC5_9ORTO	Q68cc5 influenza c
173	118	2	Q8CQW8_STAEP	Q8cqwr staphylococ	246	6	7.5	156	2	Q68CC6_9ORTO	Q68cc6 influenza c
174	119	1	Y2063_AQUAE	Q67844 aquifex aeo	247	6	7.5	156	2	Q68CC7_9ORTO	Q68cc7 influenza c
175	122	2	Q9AN42_BRAJA	Q9an42 bradyrhizob	248	6	7.5	156	2	Q68CC8_9ORTO	Q68cc8 influenza c
176	124	2	Q4S0A0_TETNG	Q4s0a0 tetraodon n	249	6	7.5	156	2	Q68CC9_9ORTO	Q68cc9 influenza c
177	125	2	Q6N4R8_RHOPA	Q6n4r8 rhodopsendo	250	6	7.5	156	2	Q68CD0_9ORTO	Q68cd0 influenza c

251	6	7.5	156	2	Q68CD1_9ORTO	Q68cd1 influenza c	324	6	7.5	164	2	Q74M85_NANEQ	Q74m85 nanoarchaeu
252	6	7.5	156	2	Q68CD2_9ORTO	Q68cd2 influenza c	325	6	7.5	165	2	P96986_RHIET	P96986 rhizobium e
253	6	7.5	156	2	Q68CD3_9ORTO	Q68cd3 influenza c	326	6	7.5	165	2	Q5L1B7_GEOKA	Q5L1B7 geobacillus
254	6	7.5	156	2	Q68CD4_9ORTO	Q68cd4 influenza c	327	6	7.5	165	2	Q8BPA3_OCEIH	Q8Bpa3 oceanobacil
255	6	7.5	156	2	Q68CD5_9ORTO	Q68cd5 influenza c	328	6	7.5	166	2	Q5QC24_9CAUD	Q5qc24 enterobacte
256	6	7.5	156	2	Q68CD6_9ORTO	Q68cd6 influenza c	329	6	7.5	167	2	Q4N377_THEPA	Q4n377 theileria p
257	6	7.5	156	2	Q68CD7_9ORTO	Q68cd7 influenza c	330	6	7.5	168	2	Q85255_STRPN	Q85255 streptococc
258	6	7.5	156	2	Q68CD8_9ORTO	Q68cd8 influenza c	331	6	7.5	168	2	Q85258_STRPN	Q85258 streptococc
259	6	7.5	156	2	Q68CD9_9ORTO	Q68cd9 influenza c	332	6	7.5	168	2	Q6J2R9_STRPN	Q6j2r9 streptococc
260	6	7.5	156	2	Q68CD10_9ORTO	Q68cd10 influenza c	333	6	7.5	168	2	Q6J2S1_STRPN	Q6j2s1 streptococc
261	6	7.5	156	2	Q68CE1_9ORTO	Q68ce1 influenza c	334	6	7.5	170	2	Q8RP60_ANAPH	Q8rp60 anaplasma p
262	6	7.5	156	2	Q68CE2_9ORTO	Q68ce2 influenza c	335	6	7.5	170	2	Q8RP63_ANAPH	Q8rp63 anaplasma p
263	6	7.5	156	2	Q68CE3_9ORTO	Q68ce3 influenza c	336	6	7.5	170	2	Q9L719_CAUCR	Q9l719 caulobacter
264	6	7.5	156	2	Q68CE4_9ORTO	Q68ce4 influenza c	337	6	7.5	171	2	Q4MEB4_PARUW	Q4meb4 parachlamyd
265	6	7.5	156	2	Q68CE5_9ORTO	Q68ce5 influenza c	338	6	7.5	172	2	Q4JAT6_SULAC	Q4jat6 sulfolobus
266	6	7.5	156	2	Q68CE6_9ORTO	Q68ce6 influenza c	339	6	7.5	172	2	Q5A5C2_CANAL	Q5a5c2 candida alb
267	6	7.5	156	2	Q91Q60_9ORTO	Q91q60 influenza c	340	6	7.5	172	2	Q8UVI8_CANAL	Q8uvi8 candida alb
268	6	7.5	156	2	Q91Q61_9ORTO	Q91q61 influenza c	341	6	7.5	172	2	Q8H9D7_SOLTU	Q8h9d7 solanum tub
269	6	7.5	156	2	Q90221_9ORTO	Q9q221 influenza c	342	6	7.5	172	2	Q9LEC7_SOLTU	Q9lec7 solanum tub
270	6	7.5	156	2	Q90224_9ORTO	Q9q224 influenza c	343	6	7.5	172	2	Q9KCV1_BACHD	Q9kcv1 bacillus ha
271	6	7.5	156	2	Q90227_9ORTO	Q9q227 influenza c	344	6	7.5	173	2	Q5SKH0_THET8	Q5skh0 thermus the
272	6	7.5	156	2	Q90232_9ORTO	Q9q232 influenza c	345	6	7.5	173	2	Q72KL9_THET2	Q72kl9 thermus the
273	6	7.5	156	2	Q90235_9ORTO	Q9q235 influenza c	346	6	7.5	176	2	Q8GTI9_9DINO	Q8gti9 symbiodinlu
274	6	7.5	156	2	Q90238_9ORTO	Q9q238 influenza c	347	6	7.5	176	2	Q606M4_METCA	Q606m4 methylococc
275	6	7.5	156	2	Q90241_9ORTO	Q9q241 influenza c	348	6	7.5	177	2	Q86Y24_HUMAN	Q86y24 homo sapien
276	6	7.5	156	2	Q90244_9ORTO	Q9q244 influenza c	349	6	7.5	177	2	Q4XX05_PLACH	Q4xx05 plasmodiium
277	6	7.5	156	2	Q90247_9ORTO	Q9q247 influenza c	350	6	7.5	179	1	RL5_BUCAK	P46178 buchnera ap
278	6	7.5	156	2	Q90250_9ORTO	Q9q250 influenza c	351	6	7.5	181	2	Q5E6G5_ANTLO	Q5e6g5 antonospora
279	6	7.5	156	2	Q90253_9ORTO	Q9q253 influenza c	352	6	7.5	181	2	Q4W0J3_9VIRU	Q4w0j3 banana stre
280	6	7.5	156	2	Q8B040_9ORTO	Q8b040 influenza c	353	6	7.5	181	2	Q4W0J4_9VIRU	Q4w0j4 banana stre
281	6	7.5	156	2	Q8B041_9ORTO	Q8b041 influenza c	354	6	7.5	181	2	Q4W0J5_9VIRU	Q4w0j5 banana stre
282	6	7.5	156	2	Q8B042_9ORTO	Q8b042 influenza c	355	6	7.5	181	2	Q4W0J6_9VIRU	Q4w0j6 banana stre
283	6	7.5	156	2	Q8B043_9ORTO	Q8b043 influenza c	356	6	7.5	181	2	Q4W0J7_9VIRU	Q4w0j7 banana stre
284	6	7.5	156	2	Q8B044_9ORTO	Q8b044 influenza c	357	6	7.5	181	2	Q4W0K0_9VIRU	Q4w0k0 banana stre
285	6	7.5	156	2	Q8B045_9ORTO	Q8b045 influenza c	358	6	7.5	181	2	Q4W0K1_9VIRU	Q4w0k1 banana stre
286	6	7.5	156	2	Q8B046_9ORTO	Q8b046 influenza c	359	6	7.5	181	2	Q4W0K2_9VIRU	Q4w0k2 banana stre
287	6	7.5	156	2	Q8B047_9ORTO	Q8b047 influenza c	360	6	7.5	181	2	Q4W0K3_9VIRU	Q4w0k3 banana stre
288	6	7.5	156	2	Q8B048_9ORTO	Q8b048 influenza c	361	6	7.5	181	2	Q4W0K4_9VIRU	Q4w0k4 banana stre
289	6	7.5	156	2	Q8B049_9ORTO	Q8b049 influenza c	362	6	7.5	181	2	Q4W0K5_9VIRU	Q4w0k5 banana stre
290	6	7.5	156	2	Q8B050_9ORTO	Q8b050 influenza c	363	6	7.5	181	2	Q4W0K6_9VIRU	Q4w0k6 banana stre
291	6	7.5	156	2	Q8B051_9ORTO	Q8b051 influenza c	364	6	7.5	181	2	Q4W0K7_9VIRU	Q4w0k7 banana stre
292	6	7.5	156	2	Q8B052_9ORTO	Q8b052 influenza c	365	6	7.5	181	2	Q4W0K8_9VIRU	Q4w0k8 banana stre
293	6	7.5	156	2	Q8B053_9ORTO	Q8b053 influenza c	366	6	7.5	181	2	Q4W0K9_9VIRU	Q4w0k9 banana stre
294	6	7.5	156	2	Q8B054_9ORTO	Q8b054 influenza c	367	6	7.5	182	2	Q8TSA5_METAC	Q8tea5 methanosarc
295	6	7.5	156	2	Q8B055_9ORTO	Q8b055 influenza c	368	6	7.5	182	2	Q73M40_TREDE	Q73m40 treponema d
296	6	7.5	156	2	Q8B056_9ORTO	Q8b056 influenza c	369	6	7.5	183	1	TBP_METJA	Q5Y930 methanococc
297	6	7.5	156	2	Q8B057_9ORTO	Q8b057 influenza c	370	6	7.5	183	2	Q97Q14_STRPN	Q97q14 streptococc
298	6	7.5	156	2	Q8B058_9ORTO	Q8b058 influenza c	371	6	7.5	184	2	Q7QN85_ANOGA	Q7qn85 anopheles g
299	6	7.5	156	2	Q8B059_9ORTO	Q8b059 influenza c	372	6	7.5	184	2	Q7VGB0_HELHP	Q7vgb0 helicobacte
300	6	7.5	156	2	Q8B060_9ORTO	Q8b060 influenza c	373	6	7.5	184	2	Q8DMA4_STRMU	Q8dma4 streptococc
301	6	7.5	156	2	Q8B061_9ORTO	Q8b061 influenza c	374	6	7.5	185	2	Q8TEK8_HUMAN	Q8tek8 homo sapien
302	6	7.5	156	2	Q8B062_9ORTO	Q8b062 influenza c	375	6	7.5	185	2	Q709F4_ARATH	Q709f4 arabidopsia
303	6	7.5	156	2	Q8B063_9ORTO	Q8b063 influenza c	376	6	7.5	186	2	Q5T981_HUMAN	Q5t981 homo sapien
304	6	7.5	156	2	Q8B064_9ORTO	Q8b064 influenza c	377	6	7.5	186	2	Q5T802_SALCH	Q5t802 salmonella
305	6	7.5	156	2	Q8B065_9ORTO	Q8b065 influenza c	378	6	7.5	186	2	Q5PCD1_SALPA	Q5pcd1 salmonella
306	6	7.5	156	2	Q8B066_9ORTO	Q8b066 influenza c	379	6	7.5	186	2	Q8ZR55_SALTY	Q8zr55 salmonella
307	6	7.5	156	2	Q8B067_9ORTO	Q8b067 influenza c	380	6	7.5	186	2	Q8Z8N1_SALTI	Q8z8n1 salmonella
308	6	7.5	156	2	Q8B068_9ORTO	Q8b068 influenza c	381	6	7.5	186	2	Q8YIF4_BRUME	Q8yif4 bruceella me
309	6	7.5	156	2	Q4U6Y3_9ORTO	Q4uey3 influenza c	382	6	7.5	187	1	Y1183_PHOLL	Q7y7g6 photorhabdu
310	6	7.5	156	2	Q4U6Y4_9ORTO	Q4uey4 influenza c	383	6	7.5	187	1	Y936_YERPE	Q8zhg3 yersinia pe
311	6	7.5	156	2	Q4U6Y5_9ORTO	Q4uey5 influenza c	384	6	7.5	187	2	Q6TA04_ANAPH	Q6ta04 anaplasma p
312	6	7.5	156	2	Q4U6Y6_9ORTO	Q4uey6 influenza c	385	6	7.5	187	2	Q666P0_YERPS	Q666p0 yersinia ps
313	6	7.5	157	2	Q9RRJ0_DEIRA	Q9rrj0 deinococcus	386	6	7.5	187	2	Q6D076_ERWCT	Q6d076 erwinia car
314	6	7.5	158	2	Q7RR40_NEUCR	Q7rr40 neurospora	387	6	7.5	188	2	Q71W82_LISMF	Q71w82 listeria mo
315	6	7.5	159	2	Q57AG7_BRUAB	Q57ag7 bruceella ab	388	6	7.5	188	2	Q8Y3Y9_LISMO	Q8y3y9 listeria mo
316	6	7.5	159	2	Q82M14_STRAW	Q82m14 streptomyce	389	6	7.5	188	2	Q927F2_LISX	Q927f2 listeria in
317	6	7.5	159	2	Q8FY02_BRUSU	Q8fy02 bruceella su	390	6	7.5	189	2	Q8D0B0_YERPE	Q8d0b0 yersinia pe
318	6	7.5	159	2	Q8YE44_BRUME	Q8ye44 bruceella me	391	6	7.5	190	2	Q556D4_DICDI	Q556d4 dictyosteli
319	6	7.5	160	2	Q5TWS3_ANOGA	Q5tws3 anopheles g	392	6	7.5	190	2	Q9G4D4_9STRA	Q9g4d4 chaustocochy
320	6	7.5	161	2	Q4JLK0_LACRE	Q4jlk0 lactobacill	393	6	7.5	190	2	Q6TNR4_BRARE	Q6tnr4 brachydanio
321	6	7.5	161	2	Q9X7P1_STRCO	Q9x7p1 streptomyce	394	6	7.5	191	2	Q4JTV48_CORJK	Q4jtv48 corynebacte
322	6	7.5	162	2	Q8ZUL0_PYRAE	Q8zul0 pyrobaculum	395	6	7.5	192	2	Q54BZ2_DICDI	Q54bz2 dictyosteli
323	6	7.5	163	2	Q63PU3_BURPS	Q63pu3 burkholderi	396	6	7.5	193	2	Q4N084_THEPA	Q4n084 theileria p

397	Q5B237	EMENI	194	7.5	6	Q5B237 aspergillus	470	6	7.5	230	Q5ZWN4	LEGPH	Q5zwn4	legionella
398	Q4UV17	XANCP	194	7.5	6	Q4uv17 xanthomonas	471	6	7.5	233	Q7VZ01	BORPE	Q7vz01	bordetella
399	Q8C702	MOUSE	194	7.5	6	Q8c702 mus musculus	472	6	7.5	235	Q5BYA8	SCHJA	Q5bya8	schistosoma
400	Q8GTH4	SYMPU	195	7.5	6	Q8gth4 symbiodinium	473	6	7.5	235	Q77103	LEITA	Q77103	leishmania
401	Q71S08	VIGNU	195	7.5	6	Q71su8 vigna unguis	474	6	7.5	235	Q9AG66	RHET	Q9ag66	rhizobium
402	Q8U4E2	PYRFU	196	7.5	6	Q8u4e2 pyrococcus	475	6	7.5	236	Q9SGX2	RATH	Q9sgx2	arabidopsis
403	Q73BM8	VRACH	196	7.5	6	Q73bm8 brucella	476	6	7.5	236	Q9SGX2	RATH	Q9sgx2	arabidopsis
404	Q44195	AGRRH	197	7.5	6	Q44195 agrobacteri	477	6	7.5	237	Q7NZ54	CHRO	Q7nz54	chromobacte
405	Q6SKP9	BACCE	198	7.5	6	Q6skp9 bacillus ce	478	6	7.5	237	Q27679	LEIDO	Q27679	leishmania
406	Q8GTH2	SYMPU	199	7.5	6	Q8gth2 symbiodinium	479	6	7.5	238	Q4Q9H8	LEIMA	Q4q9h8	leishmania
407	Q4JWS2	CORJK	199	7.5	6	Q4jws2 corynebacte	480	6	7.5	238	Y037	METUA	Q60344	methanococc
408	Q86F17	SCHJA	200	7.5	6	Q86f17 schistosoma	481	6	7.5	241	Q7RUS7	NEUCR	Q7rus7	neurospora
409	Q4XHD9	PLACH	200	7.5	6	Q4xhd9 plasmidium	482	6	7.5	242	Q7RUS7	NEUCR	Q7rus7	neurospora
410	Q97GZ6	CLOAB	201	7.5	6	Q97gz6 clostridium	483	6	7.5	242	Q89Y25	BRAJA	Q89y25	bradyrhizob
411	Q7ZW81	BRARE	201	7.5	6	Q7zw81 brachydanio	484	6	7.5	242	Q9HWJ6	PSEAE	Q9hwj6	pseudomonas
412	Q6WKK8	SERMA	202	7.5	6	Q6wkk8 serratia ma	485	6	7.5	243	Q75VH8	9BACT	Q75vh8	uncultured
413	Q61ME7	9STRA	203	7.5	6	Q61me7 phytophthor	486	6	7.5	244	ADC	CLOAB	P23670	clostridium
414	Q523K4	NOCPA	203	7.5	6	Q523k4 nocardia fa	487	6	7.5	244	Q5ZQT8	ARCVE	Q5zqt8	archaeoglob
415	Q42ZU7	PLABE	205	7.5	6	Q42zu7 plasmidium	488	6	7.5	244	Q61A69	SOLDE	Q61a69	solanum dem
416	Q33115	MYCLE	205	7.5	6	Q33115 mycobacteri	489	6	7.5	245	Q23616	ARATH	Q23616	arabidopsis
417	Q5SKG9	THEFT8	206	7.5	6	Q5skg9 thermus the	490	6	7.5	245	Q4FQMO	9GAMM	Q4fqmo	psychrobact
418	Q72KL8	THEFT2	207	7.5	6	Q72kl8 thermus the	491	6	7.5	246	Q84LB7	MALDO	Q84lb7	malus domes
419	Q69YA5	ORYSA	207	7.5	6	Q69ya5 oryza sativ	492	6	7.5	246	Q88Q72	PSEPK	Q88q72	pseudomonas
420	Q4TLU7	9SPHN	207	7.5	6	Q4tlu7 erythrobact	493	6	7.5	247	Q75VU0	9BACT	Q75vj0	uncultured
421	Q9HE35	NEUPN	208	7.5	6	Q9he35 neurospora	494	6	7.5	248	YWQC	BACSU	P96715	bacillus su
422	Q4HM62	CAMLA	208	7.5	6	Q4hm62 campylobact	495	6	7.5	248	Q5WRZ4	LEGPL	Q5wrz4	legionella
423	PEN	MOUSE	210	7.5	6	P5651 mus musculus	496	6	7.5	248	Q8D459	VIBVU	Q8d459	vibrio vuln
424	Q59PA4	CANAL	210	7.5	6	Q59pa4 candida alb	497	6	7.5	248	Q8XXK9	RALSO	Q8xxk9	raistonia s
425	Q8J2J8	NEOUN	210	7.5	6	Q8j2j8 neotyphodi	498	6	7.5	249	Q8GT10	9DINO	Q8gt10	symbiodiniu
426	Q70FW9	ANOCA	210	7.5	6	Q70fw9 anopheles g	499	6	7.5	249	Q5NF40	FRATT	Q5nf40	francigella
427	Q9QYR4	MUSSA	210	7.5	6	Q9qyr4 mus saxicol	500	6	7.5	250	Q68E87	AERPU	Q68e87	aeromonas p
428	Q9QYR5	MUSCR	210	7.5	6	Q9qyr5 mus caroli	501	6	7.5	251	Q74M76	NANEQ	Q74m76	nanorarchaeu
429	Q4TU88	MOUSE	210	7.5	6	Q4tu88 mus musculus	502	6	7.5	251	Q9HSX5	HUMAN	Q9hsx5	homo sapien
430	Q7T9N1	MOUSE	210	7.5	6	Q7t9n1 mus musculus	503	6	7.5	251	Q6V204	9BACT	Q6v204	uncultured
431	Q8LPC1	PHYPA	212	7.5	6	Q8lpc1 physcomitre	504	6	7.5	251	Q9F5F9	AGRRH	Q9f5f9	agrobacteri
432	Q6A4H9	CAMJE	213	7.5	6	Q6a4h9 campylobact	505	6	7.5	251	Q7W5U1	BORPA	Q7w5u1	bordetella
433	Q9EV56	RHIME	213	7.5	6	Q9ev56 rhizobium m	506	6	7.5	251	Q7WGJ2	BORBR	Q7wgj2	bordetella
434	Q6GZM1	9HIV1	214	7.5	6	Q6gzml human immun	507	6	7.5	251	Q98RX0	GUILTH	Q98rx0	guillardia
435	Q66KP3	XENLA	215	7.5	6	Q66kp3 xenopus lae	508	6	7.5	253	Q6V1Z8	9BACT	Q6v1z8	uncultured
436	Q81ZQ0	PLAF7	217	7.5	6	Q81zq0 plasmidium	509	6	7.5	253	Q6V1Z9	9BACT	Q6v1z9	uncultured
437	Q5Z217	NOCPA	218	7.5	6	Q5z217 nocardia fa	510	6	7.5	253	Q6V201	9BACT	Q6v201	uncultured
438	Q98HX1	RHIL0	219	7.5	6	Q98hx1 rhizobium l	511	6	7.5	253	Q6V202	9BACT	Q6v202	uncultured
439	Q57B21	BRUAB	220	7.5	6	Q57b21 brucella ab	512	6	7.5	253	Q6V203	9BACT	Q6v203	uncultured
440	Q8FZP8	BRUSU	220	7.5	6	Q8fzp8 brucella su	513	6	7.5	253	Q72LA6	THEFT2	Q72la6	thermus the
441	Q8XMS4	CLOPE	220	7.5	6	Q8xms4 clostridium	514	6	7.5	254	Q4Z243	FLABE	Q4z243	plasmodium
442	CAPA	STRAU	221	7.5	6	P39850 staphylococ	515	6	7.5	254	Q82U53	NITEU	Q82u53	nitrosomona
443	Q6VUV3	9BACT	221	7.5	6	Q6vuv3 uncultured	516	6	7.5	254	Q68FD8	MOUSE	Q68fd8	mus musculu
444	Q8E039	STRA5	221	7.5	6	Q8e039 streptococc	517	6	7.5	255	Q96HS1	HUMAN	Q96hs1	homo sapien
445	Q8E5R6	STRA3	221	7.5	6	Q8e5r6 streptococc	518	6	7.5	255	Q7Z368	HUMAN	Q7z368	homo sapien
446	Q5NHA7	FRATT	221	7.5	6	Q5nha7 francisella	519	6	7.5	255	Q6L407	SOLDE	Q6l407	solanum dem
447	FLPA	THEVO	222	7.5	6	Q979p2 thermoplasm	520	6	7.5	258	Q6MIM4	BDEBA	Q6mim4	bdellovibri
448	Q5ZE75	ORYSA	222	7.5	6	Q5ze75 oryza sativ	521	6	7.5	258	Q6LCF0	MOUSE	Q6lcf0	mus musculu
449	PURQ	RHIME	223	7.5	6	Q92pi1 rhizobium m	522	6	7.5	259	Q5F9V7	NEIG1	Q5f9v7	neisseria g
450	Q8TUA9	METAC	223	7.5	6	Q8tua9 methanosarc	523	6	7.5	259	Q9JVB4	NEIMA	Q9jvb4	neisseria m
451	Q54BL9	DICDI	223	7.5	6	Q54bl9 dictyosteli	524	6	7.5	259	Q9K0A8	NEIMB	Q9k0a8	neisseria m
452	Q847V6	VIBPA	223	7.5	6	Q847v6 vibrio para	525	6	7.5	260	Q7QDH5	ANOCA	Q7qdh5	anopheles g
453	Q87G70	VIBPA	223	7.5	6	Q87g70 vibrio para	526	6	7.5	262	Q525U4	WAGGR	Q525j4	magnaporthe
454	Q81KJ2	BACAN	224	7.5	6	Q81kj2 bacillus an	527	6	7.5	264	THIG	CHRO	Q7nrl4	chromobacte
455	Q6HCC9	BACHK	224	7.5	6	Q6hcc9 bacillus th	528	6	7.5	264	Q4KI36	PSEFS	Q4ki36	pseudomonas
456	Q632T9	BACCZ	224	7.5	6	Q632t9 bacillus ce	529	6	7.5	265	Q8WXP4	HUMAN	Q8wxf4	h ras effec
457	Q91BC9	CHICK	224	7.5	6	Q91bc9 gallus gall	530	6	7.5	265	Q4NGS7	9NICC	Q4ngs7	arthrobacte
458	Q8PWW9	METMA	225	7.5	6	Q8pww9 methanosarc	531	6	7.5	265	Q8C2E8	MOUSE	Q8c2e8	mus musculu
459	Q861U7	DICDI	225	7.5	6	Q861u7 dictyosteli	532	6	7.5	266	Q8TNX7	METAC	Q8tnx7	methanosarc
460	Q4V9X0	MOUSE	225	7.5	6	Q4v9x0 mus musculu	533	6	7.5	266	Q6W249	RHISN	Q6w249	rhizobium s
461	Q31F02	PLAF7	228	7.5	6	Q813t0 plasmidium	534	6	7.5	266	Q6F272	MESFL	Q6f272	mesoplasma
462	Q5F152	LACAC	228	7.5	6	Q5fi52 lactobacill	535	6	7.5	267	Q51X64	WAGGR	Q51x64	magnaporthe
463	Q74HN2	LACJO	228	7.5	6	Q74hn2 lactobacill	536	6	7.5	267	Q4JL32	SCHJA	Q4jl32	schistosoma
464	Q6GQES	XENLA	228	7.5	6	Q6gqe5 xenopus lae	537	6	7.5	267	Q8GSK1	9DINO	Q8gsk1	symbiodiniu
465	Q33T0C	HUMAN	229	7.5	6	Q53t06 homo sapien	538	6	7.5	267	Q8GTH5	9DINO	Q8gth5	symbiodiniu
466	Q7QRH5	GIALA	229	7.5	6	Q7qrh5 giardia lam	539	6	7.5	267	Q8GTH6	9DINO	Q8gth6	symbiodiniu
467	Q89B84	BRAJA	229	7.5	6	Q89b84 bradyrhizob	540	6	7.5	267	Q8GTH7	9DINO	Q8gth7	symbiodiniu
468	Q88T18	LACPL	229	7.5	6	Q88t18 lactobacill	541	6	7.5	267	Q9X919	STRCO	Q9x919	streptomyce
469	Q5X2Q6	LEGPA	230	7.5	6	Q5x2q6 legionella	542	6	7.5	268	Q60E71	ORYSA	Q60e71	oryza sativ



543	6	7.5	268	2	Q8GT14_9DINO	Q8gti4 symbiodiniu	616	7.5	293	2	Q6KAR0_MOUSE	Q6kar0 mus musculu
544	6	7.5	270	2	Q75FT4_LEPIC	Q75ft4 leptospira	617	7.5	293	2	Q4RP15_TETNG	Q4rp15 tetraodon n
545	6	7.5	270	2	Q8EXT7_LEPIN	Q8ext7 leptospira	618	7.5	294	2	Q5PDW4_SALPA	Q5pdw4 salmonella
546	6	7.5	272	2	Q8GEZ4_SCHJA	Q8gez4 schistosoma	619	7.5	294	2	Q8Z5F1_SALTI	Q8z5f1 salmonella
547	6	7.5	273	2	Q9NZQ0_HUMAN	Q9nzo0 homo sapien	620	7.5	294	2	Q8ZNP7_SALTY	Q8znp7 salmonella
548	6	7.5	273	2	Q5RDES_PONPY	Q5rdes pongo pygma	621	7.5	294	2	Q834B2_ENTFA	Q834b2 enterococcu
549	6	7.5	273	2	Q61ML7_RAT	Q61ml7 rattus norv	622	7.5	294	2	Q8CCX5_MOUSE	Q8ccx5 mus musculu
550	6	7.5	273	2	Q8BX00_MOUSE	Q8bx00 mus musculu	623	7.5	295	2	Q8N1A0_HUMAN	Q8n1a0 homo sapien
551	6	7.5	273	2	Q8CFP6_MOUSE	Q8cfp6 mus musculu	624	7.5	295	2	Q617J5_CAEBR	Q617j5 caenorhabdi
552	6	7.5	273	2	Q61MM1_CHICK	Q61mm1 gallus gall	625	7.5	295	2	Q65U99_MANSN	Q65u99 mannelmia
553	6	7.5	273	2	Q72YF1_XENLA	Q72yf1 xenopus lae	626	7.5	296	2	Q96ZJ4_SULTO	Q96zj4 sulfolobus
554	6	7.5	274	2	Q86FD1_SCHJA	Q86fd1 schistosoma	627	7.5	296	2	Q5VRP2_ORYSA	Q5vrp2 oryza sativ
555	6	7.5	274	2	Q8LLU9_ORYSA	Q8llu9 oryza sativ	628	7.5	297	2	Q67PA0_SYMTH	Q67pa0 symbiobacte
556	6	7.5	274	2	Q923I0_MOUSE	Q923i0 mus musculu	629	7.5	297	2	Q9I905_XENLA	Q9i905 xenopus lae
557	6	7.5	276	2	Q5DMH3_BPT5	Q5dmh3 bacterioph	630	7.5	298	2	Q7MSN2_WOLSA	Q7msn2 wolinnella s
558	6	7.5	276	2	Q5MTD1_XENLA	Q5mtd1 xenopus lae	631	7.5	298	2	Q6P818_XENTR	Q6p818 xenopus tro
559	6	7.5	278	1	CBT01_EACHD	Q929j3 bacillus ha	632	7.5	298	2	Q4SSB3_TETNG	Q4ssb3 tetraodon n
560	6	7.5	278	2	Q5URP2_HUMAN	Q5urp2 homo sapien	633	7.5	299	2	Q4L695_STAHJ	Q4l695 staphylococ
561	6	7.5	278	2	Q8VV19_CORGL	Q8vv19 corynebacte	634	7.5	299	2	Q9PVL6_CHICK	Q9pvl6 gallus gall
562	6	7.5	278	2	Q63AB0_BACCZ	Q63ab0 bacillus ce	635	7.5	300	2	Q96DH7_HUMAN	Q96dh7 homo sapien
563	6	7.5	279	1	TVSY_STRMU	Q8dui4 streptococc	636	7.5	300	2	Q8L7G8_ARATH	Q8l7g8 arabidopsis
564	6	7.5	280	2	Q721E7_TRYCR	Q721e7 trypanosoma	637	7.5	300	2	Q7X735_ORYSA	Q7x735 oryza sativ
565	6	7.5	280	2	Q4LJEG_STAHJ	Q4ljeg staphylococ	638	7.5	300	2	Q6G9H0_STAAS	Q6g9h0 staphylococ
566	6	7.5	281	2	Q8GVD6_ORYSA	Q8gvd6 oryza sativ	639	7.5	300	2	Q6GH17_STAAR	Q6gh17 staphylococ
567	6	7.5	282	2	Q9RGG2_LACCA	Q9rgg2 lactobacill	640	7.5	300	2	Q7ASQ1_STAAN	Q7asq1 staphylococ
568	6	7.5	282	2	Q5FHU4_LACAC	Q5fhu4 lactobacill	641	7.5	300	2	Q8NWS9_STAAN	Q8nws9 staphylococ
569	6	7.5	282	2	Q6GSE1_BARHE	Q6gse1 battonella	642	7.5	300	2	Q9U9U3_STAAM	Q9u9u3 staphylococ
570	6	7.5	283	2	Q8OVY8_MOUSE	Q8ovy8 mus musculu	643	7.5	300	2	Q5HG23_STAAC	Q5hg23 staphylococ
571	6	7.5	283	2	Q5L5L5_CHLUB	Q5l5l5 chlamydophi	644	7.5	300	2	Q9PUL9_BRARE	Q9pul9 brachydanio
572	6	7.5	284	2	Q612P7_PICTO	Q612p7 picrophilus	645	7.5	301	2	Q9V1P4_PYRAB	Q9v1p4 pyrococcus
573	6	7.5	284	2	Q579K3_HUMAN	Q5t9k3 homo sapien	646	7.5	301	2	Q9N3S8_CAEBL	Q9n3s8 caenorhabdi
574	6	7.5	284	2	Q5K2M2_BACLI	Q5k2m2 bacillus li	647	7.5	301	2	Q7NK17_GLOVI	Q7nk17 gloeobacter
575	6	7.5	285	2	Q5UF41_9PROT	Q5uf41 uncultured	648	7.5	301	2	Q7NM69_GLOVI	Q7nm69 gloeobacter
576	6	7.5	285	2	Q8GPA1_SCHJA	Q8gpa1 schistosoma	649	7.5	302	2	Q5QNI0_ORYSA	Q5qni0 oryza sativ
577	6	7.5	285	2	Q4NTI9_9DELT	Q4nti9 anaeronyxob	650	7.5	302	2	Q832F3_ENTFA	Q832f3 enterococcu
578	6	7.5	285	2	Q5LXD8_SILPO	Q5lxd8 silicibacte	651	7.5	302	2	P73115_SYNY3	P73115 syntechocyst
579	6	7.5	285	2	Q82R08_STRAW	Q82r08 streptomyce	652	7.5	303	1	MTCH2_BOVIN	MTch2 bos taurus
580	6	7.5	286	1	TVSY_STRT1	Q5m5b3 streptococc	653	7.5	303	1	MTCH2_MOUSE	MTch2 mus musculu
581	6	7.5	286	1	TVSY_STRT2	Q5m5b3 streptococc	654	7.5	303	1	MTCH2_PONPY	MTch2 pongo pygma
582	6	7.5	286	2	Q8TT83_METAC	Q8tt83 methanosarc	655	7.5	303	1	Q5G3G4_HUMAN	Q5g3g4 homo sapien
583	6	7.5	286	2	Q5KSB6_LORJA	Q5ksb6 locus japon	656	7.5	304	2	Q9FPFC_ORYSA	Q9fpfc oryza sativ
584	6	7.5	286	2	Q4TQM6_9SPHN	Q4tqm6 erythrobact	657	7.5	304	2	Q88XS7_LACPL	Q88xs7 lactobacill
585	6	7.5	287	2	Q9VMF2_PSEPU	Q9vmf2 pseudomonas	658	7.5	305	2	Q9NPP5_HUMAN	Q9npp5 homo sapien
586	6	7.5	287	2	Q8BM78_MOUSE	Q8bm78 m mus muscu	659	7.5	305	2	Q8C878_ARATH	Q8c878 arabidopsis
587	6	7.5	288	2	Q8TZJ1_PYRFU	Q8tzj1 pyrococcus	660	7.5	306	2	Q67RS4_SYMTH	Q67rs4 symbiobacte
588	6	7.5	288	2	Q6BPJ1_DEBHA	Q6bpj1 debaryomyce	661	7.5	306	2	Q6HCA6_BACHK	Q6hca6 bacillus th
589	6	7.5	288	2	Q4TYV9_PLABE	Q4tyv9 plasmodium	662	7.5	306	2	Q72YU8_BACCL	Q72yu8 bacillus ce
590	6	7.5	288	2	Q8BX10_MOUSE	Q8bx10 mus musculu	663	7.5	306	2	Q816Q3_BACCR	Q816q3 bacillus ce
591	6	7.5	288	2	Q5G2B5_RAT	Q5g2b5 rattus norv	664	7.5	306	2	Q8XXD9_RALSO	Q8xxd9 ralstonia s
592	6	7.5	289	2	Q8GT12_9DINO	Q8gt12 symbiodiniu	665	7.5	306	2	Q81KH1_BACAN	Q81kh1 bacillus an
593	6	7.5	289	2	Q8GT13_9DINO	Q8gt13 symbiodiniu	666	7.5	306	2	Q632R8_BACCZ	Q632r8 bacillus ce
594	6	7.5	289	2	Q8GT15_9DINO	Q8gt15 symbiodiniu	667	7.5	307	2	Q5VIC2_HALAWA	Q5vic2 haloarcula
595	6	7.5	289	2	Q8GT16_9DINO	Q8gt16 symbiodiniu	668	7.5	307	2	Q6ASD1_DESPS	Q6aad1 deaultofale
596	6	7.5	289	2	Q8GT17_9DINO	Q8gt17 symbiodiniu	669	7.5	308	2	Q7QD97_ANOGA	Q7qgd97 anophelies g
597	6	7.5	289	2	Q8GT18_9DINO	Q8gt18 symbiodiniu	670	7.5	308	2	Q61EN4_CAEBR	Q61en4 caenorhabdi
598	6	7.5	289	2	Q85066_9BROM	Q85066 peanut stun	671	7.5	308	2	Q51BW5_ENTHI	Q51bw5 entamoeba h
599	6	7.5	290	1	EX05_BPT5	P06229 bacterioph	672	7.5	308	2	Q5RD19_PONPY	Q5rdi9 pongo pygma
600	6	7.5	290	2	Q6P8A9_XENTR	Q6p8a9 xenopus tro	673	7.5	308	2	P71522_MARHA	P71522 marincoccu
601	6	7.5	291	2	Q8FY93_METNA	Q8fy93 methanosarc	674	7.5	308	2	Q7W253_BORPA	Q7w253 bordetella
602	6	7.5	291	2	Q66LT5_BPT5	Q66lt5 bacterioph	675	7.5	309	2	Q6PJ76_HUMAN	Q6pj76 homo sapien
603	6	7.5	292	1	HCHA_STAAM	P64312 staphylococ	676	7.5	310	2	Q50PX2_ENTHI	Q50px2 entamoeba h
604	6	7.5	292	1	HCHA_STAAN	P64313 staphylococ	677	7.5	310	2	Q51B62_ENTHI	Q51b62 entamoeba h
605	6	7.5	292	1	HCHA_STAAN	Q8nyx2 staphylococ	678	7.5	310	2	Q8WQ32_CAEBL	Q8wq32 caenorhabdi
606	6	7.5	292	2	Q72R49_LEPIC	Q72r49 leptospira	679	7.5	310	2	Q87988_BORBR	Q87988 bordetella
607	6	7.5	292	2	Q6GTB6_STAAS	Q6gtb6 staphylococ	680	7.5	310	2	Q7W253_BORPA	Q7w253 bordetella
608	6	7.5	292	2	Q6GJB7_STAAR	Q6gjb7 staphylococ	681	7.5	310	2	Q7WGG6_BORBR	Q7wgg6 bordetella
609	6	7.5	292	2	Q5HIC4_STAAC	Q5hic4 staphylococ	682	7.5	311	2	Q8C3A0_MOUSE	Q8c3a0 mus musculu
610	6	7.5	292	2	Q5BLC1_BRARE	Q5blc1 brachydanio	683	7.5	311	2	Q9H8F7_HUMAN	Q9h8f7 homo sapien
611	6	7.5	293	2	Q6MU03_MYCWS	Q6mu03 mycoplasma	684	7.5	311	2	Q5J5N7_HUMAN	Q5jan7 homo sapien
612	6	7.5	293	2	Q724P2_LISMP	Q724p2 listeria mo	685	7.5	311	2	Q5WC88_BACSK	Q5wc88 bacillus cl
613	6	7.5	293	2	Q8YAF9_LISMP	Q8yaf9 listeria mo	686	7.5	311	2	Q7URM1_RHOBA	Q7urm1 rhodospirell
614	6	7.5	293	2	Q92F96_LISIN	Q92f96 listeria in	687	7.5	312	2	Q9Y9N2_AERPE	Q9y9n2 aeropyrum p
615	6	7.5	293	2	Q69ZE3_MOUSE	Q69ze3 mus musculu	688	7.5	312	2	Q7MFN5_VIBVY	Q7mfns vibrio vuln

689	6	7.5	312	2	Q9D050_MOUSE	Q9D050_mus musculus	762	6	7.5	329	2	Q98GR0_RHIL0	Q98gr0 rhizobium 1
690	6	7.5	312	2	Q640V7_XENLA	Q640v7 xenopus lae	763	6	7.5	332	2	Q6FRW9_CANGA	Q6frw9 candida gla
691	6	7.5	313	2	Q42IA1_PLABE	Q42ia1 plasmodium	764	6	7.5	332	2	Q4MMV1_BACCE	Q4mmv1 bacillus ce
692	6	7.5	313	2	Q7W4Y8_BORPA	Q7w4y8 bordetella	765	6	7.5	332	2	Q4FTF0_9GAMM	Q4ftf0 psychrobact
693	6	7.5	314	2	Q4YH25_PLABE	Q4yh25 plasmodium	766	6	7.5	332	2	Q635H9_BACCZ	Q635h9 bacillus ce
694	6	7.5	314	2	Q6D5T6_ERWCT	Q6d5t6 erwinia car	767	6	7.5	332	2	Q6HEG3_BACCK	Q6heg3 bacillus th
695	6	7.5	315	2	Q6ZM20_BRARE	Q6zm20 brachydanio	768	6	7.5	332	2	Q731J5_BACCI	Q731j5 bacillus ce
696	6	7.5	315	2	Q5OSD0_ENTHI	Q5osd0 entamoeba h	769	6	7.5	332	2	Q81MC5_BACSE	Q81mc5 bacillus an
697	6	7.5	316	1	GSEP_BACLD	P80057 bacillus li	770	6	7.5	332	2	Q4VA36_MOUSE	Q4va36 mus musculus
698	6	7.5	316	2	Q9QM43_9VIRU	Q9qm43 parvo-like	771	6	7.5	334	2	Q4P0Z4_USTMA	Q4p0z4 ustilago ma
699	6	7.5	316	2	Q4U3C5_BMDNV	Q4u3c5 bombyx mori	772	6	7.5	334	2	Q4FVS3_9GAMM	Q4fvs3 psychrobact
700	6	7.5	317	2	Q6CJL1_KJULA	Q6cjl1 kluyveromyc	773	6	7.5	335	2	Q6CS23_KJULA	Q6cs23 kluyveromyc
701	6	7.5	317	2	Q8B3G8_PSESM	Q8b3g8 pseudomonas	774	6	7.5	336	2	Q8WVW9_HUMAN	Q8wvw9 homo sapien
702	6	7.5	318	2	Q5OR23_ENTHI	Q5or23 entamoeba h	775	6	7.5	336	2	Q4NMX0_9DELT	Q4nmx0 anaeromyxob
703	6	7.5	318	2	Q6MSK1_MYCMS	Q6msk1 mycoplasma	776	6	7.5	336	2	Q4NSB0_9DELT	Q4nsb0 anaeromyxob
704	6	7.5	319	2	Q61SE9_CAEOR	Q61se9 caenorhabdi	777	6	7.5	337	1	CWC2_KJULA	Q6ct50 kluyveromyc
705	6	7.5	320	2	Q743H7_MYCPA	Q743h7 mycobacteri	778	6	7.5	338	2	Q28757_ARCFU	Q28757 archaeoglob
706	6	7.5	320	2	Q16457_CAEEL	Q16457 caenorhabdi	779	6	7.5	338	2	Q5SUR5_CRYNE	Q5sur5 cryptococcu
707	6	7.5	320	2	Q5CZU2_BRARE	Q5czu2 brachydanio	780	6	7.5	338	2	Q8J0X1_CRYNE	Q8j0x1 cryptococcu
708	6	7.5	321	2	Q6LTD3_CABER	Q6ltd3 caenorhabdi	781	6	7.5	338	2	Q8J0Y7_CRYNE	Q8j0y7 cryptococcu
709	6	7.5	321	2	Q5OXU1_ENTHI	Q5oxul entamoeba h	782	6	7.5	338	2	Q5KHM4_CRYNE	Q5khm4 cryptococcu
710	6	7.5	321	2	Q8DY20_STRAS	Q8dy20 streptococc	783	6	7.5	338	2	Q4Y6H2_PLACH	Q4y6h2 silicibacte
711	6	7.5	321	2	Q5VBD2_9REOV	Q5vbd2 human rotav	784	6	7.5	338	2	Q5LP70_SILPO	Q5lp70 silicibacte
712	6	7.5	321	2	Q6XD89_9REOV	Q6xd89 human rotav	785	6	7.5	338	2	Q7TNQ4_MOUSE	Q7tnq4 mus musculu
713	6	7.5	321	2	Q77N43_9REOV	Q77n43 human rotav	786	6	7.5	339	2	Q7XFX4_ORISA	Q7xfx4 oryza sativ
714	6	7.5	321	2	Q86193_9REOV	Q86199 human rotav	787	6	7.5	339	2	Q8S841_ORISA	Q8s841 oryza sativ
715	6	7.5	321	2	Q9J454_9REOV	Q9j454 human rotav	788	6	7.5	339	2	Q6M3P6_CORGL	Q6m3p6 corynebacte
716	6	7.5	321	2	Q87697_SIVCZ	Q87697 chimpanzee	789	6	7.5	339	2	Q8F4N3_LEPIN	Q8f4n3 leptospira
717	6	7.5	322	1	DIDH_RAT	P23457 rattus norv	790	6	7.5	340	2	Q8E7C6_GUROC	Q8e7c6 oikopleura
718	6	7.5	322	2	Q9RJ06_STRCO	Q9rj06 streptomyc	791	6	7.5	340	2	Q89J65_BRAJA	Q89j65 bradyrhizob
719	6	7.5	322	2	Q5BKCB_RAT	Q5bkcb rattus norv	792	6	7.5	341	2	Q8DGH8_SYNEL	Q8dgh8 synethococc
720	6	7.5	323	1	X370_MYCSE	P47610 mycoplasma	793	6	7.5	341	2	Q726A3_DESVH	Q726a3 desulfovibr
721	6	7.5	324	1	ODPB_BACSU	P21882 bacillus su	794	6	7.5	341	2	Q9D9A3_MOUSE	Q9d9a3 mus musculu
722	6	7.5	324	1	YHDI_ECOLI	P26646 escherichia	795	6	7.5	342	2	Q6FN43_CANGA	Q6fn43 candida gla
723	6	7.5	324	2	Q4WFN6_ASPFU	Q4wfn6 aspergillus	796	6	7.5	342	2	Q4HB64_9DEIO	Q4hb64 deinococcus
724	6	7.5	324	2	Q57J92_SALCH	Q57j92 salmonella	797	6	7.5	344	1	LPXD_SVNY3	Q55612 synethocyst
725	6	7.5	324	2	Q9RJN8_STRCO	Q9rjn8 streptomyc	798	6	7.5	344	1	Q4NHJ3_9MICC	Q4nhj3 arthrobacte
726	6	7.5	324	2	Q5FJVB_SALPA	Q5fjvb salmonella	799	6	7.5	345	1	KRI_CHV9D	Q4543 carceripithe
727	6	7.5	324	2	Q7CFM2_SALTY	Q7cfm2 salmonella	800	6	7.5	345	1	LPXD2_GLOVI	Q7n24 gloeobacter
728	6	7.5	324	2	Q83P28_SHIFL	Q83pz8 shigella fl	801	6	7.5	345	2	Q727A0_DESVH	Q727a0 desulfovibr
729	6	7.5	324	2	Q8FD42_ECOL6	Q8fd42 escherichia	802	6	7.5	345	2	Q77LR7_9ALPH	Q77lr7 cercopithe
730	6	7.5	324	2	Q8X9C1_ECO57	Q8x9c1 escherichia	803	6	7.5	345	2	Q4T9X3_TETNG	Q4t9x3 tetradon n
731	6	7.5	324	2	Q8XG63_SALTI	Q8xg63 salmonella	804	6	7.5	346	2	Q9AI37_BURMA	Q9ai37 burkholderi
732	6	7.5	324	2	Q7ZUN1_BRARE	Q7zun1 brachydanio	805	6	7.5	346	2	Q6ZHG2_BURMA	Q6zhg2 burkholderi
733	6	7.5	324	2	Q4SMQ7_TETNG	Q4smq7 tetradon n	806	6	7.5	346	2	Q93UJ3_BURPS	Q93uj3 burkholderi
734	6	7.5	325	2	Q5UQZ6_HALMA	Q5uzq6 haloarcula	807	6	7.5	347	2	Q87476_SIVCZ	Q87476 chimpanzee
735	6	7.5	325	2	Q17597_CAEEL	Q17597 caenorhabdi	808	6	7.5	347	2	Q4H2C1_STRGR	Q4h2c1 streptomyce
736	6	7.5	325	2	Q4KBU0_PSEFP	Q4kbuj4 deinococcus	809	6	7.5	348	1	YLM1_CABEL	P34404 caenorhabdi
737	6	7.5	325	2	Q4KBU0_PSEFP	Q4kbuj4 pseudomonas	810	6	7.5	348	2	Q26577_METHH	Q26577 methanobact
738	6	7.5	325	2	Q665F1_YERPS	Q665f1 yerisinia ps	811	6	7.5	348	2	Q60YH9_CABBR	Q60yh9 caenorhabdi
739	6	7.5	325	2	Q6DA18_ERWCT	Q6da18 erwinia car	812	6	7.5	348	2	Q34353_BACSU	Q34353 bacillus su
740	6	7.5	325	2	Q8ZAW8_YERPE	Q8zaw8 yerisinia pe	813	6	7.5	349	2	Q8NNK7_CORGL	Q8nnk7 corynebacte
741	6	7.5	325	2	Q65K43_BACLD	Q65k43 bacillus li	814	6	7.5	349	2	Q76966_SIVCZ	Q76966 chimpanzee
742	6	7.5	326	2	Q5YBD0_9CHLO	Q5ybd0 helicospori	815	6	7.5	350	2	Q748P7_GROSJ	Q748p7 geobacter s
743	6	7.5	326	2	Q9K4S7_PSEPU	Q9k4s7 pseudomonas	816	6	7.5	350	2	Q87695_SIVCZ	Q87695 chimpanzee
744	6	7.5	326	2	Q5E8X2_VIBF1	Q5e8x8 vibrio fisc	817	6	7.5	351	2	Q4X872_PLACH	Q4x872 plasmodium
745	6	7.5	326	2	Q6NSE1_MYCMS	Q6nse1 mycoplasma	818	6	7.5	352	2	Q59GG4_HUMAN	Q59gg4 homo sapien
746	6	7.5	326	2	Q81X81_BACAN	Q81x81 bacillus an	819	6	7.5	355	2	Q7S3N7_NEUCR	Q7s3n7 neurospora
747	6	7.5	326	2	Q7VJ94_HELHP	Q7vj94 helicobacte	820	6	7.5	355	2	Q83E04_COXBU	Q83e04 coxiella bu
748	6	7.5	326	2	Q7UHE3_RHOBA	Q7uhe3 rhodopirell	821	6	7.5	355	2	Q7VC86_PROMA	Q7vc86 prochloroco
749	6	7.5	326	2	Q87TP1_VIBPA	Q87tp1 vibrio para	822	6	7.5	356	1	XARG_DRONE	P48610 drosophila
750	6	7.5	326	2	Q8DDK4_VIBVU	Q8ddk4 vibrio vuln	823	6	7.5	356	2	Q8PTS2_METMA	Q8pts2 methanosarc
751	6	7.5	326	2	Q9KW22_VIBCH	Q9kw22 vibrio chol	824	6	7.5	356	2	Q6C018_YARLI	Q6c018 yarrowia li
752	6	7.5	326	2	Q7MQ11_VIBVY	Q7mq11 vibrio vuln	825	6	7.5	356	2	Q9Y4T9_HUMAN	Q9y4t9 homo sapien
753	6	7.5	327	2	Q95J23_MACFA	Q95j23 macaca fasc	826	6	7.5	356	2	Q8H1K4_9DINO	Q8h1k4 symbiodiniu
754	6	7.5	327	2	Q6V4X1_VIGUN	Q6v4x1 vigna ungui	827	6	7.5	356	2	Q6F973_ACTAD	Q6f973 actinetobact
755	6	7.5	327	2	Q8G4Z2_BIFLO	Q8g4z2 bifidobacte	828	6	7.5	356	2	Q5LW08_PHOPR	Q5lw08 photobacter
756	6	7.5	327	2	Q9XAW1_BACHD	Q9xaw1 bacillus ha	829	6	7.5	357	2	Q7ZT12_BRARE	Q7ztt2 brachydanio
757	6	7.5	328	2	Q516U2_ENTHI	Q516u2 entamoeba h	830	6	7.5	357	2	Q87681_SIVCZ	Q87681 chimpanzee
758	6	7.5	328	2	Q6N0V2_RHOPA	Q6n0v2 rhodospseudo	831	6	7.5	357	2	Q87682_SIVCZ	Q87682 chimpanzee
759	6	7.5	329	2	Q54NY5_DICDI	Q54ny5 dictyosteli	832	6	7.5	357	2	Q87683_SIVCZ	Q87683 chimpanzee
760	6	7.5	329	2	Q7VD49_PROMA	Q7vd49 prochloroco	833	6	7.5	357	2	Q87684_SIVCZ	Q87684 chimpanzee
761	6	7.5	329	2	Q89HS0_BRAJA	Q89hs0 bradyrhizob	834	6	7.5	357	2	Q87686_SIVCZ	Q87686 chimpanzee

835	6	7.5	357	2	Q87689_SIVCZ	Q87689 chimpanzee	908	6	7.5	371	2	Q87692_SIVCZ	Q87692 chimpanzee
836	6	7.5	358	2	Q8HD78_BRANA	Q8hd78 brassica na	909	6	7.5	371	2	Q87647_SIVCZ	Q87647 chimpanzee
837	6	7.5	358	2	Q4JU24_CORJK	Q4ju24 corynebacte	910	6	7.5	371	2	Q87648_SIVCZ	Q87648 chimpanzee
838	6	7.5	358	2	Q87688_SIVCZ	Q87688 chimpanzee	911	6	7.5	371	2	Q87649_SIVCZ	Q87649 chimpanzee
839	6	7.5	358	2	Q87690_SIVCZ	Q87690 chimpanzee	912	6	7.5	371	2	Q87650_SIVCZ	Q87650 chimpanzee
840	6	7.5	360	2	Q7PPK6_ANOGA	Q7ppk6 anopheles g	913	6	7.5	371	2	Q87651_SIVCZ	Q87651 chimpanzee
841	6	7.5	360	2	Q91UR2_9ZZZZ	Q91ur2 plasmid pb	914	6	7.5	371	2	Q87652_SIVCZ	Q87652 chimpanzee
842	6	7.5	360	2	Q91UX1_9ZZZZ	Q91ux1 plasmid pip	915	6	7.5	371	2	Q87654_SIVCZ	Q87654 chimpanzee
843	6	7.5	360	2	Q4K695_PSBPF5	Q4k695 pseudomonas	916	6	7.5	371	2	Q87656_SIVCZ	Q87656 chimpanzee
844	6	7.5	361	2	Q4HSG9_CAMUP	Q4hsg9 campylobact	917	6	7.5	372	2	Q4IEQ5_GIBZE	Q4ieq5 gibberella
845	6	7.5	362	2	Q9EUI1_SALET	Q9eui1 salmonella	918	6	7.5	372	2	Q624P6_CABBR	Q624p6 caenorhabdi
846	6	7.5	362	2	Q74RI0_GEOSL	Q74ri0 geobacter s	919	6	7.5	372	2	Q72R92_SIVCZ	Q72r92 clostridium
847	6	7.5	364	2	Q8DL75_SYNEL	Q8dl75 synechococc	920	6	7.5	372	2	Q72R91_SIVCZ	Q72r91 chimpanzee
848	6	7.5	365	1	PCP_SYNSP	P51874 symbiodiniu	921	6	7.5	372	2	Q72RD5_SIVCZ	Q72rd5 chimpanzee
849	6	7.5	365	2	Q5DHJ2_SCHJA	Q5dhj2 schistosoma	922	6	7.5	372	2	Q72RD6_SIVCZ	Q72rd6 chimpanzee
850	6	7.5	365	2	Q7QB44_ANOGA	Q7qby4 anopheles g	923	6	7.5	373	2	Q93651_ARCPR	Q93651 archaeoglob
851	6	7.5	365	2	Q8HI10_SYMKA	Q8hi10 symbiodiniu	924	6	7.5	373	2	O53048_9LACO	O53048 lactobacill
852	6	7.5	365	2	Q8HI11_SYMKA	Q8hi11 symbiodiniu	925	6	7.5	373	2	Q72R89_SIVCZ	Q72r89 chimpanzee
853	6	7.5	365	2	Q8HI12_SYMKA	Q8hi12 symbiodiniu	926	6	7.5	373	2	Q72R91_SIVCZ	Q72r91 chimpanzee
854	6	7.5	365	2	Q8HI14_SYMKA	Q8hi14 symbiodiniu	927	6	7.5	373	2	Q72R93_SIVCZ	Q72r93 chimpanzee
855	6	7.5	365	2	Q8HI15_SYMKA	Q8hi15 symbiodiniu	928	6	7.5	373	2	Q72RF2_SIVCZ	Q72rf2 chimpanzee
856	6	7.5	365	2	Q8HI18_SYMKA	Q8hi18 symbiodiniu	929	6	7.5	373	2	Q72RH6_SIVCZ	Q72rh6 chimpanzee
857	6	7.5	365	2	Q8HI19_SYMKA	Q8hi19 symbiodiniu	930	6	7.5	373	2	Q87653_SIVCZ	Q87653 chimpanzee
858	6	7.5	365	2	Q8HIJ6_9DINO	Q8hi19 symbiodiniu	931	6	7.5	374	2	Q8A706_BACTN	Q8a706 bacteroides
859	6	7.5	365	2	Q8HIJ7_9DINO	Q8hi19 symbiodiniu	932	6	7.5	374	2	Q87711_SIVCZ	Q87711 chimpanzee
860	6	7.5	365	2	Q8HIJ8_9DINO	Q8hi19 symbiodiniu	933	6	7.5	374	2	Q72R82_SIVCZ	Q72r82 chimpanzee
861	6	7.5	365	2	Q8HIJ9_9DINO	Q8hi19 symbiodiniu	934	6	7.5	374	2	Q87694_SIVCZ	Q87694 chimpanzee
862	6	7.5	365	2	Q8HIK0_9DINO	Q8hik0 symbiodiniu	935	6	7.5	374	2	Q87712_SIVCZ	Q87712 chimpanzee
863	6	7.5	365	2	Q8HIK1_9DINO	Q8hik1 symbiodiniu	936	6	7.5	374	2	Q87713_SIVCZ	Q87713 chimpanzee
864	6	7.5	365	2	Q8HIK2_9DINO	Q8hik2 symbiodiniu	937	6	7.5	374	2	Q87737_SIVCZ	Q87737 chimpanzee
865	6	7.5	365	2	Q8HIK3_9DINO	Q8hik3 symbiodiniu	938	6	7.5	374	2	Q87738_SIVCZ	Q87738 chimpanzee
866	6	7.5	365	2	Q8HIK5_9DINO	Q8hik5 symbiodiniu	939	6	7.5	374	2	Q87739_SIVCZ	Q87739 chimpanzee
867	6	7.5	365	2	Q88151_SIVCZ	Q88151 chimpanzee	940	6	7.5	375	1	NUC1_YEAST	P32451 saccharomyc
868	6	7.5	365	2	Q04478_SIVCZ	Q04478 chimpanzee	941	6	7.5	375	1	NUC1_YEAST	Q17778 caenorhabdi
869	6	7.5	365	2	Q04479_SIVCZ	Q04479 chimpanzee	942	6	7.5	375	2	Q60WQ5_CABBR	Q60wq5 caenorhabdi
870	6	7.5	365	2	Q04480_SIVCZ	Q04480 chimpanzee	943	6	7.5	375	2	O17039_CABEL	O17039 caenorhabdi
871	6	7.5	365	2	Q4U283_SIVCZ	Q4u283 chimpanzee	944	6	7.5	375	2	Q7XWH9_ORISA	Q7xwh9 oryza sativ
872	6	7.5	367	2	Q4U280_SIVCZ	Q4u280 chimpanzee	945	6	7.5	375	2	Q72R88_SIVCZ	Q72r88 chimpanzee
873	6	7.5	366	2	Q6V587_CRIL0	Q6v587 cricetus	946	6	7.5	375	2	Q72RF3_SIVCZ	Q72rf3 chimpanzee
874	6	7.5	366	2	O5BJX5_RAT	O5bjx5 rattus norv	947	6	7.5	375	2	Q72RF4_SIVCZ	Q72rf4 chimpanzee
875	6	7.5	366	2	Q8C739_MOUSE	Q8c739 mus musculu	948	6	7.5	375	2	Q72RF6_SIVCZ	Q72rf6 chimpanzee
876	6	7.5	367	2	Q8SOV7_ORISA	Q8sov7 oryza sativ	949	6	7.5	375	2	Q72RF7_SIVCZ	Q72rf7 chimpanzee
877	6	7.5	367	2	Q6PFV6_ACIAD	Q6fv6 acinetobact	950	6	7.5	375	2	Q72RF8_SIVCZ	Q72rf8 chimpanzee
878	6	7.5	367	2	Q74P27_GEOSL	Q74f27 geobacter s	951	6	7.5	375	2	Q72RF9_SIVCZ	Q72rf9 chimpanzee
879	6	7.5	367	2	Q8R346_MOUSE	Q8r346 mus musculu	952	6	7.5	375	2	Q72RL1_SIVCZ	Q72rl1 chimpanzee
880	6	7.5	368	2	O53VZ4_THET8	O53vz4 thermus the	953	6	7.5	375	2	Q87691_SIVCZ	Q87691 chimpanzee
881	6	7.5	369	2	Q9C6B1_ARATH	Q9c6b1 arabidopsis	954	6	7.5	375	2	Q87693_SIVCZ	Q87693 chimpanzee
882	6	7.5	369	2	Q4G057_RAT	Q4g057 rattus norv	955	6	7.5	376	2	Q72R83_SIVCZ	Q72r83 chimpanzee
883	6	7.5	369	2	Q4SRE5_TETNG	Q4sre5 tetraodon n	956	6	7.5	376	2	Q72R84_SIVCZ	Q72r84 chimpanzee
884	6	7.5	369	2	Q87671_SIVCZ	Q87671 chimpanzee	957	6	7.5	376	2	Q72R85_SIVCZ	Q72r85 chimpanzee
885	6	7.5	370	2	Q9NUZ1_HUMAN	Q9nuz1 homo sapien	958	6	7.5	376	2	Q72R86_SIVCZ	Q72r86 chimpanzee
886	6	7.5	370	2	Q4UQNZ_XANCP	Q4uqn2 xanthomonas	959	6	7.5	376	2	Q72R87_SIVCZ	Q72r87 chimpanzee
887	6	7.5	370	2	Q8PC87_XANCP	Q8pc87 xanthomonas	960	6	7.5	376	2	Q72R94_SIVCZ	Q72r94 chimpanzee
888	6	7.5	370	2	Q8PGP6_XANCP	Q8pgp6 xanthomonas	961	6	7.5	376	2	Q72R95_SIVCZ	Q72r95 chimpanzee
889	6	7.5	370	2	Q72R90_SIVCZ	Q72r90 chimpanzee	962	6	7.5	376	2	Q72R96_SIVCZ	Q72r96 chimpanzee
890	6	7.5	370	2	Q72RD3_SIVCZ	Q72rd3 chimpanzee	963	6	7.5	376	2	Q72R97_SIVCZ	Q72r97 chimpanzee
891	6	7.5	370	2	Q72RD4_SIVCZ	Q72rd4 chimpanzee	964	6	7.5	376	2	Q72R98_SIVCZ	Q72r98 chimpanzee
892	6	7.5	370	2	Q72RD8_SIVCZ	Q72rd8 chimpanzee	965	6	7.5	376	2	Q72R99_SIVCZ	Q72r99 chimpanzee
893	6	7.5	370	2	Q87657_SIVCZ	Q87657 chimpanzee	966	6	7.5	376	2	Q72RA0_SIVCZ	Q72ra0 chimpanzee
894	6	7.5	370	2	Q87659_SIVCZ	Q87659 chimpanzee	967	6	7.5	376	2	Q72R91_SIVCZ	Q72ra1 chimpanzee
895	6	7.5	370	2	Q87660_SIVCZ	Q87660 chimpanzee	968	6	7.5	376	2	Q72RA2_SIVCZ	Q72ra2 chimpanzee
896	6	7.5	370	2	Q87662_SIVCZ	Q87662 chimpanzee	969	6	7.5	376	2	Q72RA3_SIVCZ	Q72ra3 chimpanzee
897	6	7.5	370	2	Q87663_SIVCZ	Q87663 chimpanzee	970	6	7.5	376	2	Q72RL2_SIVCZ	Q72rl2 chimpanzee
898	6	7.5	370	2	Q87664_SIVCZ	Q87664 chimpanzee	971	6	7.5	376	2	Q72RL3_SIVCZ	Q72rl3 chimpanzee
899	6	7.5	370	2	Q87665_SIVCZ	Q87665 chimpanzee	972	6	7.5	376	2	Q72RL4_SIVCZ	Q72rl4 chimpanzee
900	6	7.5	370	2	Q87666_SIVCZ	Q87666 chimpanzee	973	6	7.5	376	2	Q72RL5_SIVCZ	Q72rl5 chimpanzee
901	6	7.5	370	2	Q87672_SIVCZ	Q87672 chimpanzee	974	6	7.5	377	2	Q7XVB1_ORISA	Q7xvb1 oryza sativ
902	6	7.5	370	2	Q87674_SIVCZ	Q87674 chimpanzee	975	6	7.5	377	2	Q8LME2_ORISA	Q8lme2 oryza sativ
903	6	7.5	370	2	Q87675_SIVCZ	Q87675 chimpanzee	976	6	7.5	377	2	Q60DR0_ORISA	Q6odr0 oryza sativ
904	6	7.5	370	2	Q87676_SIVCZ	Q87676 chimpanzee	977	6	7.5	377	2	Q67U18_ORISA	Q67u18 oryza sativ
905	6	7.5	370	2	Q87678_SIVCZ	Q87678 chimpanzee	978	6	7.5	377	2	Q6F2X7_ORISA	Q6f2x7 oryza sativ
906	6	7.5	370	2	Q87679_SIVCZ	Q87679 chimpanzee	979	6	7.5	377	2	Q615J4_ORISA	Q615j4 oryza sativ
907	6	7.5	371	2	Q72RH7_SIVCZ	Q72rh7 chimpanzee	980	6	7.5	377	2	Q9HYK4_PSEAE	Q9hyk4 pseudomonas

981 6 7.5 377 2 Q728G8 DESVH  
 982 6 7.5 377 2 Q72RF5\_SIVCZ  
 983 6 7.5 378 2 Q6C6B9\_YARL1  
 984 6 7.5 378 2 Q51E56\_BACFN  
 985 6 7.5 378 2 Q9F764\_BACFR  
 986 6 7.5 378 2 Q56768\_HCMV  
 987 6 7.5 379 2 Q29504\_ARCFU  
 988 6 7.5 379 2 Q6C5N1\_YARLI  
 989 6 7.5 379 2 Q9X0Z7\_THEMA  
 990 6 7.5 379 2 Q6Q128\_RAT  
 991 6 7.5 380 1 Y079\_METJA  
 992 6 7.5 381 2 Q55JD9\_CRYNE  
 993 6 7.5 381 2 Q5CMP3\_KLULA  
 994 6 7.5 381 2 Q5KCC0\_CRYNE  
 995 6 7.5 381 2 Q61510\_ORYSA  
 996 6 7.5 381 2 Q414D2\_STAHO  
 997 6 7.5 382 2 Q8H2C3\_PEARA  
 998 6 7.5 382 2 Q835Q8\_ENTFA  
 999 6 7.5 382 2 Q7MT14\_PORGI  
 1000 6 7.5 382 2 Q7VU27\_BORPE

## ALIGNMENTS

## RESULT 1

CD9\_HUMAN  
 ID CD9\_HUMAN STANDARD; PRT; 227 AA.  
 AC P21926; Q96ES4;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE CD9 antigen (p24) (Leukocyte antigen MIC3) (Motility-related protein)  
 DE (MRP-1) (Tetraspanin-29) (TSPAN-29).  
 GN Name=CD9; Synonyms=MIC3, TSPAN29;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 [1]  
 RP NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 1-4.  
 RX MEDLINE=91093112; PubMed=1840589;  
 RA Boucheix J., Benoit P., Frachet P., Billard M., Worthington R.E.,  
 RA Gagnon J., Uzan G.;  
 RT "Molecular cloning of the CD9 antigen. A new family of cell surface  
 proteins.";  
 RL J. Biol. Chem. 266:117-122(1991).  
 [2]  
 RP NUCLEOTIDE SEQUENCE [MRNA], AND PARTIAL PROTEIN SEQUENCE.  
 RX MEDLINE=91244846; PubMed=2037603;  
 RA Lanza F., Wolf D., Fox C.F., Kieffer N., Seyer J.M., Fried V.A.,  
 RA Coughlin S.R., Phillips D.R., Jennings L.K.;  
 RT "cDNA cloning and expression of platelet p24/CD9. Evidence for a new  
 family of multiple membrane-spanning proteins.";  
 RL J. Biol. Chem. 266:10638-10645(1991).  
 [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=92078843; PubMed=1720807; DOI=10.1084/jem.174.6.1347;  
 RA Miyake M., Koyama M., Seno M., Ikegawa S.;  
 RT "Identification of the motility-related protein (MRP-1), recognized by  
 monoclonal antibody M31-15, which inhibits cell motility.";  
 RL J. Exp. Med. 174:1347-1354(1991).  
 [4]  
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 RC TISSUE=Leukocyte;  
 RX MEDLINE=93252369; PubMed=8486348;  
 RA Rubinstein E., Benoit P., Billard M., Plaisance S., Prenant M.,  
 RA Uzan G., Boucheix C.;  
 RT "Organization of the human CD9 gene.";  
 RL Genomics 16:132-138(1993).  
 [5]  
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].

RA Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O.,  
 RA Rajkumar N., Yi Q., Nickerson D.A.;  
 RT "SeattleSNPs, NHLBI HL6682 program for genomic applications, UW-  
 FHCR, Seattle, WA [URL: <http://pga.gs.washington.edu>].";  
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
 [6]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RC TISSUE=Ovary;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Heiton E., Kettman M., Madan A.C., Shevchenko Y., Bouffard G.G.,  
 RA Whiting M., Madan A., Young A.W., Green E.D., Dickson M.C.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Myers R.M.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [7]  
 RP PROTEIN SEQUENCE OF 1-20.  
 RC TISSUE=Platelet;  
 RX MEDLINE=90292223; PubMed=2358073; DOI=10.1016/0014-5793(90)80265-K;  
 RA Higashihara M., Takahata K., Yatomi Y., Nakahara K., Kurokawa K.;  
 RT "Purification and partial characterization of CD9 antigen of human  
 platelets.";  
 RL FEBS Lett. 264:270-274(1990).  
 [8]  
 RP ROLE IN CELL MOTILITY AND METASTASIS.  
 RX PubMed=8478605; DOI=10.1084/jem.177.5.1231;  
 RA Ikegawa S., Koyama M., Yamaoka M., Sasada R., Miyake M.;  
 RT "Suppression of cell motility and metastasis by transfection with  
 human motility-related protein (MRP-1/CD9) DNA.";  
 RL J. Exp. Med. 177:1231-1237(1993).  
 [9]  
 RP ROLE IN CELL ADHESION.  
 RX PubMed=7511626;  
 RA Masellis-Smith A., Shaw A.R.;  
 RT "CD9-regulated adhesion. Anti-CD9 monoclonal antibody induce pre-B  
 cell adhesion to bone marrow fibroblasts through de novo recognition  
 of fibronectin.";  
 RL J. Immunol. 152:2768-2777(1994).  
 [10]  
 RP ROLE IN GAMETE FUSION.  
 RX PubMed=14575715; DOI=10.1016/j.bbrc.2003.09.196;  
 RA Higginbottom A., Takahashi Y., Bolling L., Coonrod S.A., White J.M.,  
 RA Partridge L.J., Monk P.N.;  
 RT "Structural requirements for the inhibitory action of the CD9 large  
 extracellular domain in sperm/oocyte binding and fusion.";  
 RL Biochem. Biophys. Res. Commun. 311:208-214(2003).  
 [11]  
 RP SUBUNIT.  
 RX PubMed=14556650; DOI=10.1042/BJ20031037;  
 RA Kovalenko O.V., Yang X., Kolesnikova T.V., Hemler M.B.;  
 RT "Evidence for specific tetraspanin homodimers: inhibition of  
 palmitoylation makes cysteine residues available for cross-linking.";  
 RL Biochem. J. 377:407-417(2004).  
 [12]  
 RP PHOSPHORYLATION.  
 RX MEDLINE=93327758; PubMed=7687539;  
 RA Chalupny N.J., Kanner S.B., Schieven G.L., Wee S., Gilliland L.K.,  
 RA Aruffo A., Ledbetter J.A.;  
 RT "Tyrosine phosphorylation of CD19 in pre-B and mature B cells.";

EMBO J. 12:2691-2696(1993).  
[13]  
RN PALMITOYLATION, AND MUTAGENESIS OF CYS-8; CYS-77; CYS-78; CYS-86;  
RP CYS-217 AND CYS-218.  
RX PubMed=11959120; DOI=10.1016/S0014-5793(02)02522-X;  
RA Charin S., Manie S., Oualid M., Billard M., Bouchaix C.,  
RA Rubinstein E.;  
RT "Differential stability of tetraspanin/tetraspanin interactions: role  
RT of palmitoylation.";  
RL FEBS Lett. 516:139-144(2002).  
[14]  
RN INTERACTION WITH PTGFRN.  
RX MEDLINE=21216740; PubMed=11278880; DOI=10.1074/jbc.M011297200;  
RA Charin S., Le Nacur F., Oualid M., Billard M., Faure G., Hanash S.M.,  
RA Bouchaix C., Rubinstein E.;  
RT "The major CD9 and CD81 molecular partner. Identification and  
RT characterization of the complexes.";  
RL J. Biol. Chem. 276:14329-14337(2001).  
CC -!- FUNCTION: Involved in platelet activation and aggregation.  
CC Regulates paranodal junction formation. Required for gamete  
CC fusion. Involved in cell adhesion, cell motility and tumor  
CC metastasis.  
CC -!- SUBUNIT: Forms both disulfide-linked homodimers and higher  
CC homooligomers as well as heterooligomers with other members of the  
CC tetraspanin family. Associates with CR2/CD21 and with  
CC PTGFRN/CD9P1.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: Expressed by a variety of hematopoietic and  
CC epithelial cells.  
CC -!- PTM: Protein exists in three forms with molecular masses between  
CC 22 and 27 kDa, and is known to carry covalently linked fatty  
CC acids.  
CC -!- PTM: Phosphorylated on tyrosine following B-cell activation.  
CC -!- SIMLARTY: Belongs to the tetraspanin (TM4SF) family.  
-----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
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DR EMBL; S60489; AAC60586.1; -; Genomic\_DNA.  
DR EMBL; S60462; AAC60586.1; JOINED; Genomic\_DNA.  
DR EMBL; S60463; AAC60586.1; JOINED; Genomic\_DNA.  
DR EMBL; S60464; AAC60586.1; JOINED; Genomic\_DNA.  
DR EMBL; S60700; AAC60586.1; JOINED; Genomic\_DNA.  
DR EMBL; S60699; AAC60586.1; JOINED; Genomic\_DNA.  
DR EMBL; S60465; AAC60586.1; JOINED; Genomic\_DNA.  
DR EMBL; S60472; AAC60586.1; JOINED; Genomic\_DNA.  
DR EMBL; M38690; AAA80320.1; -; mRNA.  
DR EMBL; L34068; AAA59982.1; -; mRNA.  
DR EMBL; X50111; CA942708.1; -; mRNA.  
DR EMBL; L08118; -; NOT ANNOTATED CDS; Genomic\_DNA.  
DR EMBL; L08119; AAA51954.1; ALT SEQ; Genomic\_DNA.  
DR EMBL; L08120; AAA51955.1; ALT SEQ; Genomic\_DNA.  
DR EMBL; L08121; AAA51956.1; -; Genomic\_DNA.  
DR EMBL; L08122; AAA51957.1; -; Genomic\_DNA.  
DR EMBL; L08123; AAA51958.1; -; Genomic\_DNA.  
DR EMBL; L08124; AAA51959.1; -; Genomic\_DNA.  
DR EMBL; L08125; -; NOT ANNOTATED CDS; Genomic\_DNA.  
DR EMBL; AY422198; AAQ87878.1; -; Genomic\_DNA.  
DR EMBL; BC011988; AAH11988.1; -; mRNA.  
DR PIR; A46123; A40420.  
DR Ensembl; ENSG0000010278; Homo sapiens.  
DR HGNC; HGNC:1709; CD9.  
DR H-InvDB; HIX0010357; -.  
DR Reactome; P21926; -.  
DR MIM; 143030; -.  
DR GO; GO:0005887; C:integral to plasma membrane; NAS.  
DR GO; GO:0005886; C:plasma membrane; NAS.  
DR GO; GO:0005515; F:protein binding; IPI.  
DR GO; GO:0007155; P:cell adhesion; IDA.  
DR GO; GO:0006928; P:cell motility; IDA.

DR GO; GO:0007342; P:fusion of sperm to egg plasma membrane; IDA.  
DR GO; GO:0030913; P:paranodal junction formation; ISS.  
DR GO; GO:0030169; P:platelet activation; NAS.  
DR InterPro; IPR000301; Transmem 4.  
DR Pfam; PF00335; Tetraspanin; 1.  
DR PRINTS; PR00259; TMFOUR.  
DR PROSITE; PS00421; TM4\_1; 1.  
KW Antigen; Cell adhesion; Direct protein sequencing; Fertilization;  
KW Antigen; Cell adhesion; Direct protein sequencing; Fertilization;  
Query Match 100.0%; Score 80; DB 1; Length 227;  
Best Local Similarity 100.0%; Pred. No. 5.8e-75;  
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HKDEVIKEVQEFYKDTYTNKLTQDEPQRETLKAIHYALNCCGLAGGVQFISDIPCCKDV 60  
Db 112 HKDEVIKEVQEFYKDTYTNKLTQDEPQRETLKAIHYALNCCGLAGGVQFISDIPCCKDV 171  
QY 61 LETFTVKSCPDAIKEVFDNK 80  
Db 172 LETFTVKSCPDAIKEVFDNK 191

RESULT 2  
Q5J7W6\_HUMAN  
ID Q5J7W6 HUMAN PRELIMINARY; PRT; 228 AA.  
AC Q5J7W6;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Growth-inhibiting gene 2 protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN NUCLEOTIDE SEQUENCE.  
RP Kim J.W.;  
RA "Identification of a human growth inhibition gene 2 (GIG2).";  
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY423720; AAS00483.1; -; mRNA.  
DR EMBL; 228 AA; 25416 MW; F68333E0C20611D8 CRC64;  
SEQUENCE 228 AA; 25416 MW; F68333E0C20611D8 CRC64;  
Query Match 100.0%; Score 80; DB 2; Length 228;  
Best Local Similarity 100.0%; Pred. No. 5.8e-75;  
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HKDEVIKEVQEFYKDTYTNKLTQDEPQRETLKAIHYALNCCGLAGGVQFISDIPCCKDV 60  
Db 113 HKDEVIKEVQEFYKDTYTNKLTQDEPQRETLKAIHYALNCCGLAGGVQFISDIPCCKDV 172  
QY 61 LETFTVKSCPDAIKEVFDNK 80  
Db 173 LETFTVKSCPDAIKEVFDNK 192

RESULT 3  
Q56CY1\_HUMAN  
ID Q56CY1 HUMAN PRELIMINARY; PRT; 182 AA.  
AC Q56CY1;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Bladder cancer related CD9 variant.  
GN Name=BTCC-1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN NUCLEOTIDE SEQUENCE.  
RP Tissue=Bladder;  
RC Tissue=Bladder;

RA Ma F., Wang H., Wang X., Chang J.;  
 RT "The full-length cloning of a differentially expressed EST sequence in  
 a bladder cancer subtractive cDNA library.";  
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
 SQ EMBL; AY966455; AAX78197.1; -; mRNA.  
 DR SEQUENCE 182 AA; 20750 MW; C26F856F584AADEE CRC64;

Query Match 48.8%; Score 39; DB 2; Length 182;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-32;  
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVIKEVQFYKDTYNTKLTQDEPQRETLLKAIHYALN 39  
 |||||  
 DB 113 HKDEVIKEVQFYKDTYNTKLTQDEPQRETLLKAIHYALN 151  
 |||||

RESULT 4  
 CD9\_CERAE STANDARD; PRT; 227 AA.  
 AC P30409;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE CD9 antigen (27 kDa diphtheria toxin receptor-associated protein)  
 DE (DRAP27).  
 GN Name=CD9;  
 OS Cercopithecus aethiops (Green monkey) (Grivet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 OC Cercopitheidae; Cercopithecinae; Cercopithecus.  
 OX NCBI\_TaxID=9534;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [MRNA].  
 RX MEDLINE=92394967; PubMed=1522113; DOI=10.1093/jcb.118.6.1389;  
 RA Mitamura T., Iwanoto R., Umata T., Yomo T., Urabe I., Tsuneoka M.,  
 RA Mekada E.;  
 RT "The 27-kD diphtheria toxin receptor-associated protein (DRAP27) from  
 vero cells is the monkey homologue of human CD9 antigen: expression of  
 DRAP27 elevates the number of diphtheria toxin receptors on toxin-  
 sensitive cells.";  
 RL J. Cell Biol. 118:1389-1399(1992).  
 CC -!- FUNCTION: Involved in platelet activation and aggregation.  
 CC Regulates paranodal junction formation. Required for gamete  
 CC fusion. Involved in cell adhesion, cell motility and tumor  
 CC metastasis (By similarity).  
 CC -!- FUNCTION: Expression of DRAP27 elevates the number of diphtheria  
 CC toxin receptors on toxin-sensitive cells.  
 CC -!- SUBUNIT: Forms both disulfide-linked homodimers and higher  
 CC homooligomers as well as heterooligomers with other members of the  
 CC tetraspanin family. Associates with CR2/CD21 and with PTGFRN/CD9P1  
 CC (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- PTM: Phosphorylated on tyrosine following B-cell activation (By  
 CC similarity).  
 CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.  
 CC  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC  
 CC EMBL; D10726; BAA01569.1; -; mRNA.  
 DR F01; A42929; A42929.  
 DR GO; GO:0005887; C:integral to plasma membrane; ISS.  
 DR GO; GO:0005515; F:protein binding; ISS.  
 DR GO; GO:0007155; P:cell adhesion; ISS.  
 DR GO; GO:0006928; P:cell motility; ISS.  
 DR GO; GO:0007342; P:fusion of sperm to egg plasma membrane; ISS.  
 DR GO; GO:0030913; P:paranodal junction formation; ISS.  
 DR GO; GO:0030168; P:platelet activation; ISS.  
 DR InterPro; IPR000301; Transmem 4.  
 DR Pfam; PF00335; Tetraspanin; I.

DR PRINTS; PR00259; TMFOUR.  
 DR PROSITE; PS00421; TM4\_1; 1.  
 KW Antigen; Cell adhesion; Fertilization; Glycoprotein; Lipoprotein;  
 KW Palmitate; Phosphorylation; Transmembrane.  
 FT INIT MET 0  
 FT TOPO DOM 1 11  
 FT TRANSMEM 12 32  
 FT TOPO DOM 33 54  
 FT TRANSMEM 55 75  
 FT TOPO DOM 76 86  
 FT TRANSMEM 87 110  
 FT TOPO DOM 111 194  
 FT TRANSMEM 195 220  
 FT TOPO DOM 221 227  
 FT LIPID 8 8  
 FT LIPID 77 77  
 FT LIPID 78 78  
 FT LIPID 86 86  
 FT LIPID 217 217  
 FT LIPID 218 218  
 FT CARBOHYD 51 51  
 FT CARBOHYD 52 52  
 SQ SEQUENCE 227 AA; 25300 MW; 8E3474E7A590374A CRC64;

Query Match 47.5%; Score 38; DB 1; Length 227;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-31;  
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVIKEVQFYKDTYNTKLTQDEPQRETLLKAIHYAL 38  
 |||||  
 DB 112 HKDEVIKEVQFYKDTYNTKLTQDEPQRETLLKAIHYAL 149  
 |||||

RESULT 5  
 CD9\_FELCA STANDARD; PRT; 225 AA.  
 AC P40239;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE CD9 antigen.  
 GN Name=CD9;  
 OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;  
 OC Felinae; Felis.  
 OX NCBI\_TaxID=9685;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [MRNA].  
 RX PubMed=7753050; DOI=10.1016/0161-5890(95)00008-3;  
 RA Willett B.J., Neil J.C.;  
 RT "cDNA cloning and eukaryotic expression of feline CD9.";  
 RL Mol. Immunol. 32:417-423(1995).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE [MRNA].  
 RA Morikawa S.;  
 RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Involved in platelet activation and aggregation.  
 CC Regulates paranodal junction formation. Required for gamete  
 CC fusion. Involved in cell adhesion, cell motility and tumor  
 CC metastasis (By similarity).  
 CC -!- SUBUNIT: Forms both disulfide-linked homodimers and higher  
 CC homooligomers as well as heterooligomers with other members of the  
 CC tetraspanin family. Associates with CR2/CD21 and with PTGFRN/CD9P1  
 CC (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- PTM: Phosphorylated on tyrosine following B-cell activation (By  
 CC similarity).  
 CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.  
 CC  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.









RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [4]  
RP ROLE IN GAMETE FUSION.  
RX Pubmed=10700183; DOI=10.1038/73502;  
RA Kajji K., Oda S., Shikano T., Ohnuki T., Uematsu Y., Sakagami J.,  
RA Tada N., Miyazaki S., Kudo A.;  
RT "The gamete fusion process is defective in eggs of Cd9-deficient  
mice.";  
RT Nat. Genet. 24:279-282(2000).  
RN [5]  
RN ROLE IN PARANODAL FORMATION, AND TISSUE SPECIFICITY.  
RX Pubmed=14715942; DOI=10.1523/JNEUROSCI.1484-03.2004;  
RA Ishibashi T., Ding L., Ikenaka K., Inoue Y., Miyado K., Mekada E.,  
RA Baba H.;  
RT "Tetraspanin protein CD9 is a novel paranodal component regulating  
paranodal junctional formation.";  
RL J. Neurosci. 24:96-102(2004).  
RN [6]  
RN FUNCTION AS RECEPTOR FOR PSG17.  
RX Pubmed=11805154; DOI=10.1084/jem.20011741;  
RA Waterhouse R., Ha C., Dreksler G.S.;  
RT "Murine CD9 is the receptor for pregnancy-specific glycoprotein 17.";  
RL J. Exp. Med. 195:277-282(2002).  
CC -!- FUNCTION: Involved in platelet activation and aggregation.  
CC Regulates paranodal junction formation. Required for gamete  
CC fusion. Involved in cell adhesion, cell motility and tumor  
CC metastasis. Acts as a receptor for PSG17.  
CC -!- SUBUNIT: Forms both disulfide-linked homodimers and higher  
CC homooligomers as well as heterooligomers with other members of the  
CC tetraspanin family. Associates with CR2/CD21 and with PTGFRN/CD9P1  
CC (By similarity).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: Expressed predominantly in the peripheral  
CC nervous system.  
CC -!- PTM: Phosphorylated on tyrosine following B-cell activation (By  
CC similarity).  
CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.  
CC  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC  
CC EMBL; L08115; AAA37405.1; -; mRNA.  
CC EMBL; AK002251; BAB21965.1; -; mRNA.  
CC EMBL; AK012793; BAB28473.1; -; mRNA.  
CC EMBL; BC070474; AAH70474.1; -; mRNA.  
CC PIR; I49589; I49589.  
CC Ensembl; ENSMUSG00000030342; Mus musculus.  
CC MGI; MGI:88348; Cd9.  
CC DR GO; GO:0005887; C:integral to plasma membrane; ISS.  
CC DR GO; GO:0005886; C:plasma membrane; TAS.  
CC DR GO; GO:0005515; F:protein binding; IPI.  
CC DR GO; GO:0007155; P:cell adhesion; ISS.  
CC DR GO; GO:0006928; P:cell motility; ISS.  
CC DR GO; GO:0007342; P:fusion of sperm to egg plasma membrane; IDA.  
CC DR GO; GO:0030913; P:paranodal junction formation; IDA.  
CC DR GO; GO:0030168; P:platelet activation; ISS.  
CC DR InterPro; IPR00301; Transmem 4.  
CC DR Pfam; PF00335; Tetraspanin, I.  
CC DR PRINTS; PR00259; TMFOUR.  
CC DR PROSITE; PS00421; TM4\_1; 1.  
CC DR Antigen; Cell adhesion; Fertilization; Glycoprotein; Lipoprotein;  
KW Palmitate; Phosphorylation; Transmembrane.  
FT INIT MET 0 0 By similarity.  
FT TOPO\_DOM 1 11 Cytoplasmic (Potential).  
FT TRANSMEM 12 32 Potential.  
FT TOPO\_DOM 33 52 Extracellular (Potential).  
FT TRANSMEM 53 73 Potential.

FT TOPO\_DOM 74 84 Cytoplasmic (Potential).  
FT TRANSMEM 85 108 Potential.  
FT TOPO\_DOM 109 192 Extracellular (Potential).  
FT TRANSMEM 193 218 Potential.  
FT TOPO\_DOM 219 225 Cytoplasmic (Potential).  
FT LIPID 8 8 S-palmitoyl cysteine (By similarity).  
FT LIPID 75 75 S-palmitoyl cysteine (By similarity).  
FT LIPID 76 76 S-palmitoyl cysteine (By similarity).  
FT LIPID 84 84 S-palmitoyl cysteine (By similarity).  
FT LIPID 215 215 S-palmitoyl cysteine (By similarity).  
FT LIPID 216 216 S-palmitoyl cysteine (By similarity).  
FT CARBOHYD 49 49 N-linked (GlcNAc...) (Potential).  
SQ SEQUENCE 225 AA; 25127 MW; 2BBE40B8D7C31BC0 CRC64;  
  
Query Match 16.2%; Score 13; DB 1; Length 225;  
Best Local Similarity 100.0%; Pred. No. 5.4e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 23 KDEPQRETLKAIH 35  
|||||  
DB 132 KDEPQRETLKAIH 144  
  
RESULT 9  
ID CD9\_PIG STANDARD; PRT; 225 AA.  
AC Q8WMQ3;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE CD9 antigen.  
GN Name=CD9;  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
OC Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [MRNA].  
RC TISSUE=Smooth muscle;  
RX Pubmed=14610355; DOI=10.1159/000074170;  
RA Yubero N., Jimenez-Marin A., Yerle M., Moreza L., Barbancho M.J.,  
RA Llanes D., Garrido J.J.;  
RT "Molecular cloning, expression pattern and chromosomal mapping of pig  
CD9 antigen.";  
RL Cytogenet. Genome Res. 101:143-146(2003).  
CC -!- FUNCTION: Involved in platelet activation and aggregation.  
CC Regulates paranodal junction formation. Required for gamete  
CC fusion. Involved in cell adhesion, cell motility and tumor  
CC metastasis (By similarity).  
CC -!- SUBUNIT: Forms both disulfide-linked homodimers and higher  
CC homooligomers as well as heterooligomers with other members of the  
CC tetraspanin family. Associates with CR2/CD21 and with PTGFRN/CD9P1  
CC (By similarity).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- PTM: Phosphorylated on tyrosine following B-cell activation (By  
CC similarity).  
CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.  
CC  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC  
CC EMBL; AY072785; AAL68966.1; -; mRNA.  
CC DR GO; GO:0005887; C:integral to plasma membrane; ISS.  
CC DR GO; GO:0005515; F:protein binding; ISS.  
CC DR GO; GO:0007155; P:cell adhesion; ISS.  
CC DR GO; GO:0006928; P:cell motility; ISS.  
CC DR GO; GO:0007342; P:fusion of sperm to egg plasma membrane; ISS.  
CC DR GO; GO:0030913; P:paranodal junction formation; ISS.  
CC DR GO; GO:0030168; P:platelet activation; ISS.

DR InterPro; IPR000301; Transmem\_4.  
 DR Pfam; PF00335; Tetraspannin; 1.  
 DR PRINTS; PR00259; TMFOUR.  
 DR PROSITE; PS00421; TM4\_1; 1.  
 KW Antigen; Cell adhesion; Fertilization; Glycoprotein; Lipoprotein;  
 KW Palmitate; Phosphorylation; Transmembrane.  
 FT INIT\_MET 0 0  
 FT TOPO\_DOM 1 11  
 FT TRANSMEM 12 32  
 FT TOPO\_DOM 33 52  
 FT TRANSMEM 53 73  
 FT TOPO\_DOM 74 84  
 FT TRANSMEM 85 108  
 FT TOPO\_DOM 109 192  
 FT TRANSMEM 193 218  
 FT TOPO\_DOM 219 225  
 FT LIPID 8 8  
 FT LIPID 75 75  
 FT LIPID 76 76  
 FT LIPID 84 84  
 FT LIPID 215 215  
 FT LIPID 216 216  
 FT CARBOHYD 49 49  
 FT CARBOHYD 50 50  
 SQ SEQUENCE 225 AA; 25070 MW; FF280FE39BC11545 CRC64;  
 Query Match 16.2%; Score 13; DB 1; Length 225;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 26 PORETLKAIHYAL 38  
 Db 135 PORETLKAIHYAL 147  
 |||||  
 RESULT 10  
 Q8MJ48\_PIG  
 ID Q8MJ48\_PIG PRELIMINARY; PRT; 226 AA.  
 AC Q8MJ48;  
 DT 01-OCT-2002 (TREMBlrel. 22, Created)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Transmembrane protein CD9.  
 GN Name=CD9;  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
 OC Sus.  
 NCBI\_TaxID=9923;  
 [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Heinz M., Huang C.A., Emery D.W., Giovino M.A., LeGuern A.,  
 RA Kurilla-Nahon B., Theodore P., Arn J.S., Sykes M., Mulligan R.C.,  
 RA Down J.D., Sachs D.H., Goodell M.A.;  
 RT "Use of CD9 Expression to Enrich for Porcine Hematopoietic  
 RT Progenitors";  
 RL Exp. Hematol. 0:0-0(2002).  
 DR EMBL; AF25029; AAM81376.1; -; mRNA.  
 DR HSSP; P60033; IG8Q.  
 GO; GO:0016021; C: integral to membrane; IEA.  
 DR InterPro; IPR000301; Transmem 4.  
 DR Pfam; PF00335; Tetraspannin; 1.  
 DR PRINTS; PR00259; TMFOUR.  
 DR PROSITE; PS00421; TM4\_1; 1.  
 KW Transmembrane.  
 SQ SEQUENCE 226 AA; 25127 MW; 885C244477F95C23 CRC64;  
 Query Match 16.2%; Score 13; DB 2; Length 226;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 26 PORETLKAIHYAL 38  
 Db 135 PORETLKAIHYAL 147  
 |||||

Query Match 10.0%; Score 8; DB 2; Length 298;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 PDAIKSVF 77  
| | | | | | | |  
Db 252 PDAIKSVF 259

## RESULT 13

Q5AJ90 CANAL PRELIMINARY; PRT; 410 AA.  
AC Q5AJ90;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Potential peroxisomal 3-ketoacyl-CoA thiolase.  
GN Name=PO2; ORFNames=CaO19.1704, CaO19.9271;  
OS Candida albicans SC5314.  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.  
OX NCBI\_TaxID=237561;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=SC5314;  
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;  
RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S., Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T., Davis R.W., Scherer S.;  
RA "The diploid genome sequence of Candida albicans.";  
RT Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=SC5314;  
RA Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola O., Roberts J., Persson K., Donnelly S., Favoreto S., Tzung K.-W., Jones T., Scherer S., Agabian N.;  
RA "Annotation of the Genome of Candida albicans.";  
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AACQ01000014; EAL02864.1; -; Genomic DNA.  
DR EMBL; AACQ01000013; EAL02993.1; -; Genomic DNA.  
DR GO; GO:0008415; F:acyltransferase activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
KW Acyltransferase; Transferase.  
SQ SEQUENCE 410 AA; 43877 MW; 65CBECS99E39B4692 CRC64;

Query Match 10.0%; Score 8; DB 2; Length 410;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 CGLAGGVE 48  
| | | | | | | |  
Db 121 CGLAGGVE 128

## RESULT 14

Q4XU05 PLACH PRELIMINARY; PRT; 29 AA.  
AC Q4XU05;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Hypothetical protein (Fragment).  
GN ORFNames=PC105993.00.0;  
OS Plasmodium chabaudi.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5825;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A., Berrihan M., Florens L., Janssen C.S., Pain A., Christophides G.K., James K., Rutherford K., Harris B., Harris D., Churcher C.,

Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J., Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C., Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;  
RA "A comprehensive survey of the Plasmodium life cycle by genomic, transcriptomic, and proteomic analyses.";  
RL Science 307:82-86(2005).  
CC -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.  
CC EMBL; CAAJ01003007; CAH79356.1; -; Genomic DNA.  
DR Hypothetical protein.  
FT NON\_TER 1  
SQ SEQUENCE 29 AA; 3541 MW; A386F2C2D29442CC CRC64;

Query Match 8.8%; Score 7; DB 2; Length 29;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 YNKLKTK 23  
| | | | | | | |  
Db 2 YNKLKTK 8

## RESULT 15

Q6LHC2 PROPR PRELIMINARY; PRT; 91 AA.  
AC Q6LHC2;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
GN OrderedLocusNames=PBPRB1442;  
OS Photobacterium profundum (Photobacterium sp. (strain SS9)).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
OC Vibrionaceae; Photobacterium.  
OX NCBI\_TaxID=74109;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RX PubMed=15746425; DOI=10.1126/science.1103341;  
RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.M., Cestaro A., Malacrida G., Simonati B., Cannata N., Romualdi C., Bartlett D.H., Valle G.;  
RA "Life at depth: Photobacterium profundum genome sequence and expression analysis.";  
RL Science 307:1459-1461(2005).  
DR EMBL; CR378679; CAG33308.1; -; Genomic DNA.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 91 AA; 11346 MW; 47435EB3848A1126 CRC64;

Query Match 8.8%; Score 7; DB 2; Length 91;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 KDEPQRE 29  
| | | | | | | |  
Db 29 KDEPQRE 35

Search completed: January 20, 2006, 17:44:43  
Job time : 129.769 secs

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Result No.	Score	Query		Length	DB	ID	Description
		Match	\$				
1	24	100.0		95	3	AAG01570	Human sec
2	24	100.0		209	4	ACG76051	Human col
3	24	100.0		227	2	AAR86934	Human CD9
4	24	100.0		227	5	ABB78366	Amino aci
5	24	100.0		227	5	AAE14636	Human CD9
6	24	100.0		227	6	ABU05057	Human exp
7	24	100.0		227	6	ABU05060	Human exp
8	24	100.0		227	7	ABW00436	Human CD9
9	24	100.0		227	7	ADK69862	Human CD9
10	24	100.0		227	8	ADL19366	Human CD9
11	24	100.0		227	9	AEA89005	Human CD9
12	24	100.0		228	4	ABB44581	Human wou
13	24	100.0		228	6	ABU05059	Human exp
14	24	100.0		228	6	ABU05052	Human exp
15	24	100.0		228	6	ABU05048	Human exp
16	24	100.0		228	6	ABU05049	Human exp
17	24	100.0		228	6	ABU05050	Human exp
18	24	100.0		228	6	ABU05053	Human exp
19	24	100.0		228	7	ABW01519	Protein #
20	24	100.0		228	7	ADH89037	TAT278. 1
21	24	100.0		228	7	ADG32002	Human hom
22	24	100.0		228	8	ADJ57558	Human CD9
23	24	100.0		228	8	ADL26782	Human CD9
24	24	100.0		228	8	ADL82853	Human PRO

98	6	25.0	203	8	ADT58596	Adt58596 Plant pol	171	6	25.0	398	4	ABB70325	Abb70325 Drosophil
99	6	25.0	214	4	ABB70772	Abb70772 Drosophil	172	6	25.0	402	4	ABB70534	Abb70534 Drosophil
100	6	25.0	221	4	ABB64291	Abb64291 Drosophil	173	6	25.0	402	7	ABO77783	AbO77783 Pseudomon
101	6	25.0	228	4	ABB62497	Abb62497 Drosophil	174	6	25.0	405	3	AAG49723	Aag49723 Arabidops
102	6	25.0	236	2	AAW99456	Aaw99456 Amino aci	175	6	25.0	405	8	ADS24369	AdS24369 Bacterial
103	6	25.0	236	5	AAE19800	Aae19800 Candida a	176	6	25.0	406	8	ADN47627	Adn47627 Thermococ
104	6	25.0	236	7	ADM33265	Adm33265 Candida a	177	6	25.0	409	6	ABR40849	AbR40849 Momordica
105	6	25.0	242	7	ADD30644	Add30644 Plant yie	178	6	25.0	410	9	ABE40766	Abe40766 L. pneumo
106	6	25.0	242	8	ADL43685	Adl43685 Plant tra	179	6	25.0	411	3	AAG35679	Aag35679 Arabidops
107	6	25.0	242	8	ADO03477	Ado03477 Thalecres	180	6	25.0	416	4	ABB59251	Abb59251 Drosophil
108	6	25.0	242	8	ADO63011	Ado63011 Transcrip	181	6	25.0	417	9	ABE37451	Aeb37451 L. pneumo
109	6	25.0	242	8	ADG66575	Adg66575 Plant ful	182	6	25.0	426	4	ABE67253	AbE67253 Drosophil
110	6	25.0	242	9	AEA26613	Aea26613 Stress to	183	6	25.0	431	6	ABR53542	Abr53542 Protein s
111	6	25.0	244	4	ABB65539	Abb65539 Drosophil	184	6	25.0	431	7	ADK64408	Adk64408 Disease t
112	6	25.0	249	4	ABM60887	Abm60887 Drosophil	185	6	25.0	431	8	ADT87238	Adt87238 Yeast Str
113	6	25.0	252	6	ADA15537	Ada15537 A. thalia	186	6	25.0	437	4	ABB62782	Abb62782 Drosophil
114	6	25.0	252	7	ADB31901	Adb31901 Plant (A.	187	6	25.0	440	3	AAB18146	Aab18146 Plaasmodiu
115	6	25.0	252	7	ADC46655	Adc46655 Thalecres	188	6	25.0	440	4	ABB72014	Abb72014 Drosophil
116	6	25.0	252	8	ADO02097	Ado02097 Thalecres	189	6	25.0	443	4	ABB65770	Abb65770 Drosophil
117	6	25.0	270	4	ABB66659	Abb66659 Drosophil	190	6	25.0	443	4	ABM00060	AbM00060 VRN2 poly
118	6	25.0	272	2	AKR05876	Akr05876 Merozite	191	6	25.0	445	3	AAG70714	Aag70714 S cerevis
119	6	25.0	272	3	AAE18202	Aae18202 Plasmodiu	192	6	25.0	447	4	AAG70714	Aag70714 S cerevis
120	6	25.0	274	3	AAG48240	Aag48240 Arabidops	193	6	25.0	467	3	RAY54602	Ray54602 AV37 anti
121	6	25.0	274	3	AGL14699	Agl14699 Arabidops	194	6	25.0	477	4	ABB66931	Abb66931 Drosophil
122	6	25.0	275	3	AGL48239	Agl48239 Arabidops	195	6	25.0	478	3	RAA42226	Raa42226 Human ORF
123	6	25.0	275	3	AGL14598	Agl14598 Arabidops	196	6	25.0	478	3	RAY57603	Ray57603 Human pro
124	6	25.0	276	9	ADG765378	Adg765378 S. mansoni	197	6	25.0	479	7	ADK64948	Adk64948 Protein s
125	6	25.0	278	4	ABB69939	Abb69939 Drosophil	198	6	25.0	479	7	ADK64948	Adk64948 Disease t
126	6	25.0	280	4	ABB65783	Abb65783 Drosophil	199	6	25.0	480	4	ABB69134	Abb69134 Drosophil
127	6	25.0	284	4	ABB69768	Abb69768 Drosophil	200	6	25.0	480	8	ADU69147	Adu69147 Fruit fly
128	6	25.0	287	2	AR05877	Aar05877 Merozite	201	6	25.0	482	8	ADJ49010	Adj49010 Oil-assoc
129	6	25.0	287	2	AR888002	Aar888002 Delta-end	202	6	25.0	483	8	ADJ50397	Adj50397 Oil-assoc
130	6	25.0	287	8	AXG66164	Axg66164 Plant ful	203	6	25.0	483	8	ADJ49009	Adj49009 Oil-assoc
131	6	25.0	288	3	AGL14697	Agl14697 Arabidops	204	6	25.0	485	8	ADJ50209	Adj50209 Oil-assoc
132	6	25.0	288	3	AGL48238	Agl48238 Arabidops	205	6	25.0	490	8	ADJ50209	Adj50209 Oil-assoc
133	6	25.0	293	8	ADT58681	Adt58681 Plant pol	206	6	25.0	493	4	ABB71880	Abb71880 Drosophil
134	6	25.0	298	7	ADC46637	Adc46637 Thalecres	207	6	25.0	496	8	ADG76671	Adg76671 Phospholi
135	6	25.0	298	7	ADJ55830	Adj55830 Thalecres	208	6	25.0	498	3	RAG54168	Rag54168 Arabidops
136	6	25.0	298	8	ADU61459	Adu61459 A. thalia	209	6	25.0	500	3	AAG21939	Aag21939 Arabidops
137	6	25.0	298	8	ADO02451	Ado02451 Thalecres	210	6	25.0	506	4	AAG78226	Aag78226 Lepomis c
138	6	25.0	300	2	AR05878	Aar05878 Merozite	211	6	25.0	508	4	ABB71345	Abb71345 Drosophil
139	6	25.0	304	8	ADT57907	Adt57907 Plant pol	212	6	25.0	509	8	ADT77459	Adt77459 Human nuc
140	6	25.0	313	8	ADK89567	Adk89567 Plant ful	213	6	25.0	512	5	ABP29785	Abp29785 Streptoco
141	6	25.0	323	4	ABB60025	Abb60025 Drosophil	214	6	25.0	512	5	ABP27229	Abp27229 Streptoco
142	6	25.0	337	8	ADK69102	Adk69102 Plant ful	215	6	25.0	512	8	ADV89570	Adv89570 Streptoco
143	6	25.0	339	3	AGS54170	Ags54170 Arabidops	216	6	25.0	512	8	ADV82977	Adv82977 Streptoco
144	6	25.0	341	8	ADX66275	Adx66275 Plant ful	217	6	25.0	512	8	ADV80823	Adv80823 Streptoco
145	6	25.0	351	5	ABG79591	Abg79591 Candida g	218	6	25.0	513	3	AAV91276	Aav91276 Group B S
146	6	25.0	354	4	ABB30793	Abb30793 Amino aci	219	6	25.0	520	8	ADK68098	Adk68098 Plant ful
147	6	25.0	355	8	ADX95777	Adx95777 Plant ful	220	6	25.0	526	4	ABB67142	Abb67142 Drosophil
148	6	25.0	367	3	AGS54169	Ags54169 Arabidops	221	6	25.0	526	4	ABB68634	Abb68634 Drosophil
149	6	25.0	368	4	ABB58030	Abb58030 Drosophil	222	6	25.0	533	5	ABB54316	Abb54316 Lactococc
150	6	25.0	368	4	ABM96585	Abm96585 Putative	223	6	25.0	535	4	ABB58915	Abb58915 Drosophil
151	6	25.0	368	5	ABG93036	Abg93036 S. cerevi	224	6	25.0	561	4	ABB67878	Abb67878 Drosophil
152	6	25.0	368	8	ADS43197	Ads43197 Bacterial	225	6	25.0	570	4	ABB64692	Abb64692 Drosophil
153	6	25.0	369	7	ADD30364	Add30364 Plant yie	226	6	25.0	575	3	AAG21938	Aag21938 Arabidops
154	6	25.0	369	8	ADL44287	Adl44287 Plant tra	227	6	25.0	578	6	ABU30855	Abu30855 Protein e
155	6	25.0	370	5	ABP11368	Abp11368 Human ORF	228	6	25.0	578	8	ADU05598	Adu05598 H. pylori
156	6	25.0	372	5	ABB93414	Abb93414 Herbicida	229	6	25.0	581	7	ADU05598	Adu05598 H. pylori
157	6	25.0	374	3	AGS35680	Ags35680 Arabidops	230	6	25.0	582	4	AAG78227	Aag78227 Lepomis c
158	6	25.0	375	8	ADN19891	Adn19891 Bacterial	231	6	25.0	582	4	ABM82297	Abm82297 Arabidops
159	6	25.0	378	4	ABB68211	Abb68211 Drosophil	232	6	25.0	592	4	ABM82296	Abm82296 Arabidops
160	6	25.0	381	8	ADL42928	Adl42928 Plant tra	233	6	25.0	592	5	ABP99405	Abp99405 Arabidops
161	6	25.0	384	3	AGL13903	Agl13903 Arabidops	234	6	25.0	592	8	ADM98799	Adm98799 HMG-CoA r
162	6	25.0	386	4	ABB70630	Abb70630 Drosophil	235	6	25.0	592	8	ADM98789	Adm98789 HMG-CoA r
163	6	25.0	388	4	ABG49725	Abg49725 Arabidops	236	6	25.0	592	8	ADM98937	Adm98937 HMG-CoA r
164	6	25.0	388	3	ADK13902	Adk13902 Arabidops	237	6	25.0	592	8	ADM98827	Adm98827 HMG-CoA r
165	6	25.0	390	8	ADX72319	Adx72319 Plant ful	238	6	25.0	592	9	ADY52924	Ady52924 Thale cre
166	6	25.0	391	6	ABM68619	Abm68619 Photornab	239	6	25.0	592	9	ADY52374	Ady52374 Novel ket
167	6	25.0	392	9	ABE53803	Aeb53803 Drosophil	240	6	25.0	592	9	ADY51371	Ady51371 Arabidops
168	6	25.0	396	3	AGL13901	Agl13901 Arabidops	241	6	25.0	593	9	ADW18652	Adw18652 Pinus rad
169	6	25.0	396	3	AAG49724	Aag49724 Arabidops	242	6	25.0	598	3	AAG21937	Aag21937 Arabidops
170	6	25.0	398	3	AAG29336	Aag29336 Arabidops	243	6	25.0	601	4	ABB61643	Abb61643 Drosophil

244	6	25.0	602	7	AD030578	Add30578 Plant yie	317	6	25.0	960	7	ADK11471	Adk11471 Drosophil
245	6	25.0	602	8	AD141669	Adi14669 Plant tra	318	6	25.0	960	7	ADK11488	Adk11488 Drosophil
246	6	25.0	602	8	AD161491	Adi61491 A. thalia	319	6	25.0	968	8	ADO01020	ADO01020 Fruit fly
247	6	25.0	602	8	ADO02005	Ado02005 Thalecree	320	6	25.0	998	4	ABB60423	ABB60423 Drosophil
248	6	25.0	603	8	ADA89359	Ada89359 Drosophil	321	6	25.0	1001	6	ABU30822	ABU30822 Protein e
249	6	25.0	605	8	ADS43586	Ads43586 Bacterial	322	6	25.0	1023	6	ABP97078	ABP97078 Human G p
250	6	25.0	608	4	AAH82298	Aah82298 Arabidops	323	6	25.0	1046	4	ABB59307	Abb59307 Drosophil
251	6	25.0	610	4	ABE71317	Abb71317 Drosophil	324	6	25.0	1058	4	AAH68341	Aah68341 A human d
252	6	25.0	610	9	AD207750	Ad207750 HIV CON-S	325	6	25.0	1083	7	ABW85355	Abw85355 Human pro
253	6	25.0	613	4	ABB65716	Abb65716 Drosophil	326	6	25.0	1100	8	ADP99064	Adp99064 C. albica
254	6	25.0	623	3	AG41366	Ag41366 Arabidops	327	6	25.0	1111	7	ABW67097	Abw67097 Kinesin-1
255	6	25.0	627	3	AG41365	Ag41365 Arabidops	328	6	25.0	1111	8	ADL99368	Adl99368 Nanostroc
256	6	25.0	628	2	AAH88424	Aah88424 Arabidops	329	6	25.0	1111	8	ADN18760	Adn18760 Bacterial
257	6	25.0	628	3	AG41364	Ag41364 Arabidops	330	6	25.0	1113	6	ABR53293	ABR53293 Protein s
258	6	25.0	628	4	AAE01936	Aae01936 Arabidops	331	6	25.0	1113	7	ADK63560	Adk63560 Disease t
259	6	25.0	628	5	AAU93141	Aau93141 Arabidops	332	6	25.0	1138	2	AAH06461	Aah06461 BtPGS1245
260	6	25.0	628	7	AD015138	Ad015138 Thale cre	333	6	25.0	1138	2	AAH37214	Aah37214 B. t. toxi
261	6	25.0	628	7	ADH86843	Adh86843 Arabidops	334	6	25.0	1138	2	AAH46226	Aah46226 Bacillus
262	6	25.0	628	8	ADN73205	Adn73205 Thale cre	335	6	25.0	1138	9	ADR89429	Adr89429 cry7Aa. 1
263	6	25.0	645	4	ABB61545	Abb61545 Drosophil	336	6	25.0	1138	9	ADY59864	Ady59864 Bacillus
264	6	25.0	649	7	ADD25125	Ad25125 Drosophil	337	6	25.0	1164	4	ABB61495	Abb61495 Drosophil
265	6	25.0	653	6	ABU03135	Abu03135 Alpha amy	338	6	25.0	1169	4	ABB71663	Abb71663 Drosophil
266	6	25.0	653	8	ADU07484	Adu07484 Amino aci	339	6	25.0	1173	4	ABB62245	Abb62245 Drosophil
267	6	25.0	659	4	ABB64863	Abb64863 Drosophil	340	6	25.0	1173	4	ABB59646	Abb59646 Drosophil
268	6	25.0	660	4	ABB68167	Abb68167 Drosophil	341	6	25.0	1194	4	ABB59646	Abb59646 Drosophil
269	6	25.0	669	4	ABB59622	Abb59622 Drosophil	342	6	25.0	1195	4	ABB63694	Abb63694 Drosophil
270	6	25.0	674	7	ADK62474	Adk62474 Disease t	343	6	25.0	1234	8	ADP25437	Adp25437 Plasmodi
271	6	25.0	675	2	AAW00136	Aaw00136 Drosophil	344	6	25.0	1234	8	ADN20779	Adn20779 Bacterial
272	6	25.0	676	5	ABG93314	Abg93314 S. cerevi	345	6	25.0	1244	6	ABR53280	ABR53280 Protein s
273	6	25.0	688	5	ABP74039	Abp74039 Candida a	346	6	25.0	1244	7	ADK63590	Adk63590 Disease t
274	6	25.0	704	2	AAW11843	Aaw11843 Full leng	347	6	25.0	1244	8	ADN18772	Adn18772 Bacterial
275	6	25.0	706	4	ABB59652	Abb59652 Drosophil	348	6	25.0	1266	7	ADB70308	Adb70308 C. neofo
276	6	25.0	713	7	ADK11383	Adk11383 Drosophil	349	6	25.0	1266	7	ADP74638	Adp74638 Amino aci
277	6	25.0	716	4	ABB71561	Abb71561 Drosophil	350	6	25.0	1283	8	ADP74638	Adp74638 Amino aci
278	6	25.0	720	8	ADU23416	Adu23416 Bacterial	351	6	25.0	1314	6	ABR53132	ABR53132 Protein s
279	6	25.0	722	6	ABU23638	Abu23638 Protein e	352	6	25.0	1314	7	ADK63086	Adk63086 Disease t
280	6	25.0	732	4	ABB65450	Abb65450 Drosophil	353	6	25.0	1402	8	ADN22849	Adn22849 Bacterial
281	6	25.0	742	8	ADP99099	Adp99099 C. albica	354	6	25.0	1420	9	ABM92747	Abm92747 M. xanthu
282	6	25.0	761	4	ABB71561	Abb71561 Drosophil	355	6	25.0	1423	4	ABB71866	Abb71866 Drosophil
283	6	25.0	764	5	ABP73760	Abp73760 Candida a	356	6	25.0	1436	3	ABR18199	ABR18199 Plasmodi
284	6	25.0	765	4	ABR70099	ABR70099 Drosophil	357	6	25.0	1436	8	ABM82922	ABM82922 Human dia
285	6	25.0	790	4	ABE60771	ABE60771 Drosophil	358	6	25.0	1447	8	ADQ89646	ADQ89646 Antagonis
286	6	25.0	814	4	ABB68374	Abb68374 Drosophil	359	6	25.0	1464	4	ABB61199	Abb61199 Drosophil
287	6	25.0	837	6	ADU63527	Adu63527 Maliganat	360	6	25.0	1476	4	ABB58706	Abb58706 Drosophil
288	6	25.0	842	2	AAW00137	Aaw00137 Drosophil	361	6	25.0	1487	7	ABM88950	ABM88950 Rice abio
289	6	25.0	844	4	ABR65418	ABR65418 Drosophil	362	6	25.0	1491	8	ABM82920	ABM82920 Human dia
290	6	25.0	848	5	ABR53582	ABR53582 Lactococc	363	6	25.0	1491	8	ABM82921	ABM82921 Human dia
291	6	25.0	848	8	ADS29320	AdS29320 Bacterial	364	6	25.0	1501	5	AAU76762	Aau76762 Plasmodi
292	6	25.0	849	9	ABE10634	Aeb10634 Clade C e	365	6	25.0	1504	8	ADN19818	Adn19818 Bacterial
293	6	25.0	852	9	AD207734	Ad207734 HIV CON-S	366	6	25.0	1518	9	AEA23186	Aea23186 GPCR prot
294	6	25.0	856	4	ABB68808	Abb68808 Drosophil	367	6	25.0	1520	8	ADN22943	Adn22943 Bacterial
295	6	25.0	856	4	ABR60983	ABR60983 Drosophil	368	6	25.0	1520	8	ADN22944	Adn22944 Bacterial
296	6	25.0	856	7	ADJ37949	Adj37949 D melanog	369	6	25.0	1523	8	ABM84812	ABM84812 Human dia
297	6	25.0	865	7	ADH99075	Adh99075 LRPS-rela	370	6	25.0	1526	7	ADH61230	Adh61230 Rat Prote
298	6	25.0	916	4	ABB63615	Abb63615 Drosophil	371	6	25.0	1526	7	ADH44993	Adh44993 Rat Probe
299	6	25.0	916	8	ADO01008	Ado01008 Fruit fly	372	6	25.0	1530	7	ADN95295	Adn95295 Human BSC
300	6	25.0	916	8	ADS96718	Ads96718 Drosophil	373	6	25.0	1531	5	ABP67994	ABP67994 Human col
301	6	25.0	920	4	ABR62023	ABR62023 Drosophil	374	6	25.0	1531	5	AAO18890	Aao18890 Human ova
302	6	25.0	921	8	ADH99074	Adh99074 LRPS-rela	375	6	25.0	1531	5	ABG80433	ABG80433 Ant1-huma
303	6	25.0	921	8	ADJ49846	Adj49846 Oil-assoc	376	6	25.0	1531	6	ABU56492	Abu56492 Lung canc
304	6	25.0	922	8	ADJ49844	Adj49844 Oil-assoc	377	6	25.0	1531	6	ABR92156	ABR92156 Human cer
305	6	25.0	924	8	ADJ49847	Adj49847 Oil-assoc	378	6	25.0	1531	7	ADH44995	Adh44995 Human PRO
306	6	25.0	924	8	ADJ49845	Adj49845 Oil-assoc	379	6	25.0	1531	7	ADH61232	Adh61232 Human PRO
307	6	25.0	938	4	ABR60562	ABR60562 Drosophil	380	6	25.0	1531	8	ADH13197	Adh13197 Human mal
308	6	25.0	941	4	ABG25801	Abg25801 Novel hum	381	6	25.0	1531	8	ADL12474	Adl12474 Human ste
309	6	25.0	941	5	ABP74093	Abp74093 Candida a	382	6	25.0	1531	8	ADL70599	Adl70599 Cervical
310	6	25.0	943	4	ABR62085	ABR62085 Drosophil	383	6	25.0	1531	8	ADL26776	Adl26776 Human TOP
311	6	25.0	950	2	AAH06376	Aah06376 Product o	384	6	25.0	1531	8	ADN03718	Adn03718 Antipsori
312	6	25.0	950	8	ABH71271	ABH71271 Drosophil	385	6	25.0	1531	8	ADQ19281	Adq19281 Human sof
313	6	25.0	950	8	ADH43488	ADH43488 Bacterial	386	6	25.0	1531	8	ADQ89838	ADQ89838 Antagonis
314	6	25.0	959	3	ABH18194	ABH18194 Plasmodi	387	6	25.0	1531	9	ADX05548	ADX05548 Cyclin-de
315	6	25.0	960	4	ABH58434	ABH58434 Drosophil	388	6	25.0	1531	9	ADY14470	ADY14470 PRO poly
316	6	25.0	960	7	ADK11469	Adk11469 Drosophil	389	6	25.0	1531	9	ADY14468	ADY14468 PRO poly

390	6	25.0	1531	9	AE15084	Aea15084 Human pol	463	5	20.8	9	5	AAE31351	Aae31351 Human tyr
391	6	25.0	1540	8	ABM84811	Abm84811 Human dia	464	5	20.8	9	5	AAE31352	Aae31352 Human tyr
392	6	25.0	1545	8	ADSL10988	Adsl10988 Human the	465	5	20.8	9	6	ABJ20142	Abj20142 MHC bindi
393	6	25.0	1562	8	ABM82919	Abm82919 Human dia	466	5	20.8	9	8	ADP25771	Adp25771 Plaemodiu
394	6	25.0	1568	6	ABP70152	Abp70152 Amino aci	467	5	20.8	9	8	ADP25547	Adp25547 Plaemodiu
395	6	25.0	1572	2	AAW99301	Aaw99301 Human BAI	468	5	20.8	9	8	ADT40166	Adt40166 hSARS vir
396	6	25.0	1572	6	ABP81929	Abp81929 Human bra	469	5	20.8	9	8	ADS79583	Ads79583 SARS viru
397	6	25.0	1572	6	ADQ29004	Adq29004 Human nov	470	5	20.8	9	8	ADT37696	Adt37696 hSARS vir
398	6	25.0	1572	8	ADQ05172	Adq05172 Human G p	471	5	20.8	9	9	ADZ50678	Adz50678 Y. pestis
399	6	25.0	1573	7	ADC86417	Adc86417 Human GPC	472	5	20.8	10	4	AAAG86662	Aaag86662 Saccharom
400	6	25.0	1591	8	ADO29005	Ado29005 Mouse nov	473	5	20.8	10	4	AAAG86800	Aaag86800 Saccharom
401	6	25.0	1609	8	ADM90833	Adm90833 Human pha	474	5	20.8	10	4	ABP12285	Abp12285 HIV A02 s
402	6	25.0	1613	6	ABR41134	AbR41134 Human LRP	475	5	20.8	10	4	ABP12285	Abp12285 HIV A02 s
403	6	25.0	1613	7	ADB98801	Adb98801 Human LRP	476	5	20.8	10	5	ABB94839	Abb94839 CTL epito
404	6	25.0	1613	8	ADI27182	Adi27182 Mouse LRP	477	5	20.8	10	5	ABB95132	Abb95132 CTL epito
405	6	25.0	1613	8	ADI27183	Adi27183 Human LRP	478	5	20.8	12	5	ABG93666	Abg93666 Human Mit
406	6	25.0	1613	9	ADX06321	Adx06321 Cyclin-de	479	5	20.8	12	5	ABG93725	Abg93725 Human Mit
407	6	25.0	1621	4	AM25646	Aam25646 Human pro	480	5	20.8	14	7	ADF71051	Adf71051 Saccharom
408	6	25.0	1621	8	ABM80429	Abm80429 Tumour-as	481	5	20.8	15	8	ADM36120	Adm36120 RTN3 pept
409	6	25.0	1621	8	ADS12217	Ads12217 Human the	482	5	20.8	16	4	AAAM99487	Aaam99487 Vaccine r
410	6	25.0	1626	7	ADJ71211	Adj71211 Human hea	483	5	20.8	16	5	AAE17169	Aae17169 Meningoco
411	6	25.0	1626	8	ADQ89840	Adq89840 Antagonis	484	5	20.8	17	2	AAW17549	Aaw17549 Beta-B2-c
412	6	25.0	1664	2	AAW99462	Aaw99462 C.albican	485	5	20.8	17	5	AAU89944	Aau89944 Insulin/i
413	6	25.0	1664	5	AAE19799	Aae19799 Candida a	486	5	20.8	17	9	AEA43954	Aea43954 Anti-TPO
414	6	25.0	1664	5	AAU79331	Aau79331 Candida a	487	5	20.8	18	6	ABP82477	Abp82477 G protein
415	6	25.0	1664	7	ADC73265	Adc73265 Yeast Int	488	5	20.8	18	6	ABP82915	Abp82915 G protein
416	6	25.0	1664	7	ADM33264	Adm33264 Candida a	489	5	20.8	18	6	ADH16103	Adh16103 Gliadin r
417	6	25.0	1665	4	ABB64010	Abb64010 Drosophil	490	5	20.8	20	8	ADH16104	Adh16104 Gliadin r
418	6	25.0	1677	8	ADO17159	Ado17159 Novel exp	491	5	20.8	20	8	ADH15373	Adh15373 Gliadin r
419	6	25.0	1703	4	ABB66223	Abb66223 Drosophil	492	5	20.8	20	8	ADH15374	Adh15374 Gliadin r
420	6	25.0	1778	4	ABB60081	Abb60081 Drosophil	493	5	20.8	20	8	ADH15374	Adh15374 Gliadin r
421	6	25.0	1805	4	ABB65262	Abb65262 Drosophil	494	5	20.8	21	5	AAU89040	Aau89040 Insulin/i
422	6	25.0	1810	7	ADF70505	Adf70505 Orphan re	495	5	20.8	21	6	ADA03870	Ada03870 Insulin r
423	6	25.0	1893	4	ABB59829	Abb59829 Drosophil	496	5	20.8	21	7	ADH95083	Adh95083 Insulin r
424	6	25.0	1926	4	AAAG84915	Aaag84915 Shrimp wh	497	5	20.8	21	7	ADW35382	Adw35382 HLA bindi
425	6	25.0	1954	4	ABB59197	Abb59197 Drosophil	498	5	20.8	21	7	ADW34149	Adw34149 HLA bindi
426	6	25.0	1980	4	ABB67589	Abb67589 Drosophil	499	5	20.8	21	8	ADL67774	Adl67774 IGF-1R/IR
427	6	25.0	1987	4	ABB61083	Abb61083 Drosophil	500	5	20.8	21	8	ADM37619	Adm37619 Anti-IR f
428	6	25.0	2000	6	ABR52731	AbR52731 Protein s	501	5	20.8	21	9	ADX85960	Adx85960 HIV gp120
429	6	25.0	2000	7	ADK61970	Adk61970 Disease t	502	5	20.8	22	2	AAAR06590	Aaar06590 Interleuk
430	6	25.0	2006	8	ADB71277	Adb71277 Drosophil	503	5	20.8	22	9	ADV55048	Adv55048 G protein
431	6	25.0	2006	8	ADS96448	AdS96448 Drosophil	504	5	20.8	22	9	ADV54935	Adv54935 G protein
432	6	25.0	2023	4	ABB63487	Abb63487 Drosophil	505	5	20.8	22	9	ADV55154	Adv55154 G protein
433	6	25.0	2053	4	AAAB69135	AaB69135 M. catarr	506	5	20.8	23	2	AAW82478	Aaw82478 Neurospor
434	6	25.0	2071	3	AAAY84686	Aay84686 Amino aci	507	5	20.8	23	5	AAE22579	Aae22579 Drosophil
435	6	25.0	2071	4	AAE11052	Aae11052 Ashbya go	508	5	20.8	23	8	ADO55733	Ado55733 Neurospor
436	6	25.0	2150	5	AAO22566	Aao22566 Wooden le	509	5	20.8	24	2	AAAR06593	Aaar06593 Interleuk
437	6	25.0	2167	8	ADN19120	Adn19120 Bacterial	510	5	20.8	25	2	AAAR06594	Aaar06594 Interleuk
438	6	25.0	2175	4	ABB65698	Abb65698 Drosophil	511	5	20.8	25	5	ABG62549	Abg62549 Eubacteri
439	6	25.0	2280	4	ABB61650	Abb61650 Drosophil	512	5	20.8	26	2	AAAR06595	Aaar06595 Interleuk
440	6	25.0	2370	4	ABB60250	Abb60250 Drosophil	513	5	20.8	27	2	AAAR06596	Aaar06596 Interleuk
441	6	25.0	2406	4	ABB64198	Abb64198 Drosophil	514	5	20.8	28	2	AAAR06597	Aaar06597 Interleuk
442	6	25.0	3056	8	ADR43499	Adr43499 CSA-bind	515	5	20.8	28	6	ABR81914	AbR81914 Human int
443	6	25.0	3190	4	AAAB84634	AaB84634 Amino aci	516	5	20.8	28	9	ADZ36485	Adz36485 Human bra
444	6	25.0	3275	4	ABB70437	Abb70437 Drosophil	517	5	20.8	30	4	AAAM22035	Aam22035 Peptide #
445	6	25.0	3275	7	ADK11301	Adk11301 Drosophil	518	5	20.8	30	4	ABB44421	Abb44421 Peptide #
446	6	25.0	3536	4	ABB65480	Abb65480 Drosophil	519	5	20.8	30	4	AAAM38408	Aam38408 Peptide #
447	6	25.0	3614	4	ABB62664	Abb62664 Drosophil	520	5	20.8	30	4	ABB27268	Abb27268 Protein #
448	6	25.0	3973	3	AAAB18253	AaB18253 Plaemodiu	521	5	20.8	30	4	AAAM78163	Aam78163 Human bon
449	5	20.8	5	2	AAW00431	Aaw00431 Interleuk	522	5	20.8	30	4	AAAM65501	Aam65501 Human liv
450	5	20.8	7	1	AAAP71426	Aap71426 Immunomod	523	5	20.8	30	4	ABG59809	Abg59809 Human bra
451	5	20.8	8	2	AAW11529	Aaw11529 Interleuk	524	5	20.8	30	5	ABG47175	Abg47175 Human pep
452	5	20.8	9	2	AAW11528	Aaw11528 Interleuk	525	5	20.8	30	5	AAU84914	Aau84914 Human Tyr
453	5	20.8	9	2	AAW147083	Aaw147083 Immunogen	526	5	20.8	30	5	AAU84915	Aau84915 Human Tyr
454	5	20.8	9	4	ABP12131	Abp12131 HIV A02 s	527	5	20.8	31	9	ABM95343	Abm95343 M. xanthu
455	5	20.8	9	5	ABB94781	Abb94781 CTL epito	528	5	20.8	33	3	AAAG56606	Aaag56606 Arabidops
456	5	20.8	9	5	ABB94700	Abb94700 CTL epito	529	5	20.8	33	3	ADX91570	Adx91570 Plant ful
457	5	20.8	9	5	ABB94890	Abb94890 CTL epito	530	5	20.8	35	3	AAAG55191	Aaag55191 Arabidops
458	5	20.8	9	5	ABB94512	Abb94512 CTL epito	531	5	20.8	37	6	ABP59758	Abp59758 HIV immun
459	5	20.8	9	5	ABB95000	Abb95000 CTL epito	532	5	20.8	37	6	ABP59815	Abp59815 HIV immun
460	5	20.8	9	5	ABB94602	Abb94602 CTL epito	533	5	20.8	37	8	ADR58083	Adr58083 Novel ant
461	5	20.8	9	5	ABB95087	Abb95087 CTL epito	534	5	20.8	37	8	ADR58140	Adr58140 Novel ant
462	5	20.8	9	5	AAE31350	Aae31350 Human tyr	535	5	20.8	37	9	ADX85928	Adx85928 HIV gp120



536	5	20.8	37	9	ADX85770	Adx85770 HIV clade	609	5	20.8	66	7	ADI15883	Adi15883 Human pp
537	5	20.8	39	3	AAG59863	Aag59863 Arabidops	610	5	20.8	67	5	Aao22532	Aao22532 Small aci
538	5	20.8	39	8	ADH12867	Adh12867 Francisel	611	5	20.8	67	5	Aao22524	Aao22524 Small aci
539	5	20.8	40	8	ABO57415	Abos7415 Human gen	612	5	20.8	67	9	ADV86780	Adv86780 Alpha/bet
540	5	20.8	41	4	ABBA40366	Abba40366 Peptide #	613	5	20.8	67	9	ADV86772	Adv86772 Alpha/bet
541	5	20.8	41	4	AAW34072	Aam34072 Peptide #	614	5	20.8	68	5	Aao22518	Aao22518 Small aci
542	5	20.8	41	4	AAW33890	Aam33890 Human bon	615	5	20.8	68	5	ADK36086	Adk36086 Novel hum
543	5	20.8	41	4	AAW61175	Aam61175 Human bra	616	5	20.8	68	7	ABO63943	Abos63943 Klebsiell
544	5	20.8	41	4	ABG55641	Abg55641 Human liv	617	5	20.8	68	9	ADV86766	Adv86766 Alpha/bet
545	5	20.8	41	4	ABG19605	Abg19605 Novel hum	618	5	20.8	69	4	ABB62675	Abb62675 Drosophil
546	5	20.8	41	5	ABG43778	Abg43778 Human pep	619	5	20.8	69	5	Aao22513	Aao22513 Small aci
547	5	20.8	42	4	AAU17733	Aau17733 Novel hum	620	5	20.8	69	5	Aao22506	Aao22506 Small aci
548	5	20.8	42	7	ADG41113	Adg41113 Human res	621	5	20.8	69	9	ADV86761	Adv86761 Alpha/bet
549	5	20.8	42	7	ADG41113	Adg41113 Human res	622	5	20.8	69	9	ADV86761	Adv86761 Alpha/bet
550	5	20.8	42	9	AEBA3263	Aeb43263 Human LRP	623	5	20.8	70	9	ADV86753	Adv86753 Alpha/bet
551	5	20.8	44	6	AAE30231	Aae30231 Human Lp2	624	5	20.8	70	9	ADV86773	Adv86773 Alpha/bet
552	5	20.8	44	6	AAE30243	Aae30243 Human Lp2	625	5	20.8	71	5	ABP00056	Abp00056 Human ORF
553	5	20.8	44	8	ADS06191	Adso6191 Staphyloc	626	5	20.8	72	5	Aao22530	Aao22530 Small aci
554	5	20.8	46	4	AAW18239	Aam18239 Peptide #	627	5	20.8	72	9	ADV86778	Adv86778 Alpha/bet
555	5	20.8	46	4	ABB37270	Abb37270 Peptide #	628	5	20.8	73	9	ADV86778	Adv86778 Alpha/bet
556	5	20.8	46	4	AAW30730	Aam30730 Peptide #	629	5	20.8	73	4	AAW58205	Aab58205 Lung canc
557	5	20.8	46	4	ABB32018	Abb32018 Peptide #	630	5	20.8	73	4	AAW58561	Aam58561 Human imm
558	5	20.8	46	4	ABP22559	Abp22559 Protein #	631	5	20.8	73	5	ABG59908	Abg59908 Human liv
559	5	20.8	46	4	AAW70400	Aam70400 Human bon	632	5	20.8	73	5	ABP03388	Abp03388 Human ORF
560	5	20.8	46	4	AAW57970	Aam57970 Human bra	633	5	20.8	74	5	AAG32700	Aag32700 Zea mays
561	5	20.8	46	4	ABG52092	Abg52092 Human liv	634	5	20.8	74	5	ABP02044	Abp02044 Human ORF
562	5	20.8	46	5	ABG40041	Abg40041 Human pep	635	5	20.8	74	5	ABP03426	Abp03426 Human ORF
563	5	20.8	46	9	AEA32754	Aea32754 HTH AraC	636	5	20.8	75	4	ABP07318	Abp07318 Human ORF
564	5	20.8	49	4	AAQ80066	Aag80066 Chemokine	637	5	20.8	75	4	ABP11033	Abp11033 Drosophil
565	5	20.8	49	4	AAO05160	Aao05160 Human pol	638	5	20.8	75	8	ADO41438	Ado41438 Therapeut
566	5	20.8	50	5	ABP09330	Abp09330 Human ORF	639	5	20.8	75	8	ADP96016	Adp96016 Human bin
567	5	20.8	51	3	AAQ39100	Aab39100 Human sec	640	5	20.8	77	5	ABP97784	Abp97784 Human sec
568	5	20.8	51	4	ABP69142	Abp69142 Drosophil	641	5	20.8	77	7	ADC00298	Adc00298 Enterohae
569	5	20.8	52	6	ABP79893	Abp79893 N. gonorr	642	5	20.8	78	2	AAV36173	Aay36173 Human sec
570	5	20.8	52	7	ADC21299	Adc21299 Mouse MHC	643	5	20.8	78	2	AAV36220	Aay36220 Human sec
571	5	20.8	52	7	ADC21295	Adc21295 Mouse MHC	644	5	20.8	78	7	ADJ45978	Adj45978 Novel hum
572	5	20.8	52	7	ADC21298	Adc21298 Mouse MHC	645	5	20.8	78	7	ADJ46072	Adj46072 Novel hum
573	5	20.8	52	8	ADO41426	Ado41426 Therapeut	646	5	20.8	78	8	ADP19481	Adp19481 Human sec
574	5	20.8	52	8	ADO41424	Ado41424 Therapeut	647	5	20.8	79	3	AAW61490	Aag61490 Arabidops
575	5	20.8	52	8	ADP96004	Adp96004 Human bin	648	5	20.8	79	3	AAW57366	Aag57366 Arabidops
576	5	20.8	52	8	ADP96002	Adp96002 Human bin	649	5	20.8	79	4	AAW82427	Aam82427 Human imm
577	5	20.8	54	3	AAQ02193	Aag02193 Human sec	650	5	20.8	79	4	AAW94524	Aam94524 Human rep
578	5	20.8	54	7	ADB46138	Adb46138 Plasmodi	651	5	20.8	79	4	ABB10848	Aab10848 Human ova
579	5	20.8	54	8	ADSO7766	Adso7766 Staphyloc	652	5	20.8	80	2	AAW13397	Aar13397 HLA-DRW12
580	5	20.8	55	4	AAO11300	Aao11300 Human pol	653	5	20.8	80	2	AAW13396	Aar13396 HLA-DRW12
581	5	20.8	56	2	AAQ05437	Ado05437 Staphyloc	654	5	20.8	80	5	ADH32781	Adh32781 Yeast smo
582	5	20.8	56	2	AAW60476	Aay60476 Human nor	655	5	20.8	82	3	AAW83381	Abos83381 Arabidops
583	5	20.8	56	4	ABB15194	Abp15194 Human ner	656	5	20.8	82	3	ADY24612	Ady24612 Plant ful
584	5	20.8	56	5	ABP10450	Abp10450 Human ORF	657	5	20.8	82	8	ABO83381	Abos83381 Pseudomon
585	5	20.8	56	6	ABP18948	Abp18948 Human ORF	658	5	20.8	83	5	ABP34141	Abp34141 Human DNA
586	5	20.8	56	6	ABP80177	Abp80177 N. gonorr	659	5	20.8	83	6	ABU32019	Abu32019 Protein e
587	5	20.8	56	6	ADA95369	Ada95369 Protein d	660	5	20.8	83	7	ADH87090	Adh87090 Enterococ
588	5	20.8	57	5	ABP07846	Abp07846 Human ORF	661	5	20.8	83	8	ADK99934	Adk99934 Streptoco
589	5	20.8	58	2	AAW10753	Aar10753 Non-A non	662	5	20.8	84	8	ADK99932	Adk99932 Streptoco
590	5	20.8	58	2	AAW10756	Aar10756 Non-A non	663	5	20.8	84	8	ADK99932	Adk99932 Streptoco
591	5	20.8	59	2	AAW12736	Aay12736 Human 5'	664	5	20.8	85	8	ADK99929	Adk99929 Streptoco
592	5	20.8	59	4	ABB17799	Abb17799 Human ner	665	5	20.8	85	8	ADK99930	Adk99930 Streptoco
593	5	20.8	60	3	AAW19825	Aag19825 Arabidops	666	5	20.8	85	8	ADK99927	Adk99927 Streptoco
594	5	20.8	60	4	AAO05547	Aao05547 Human pol	667	5	20.8	85	8	ADK99931	Adk99931 Streptoco
595	5	20.8	61	4	AAU52950	Aau52950 Propionib	668	5	20.8	85	8	ADK99933	Adk99933 Streptoco
596	5	20.8	61	5	ABP10643	Abp10643 Human ORF	669	5	20.8	86	3	AAW57365	Aag57365 Arabidops
597	5	20.8	61	6	ABM49469	Abm49469 Propionib	670	5	20.8	86	3	AAW61489	Aag61489 Arabidops
598	5	20.8	63	3	AAQ02818	Aag02818 Human sec	671	5	20.8	86	8	ADK99928	Adk99928 Streptoco
599	5	20.8	63	7	ADB46137	Adb46137 Plasmodi	672	5	20.8	86	8	ADK99935	Adk99935 Streptoco
600	5	20.8	63	7	ADC96482	Adc96482 E. faeciu	673	5	20.8	88	6	ABO14007	Abol14007 Novel hum
601	5	20.8	63	8	ADJ06020	Adj06020 M. catarr	674	5	20.8	88	6	ADN60704	Adn60704 Human sec
602	5	20.8	64	4	AAW488153	Aam488153 Human imm	675	5	20.8	89	2	AAW14301	Aay14301 Protein e
603	5	20.8	64	4	AAU44970	Aau44970 Propionib	676	5	20.8	89	2	AAW14306	Aay14306 Protein e
604	5	20.8	64	6	ABW41489	Abw41489 Propionib	677	5	20.8	89	2	AAW14336	Aay14336 Protein e
605	5	20.8	65	4	ABG05578	Abg05578 Novel hum	678	5	20.8	89	2	AAW14307	Aay14307 Protein e
606	5	20.8	65	7	ADF06501	Adf06501 Bacterial	679	5	20.8	89	2	AAW27602	Aay27602 Human sec
607	5	20.8	66	2	AAR97241	Aar97241 Mutant fo	680	5	20.8	89	3	AAW61072	Aag61072 Arabidops
608	5	20.8	66	7	ADD22416	Add22416 HLA-B46 T	681	5	20.8	89	3	AAW44502	Aag44502 Arabidops

682	5	20.8	89	4	ABB68584	Abb68584 Drosophil	755	5	20.8	103	8	ADM32932	Adm32932 Amino aci
683	5	20.8	89	4	AAB87848	Aab87848 Protein e	756	5	20.8	104	4	AAO00241	Aao00241 Human pol
684	5	20.8	89	4	AAB87868	Aab87868 Protein e	757	5	20.8	104	5	ABP08659	Abp08659 Human ORF
685	5	20.8	89	4	AAB87849	Aab87849 Protein e	758	5	20.8	104	6	ABU02257	Abu02257 S. pneumo
686	5	20.8	89	4	AAB87875	Aab87875 Protein e	759	5	20.8	104	6	ADK46563	Adk46563 Streptoco
687	5	20.8	89	8	ADG78413	Adg78413 Human sec	760	5	20.8	104	8	ADK46563	Adk46563 Streptoco
688	5	20.8	90	4	AAm18336	Aam18336 Peptide #	761	5	20.8	105	4	AAU20778	Aau20778 Human nov
689	5	20.8	90	4	ABB37369	Abb37369 Peptide #	762	5	20.8	105	8	ADX71269	Adx71269 Plant ful
690	5	20.8	90	4	AAm30822	Aam30822 Peptide #	763	5	20.8	105	8	ADG75279	Adg75279 Human col
691	5	20.8	90	4	ABB32118	Abb32118 Peptide #	764	5	20.8	106	4	AAO13415	Aao13415 Human pol
692	5	20.8	90	4	ABB22659	Abb22659 Protein #	765	5	20.8	107	9	AEb38713	Aeb38713 L. pneumo
693	5	20.8	90	4	AAm70499	Aam70499 Human bon	766	5	20.8	108	4	ABB62825	Abb62825 Drosophil
694	5	20.8	90	4	AAm58059	Aam58059 Human bra	767	5	20.8	108	4	AAU69511	Aau69511 Human pur
695	5	20.8	90	4	AGS52181	Ag52181 Human liv	768	5	20.8	108	5	ABP26894	Abp26894 Streptoco
696	5	20.8	90	4	AAO05942	Aao05942 Peptide #	769	5	20.8	108	5	AAU83193	Aau83193 Novel sec
697	5	20.8	90	4	ABG04097	Abg04097 Novel hum	770	5	20.8	108	6	ABU46750	Abu46750 Protein e
698	5	20.8	90	5	ABG40139	Abg40139 Human pep	771	5	20.8	108	7	ADB65292	Adb65292 Synchocy
699	5	20.8	91	2	AAW10494	Aaw10494 Beta1 reg	772	5	20.8	109	5	ABP60792	Abp60792 Synchocy
700	5	20.8	91	2	AAW10501	Aaw10501 Beta1 reg	773	5	20.8	109	5	ABP60836	Abp60836 Synchocy
701	5	20.8	91	5	ABP06061	Abp06061 Human ORF	774	5	20.8	109	6	ABU00723	Abu00723 S. pneumo
702	5	20.8	91	8	ADO59295	Ado59295 TRAC*01 g	775	5	20.8	109	7	ADF58816	Adf58816 Human pol
703	5	20.8	92	2	AAW74820	Aaw74820 Human sec	776	5	20.8	109	8	ADK47455	Adk47455 Streptoco
704	5	20.8	92	2	AAy13124	Aay13124 Human sec	777	5	20.8	110	4	ABB70506	Abb70506 Drosophil
705	5	20.8	92	3	ABG19824	Abg19824 Arabidops	778	5	20.8	110	5	ABG64921	Abg64921 Human alb
706	5	20.8	92	5	ABG95271	Abg95271 Human nov	779	5	20.8	110	5	ABG64923	Abg64923 Human alb
707	5	20.8	92	6	ABO34465	Ab034465 Region of	780	5	20.8	110	5	ABB77008	Abb77008 Human pro
708	5	20.8	92	7	AD123126	Ad123126 Novel hum	781	5	20.8	110	5	ABB77030	Abb77030 Human pro
709	5	20.8	92	8	ADH74128	Adh74128 Human sec	782	5	20.8	110	6	ADA54138	Ada54138 Human pro
710	5	20.8	93	4	ABB56498	Abb56498 Murine si	783	5	20.8	110	8	ADL78190	Adl78190 Albumin f
711	5	20.8	94	3	AAb52507	Aab52507 Helicobac	784	5	20.8	110	8	ADL78188	Adl78188 Albumin f
712	5	20.8	95	3	AAb24088	Aab24088 Arabidops	785	5	20.8	111	3	ABb32917	Abb32917 Pinus rad
713	5	20.8	95	4	AAO240476	Aao240476 Human pol	786	5	20.8	111	6	ADB09627	Adb09627 Alloiococ
714	5	20.8	96	4	AAU18132	Aau18132 Novel hum	787	5	20.8	111	7	ABM87142	Abm87142 Rice abio
715	5	20.8	96	4	AAU17045	Aau17045 Human nov	788	5	20.8	111	8	ADT56893	Adt56893 Plant T-c
716	5	20.8	96	4	ABB10351	Abb10351 Human cDN	789	5	20.8	112	3	AAW36112	Aaw36112 Human T-c
717	5	20.8	96	4	AAU19897	Aau19897 Novel hum	790	5	20.8	112	3	AAg61071	Aag61071 Arabidops
718	5	20.8	96	5	ABJ05759	Abj05759 Novel hum	791	5	20.8	112	3	ABP41468	Abp41468 Human ova
719	5	20.8	96	5	ABP69398	Abp69398 Human pol	792	5	20.8	112	6	ABU44610	Abu44610 Protein e
720	5	20.8	97	2	AAW72386	Aaw72386 Pathogen	793	5	20.8	113	2	AAW36108	Aaw36108 Human T-c
721	5	20.8	97	3	AAg61700	Aag61700 Arabidops	794	5	20.8	113	3	AAb33318	Aab33318 Pinus rad
722	5	20.8	97	4	AAm14490	Aam14490 Peptide #	795	5	20.8	113	3	AAg58716	Aag58716 Arabidops
723	5	20.8	97	4	AAg62689	Aag62689 Human sac	796	5	20.8	113	3	AAg59230	Aag59230 Arabidops
724	5	20.8	97	4	ABb33438	Abb33438 Peptide #	797	5	20.8	113	4	AAU37831	Aau37831 Streptoco
725	5	20.8	97	4	AAm26903	Aam26903 Peptide #	798	5	20.8	113	6	ABP81549	Abp81549 Streptoco
726	5	20.8	97	4	ABB28263	Abb28263 Human pep	799	5	20.8	113	6	ABU45863	Abu45863 Protein e
727	5	20.8	97	4	ABB18897	Abb18897 Protein #	800	5	20.8	113	7	ABO61614	Ab061614 Klebsiell
728	5	20.8	97	4	AAm66617	Aam66617 Human bra	801	5	20.8	114	6	ABP79241	Abp79241 N. gonorr
729	5	20.8	97	4	AAm54223	Aam54223 Human bra	802	5	20.8	114	6	ADR94295	Adr94295 Novel S.
730	5	20.8	97	4	ABG48285	Abg48285 Human liv	803	5	20.8	114	9	AEA58165	Aea58165 Streptoco
731	5	20.8	97	4	AAm02217	Aam02217 Peptide #	804	5	20.8	115	4	AAm91128	Aam91128 Human imm
732	5	20.8	97	5	ABG36269	Abg36269 Human pep	805	5	20.8	115	8	ADY24879	Ady24879 Plant ful
733	5	20.8	97	9	ADW97159	Adw97159 Human IL-	806	5	20.8	116	8	AAy11126	Aay11126 S. pneumo
734	5	20.8	98	6	ADA41194	Ada41194 Human sec	807	5	20.8	117	2	AAU21852	Aau21852 Human car
735	5	20.8	98	7	ADC74396	Adc74396 Human sec	808	5	20.8	118	4	AAU21852	Aau21852 Human car
736	5	20.8	98	8	ADX94498	Adx94498 Plant ful	809	5	20.8	118	6	ADB09625	Adb09625 Alloiococ
737	5	20.8	99	3	AAg19823	Ag19823 Arabidops	810	5	20.8	118	7	ADE45820	Ade45820 Human car
738	5	20.8	99	3	AAb38393	Abb38393 Human sec	811	5	20.8	118	7	ABO66138	Ab066138 Klebsiell
739	5	20.8	99	9	AEA32810	Aea32810 HTH AraC	812	5	20.8	118	8	ADJ07238	Adj07238 Human car
740	5	20.8	99	9	AEA32637	Aea32637 AraC-Xy1S	813	5	20.8	118	9	AEA89797	Aea89797 Antibody
741	5	20.8	102	3	AAg15648	Aag15648 Arabidops	814	5	20.8	118	9	AEA89796	Aea89796 Antibody
742	5	20.8	102	4	AAm14940	Aam14940 Peptide #	815	5	20.8	118	9	AEA44069	Aea44069 Anti-TPO
743	5	20.8	102	4	ABB33909	Abb33909 Peptide #	816	5	20.8	118	9	AEA44073	Aea44073 Anti-TPO
744	5	20.8	102	4	AAm27370	Aam27370 Peptide #	817	5	20.8	119	3	AAO20095	Aao20095 Protein e
745	5	20.8	102	4	ABB28730	Abb28730 Peptide #	818	5	20.8	119	4	AAO10522	Aao10522 Human pol
746	5	20.8	102	4	ABB19350	Abb19350 Protein #	819	5	20.8	119	9	AAg91781	Aag91781 C. glutami
747	5	20.8	102	4	AAm67078	Aam67078 Human bon	820	5	20.8	119	9	ABE41904	Aeb41904 L. pneumo
748	5	20.8	102	4	AAW54676	Aaw54676 Human bra	821	5	20.8	120	3	AAg00209	Aag00209 Human sec
749	5	20.8	102	4	ABG48744	Abg48744 Peptide #	822	5	20.8	121	3	AAg24879	Aag24879 Arabidops
750	5	20.8	102	4	AAW02668	Aaw02668 Peptide #	823	5	20.8	121	1	AAp90402	Aap90402 Plasmodiu
751	5	20.8	102	5	ABG36737	Abg36737 Human pep	824	5	20.8	122	3	AAg57502	Aag57502 Arabidops
752	5	20.8	102	8	ADY12921	Ady12921 Plant ful	825	5	20.8	122	8	ADX90625	Adx90625 Plant ful
753	5	20.8	103	5	ABP60775	Abp60775 Listeria	826	5	20.8	123	2	AAy20151	Aay20151 B. burgdo
754	5	20.8	103	5	ABb48334	Abb48334 Listeria	827	5	20.8	124	8	ADx91889	Adx91889 Plant ful

828	2	AY20107	B. burgdo	901	5	20.8	149	3	AAG37353	Arabidops
829	4	AA19366	Peptide #	902	5	20.8	149	4	ABG05579	Novel hum
830	4	ABB38735	Peptide #	903	5	20.8	150	3	AG49726	Arabidops
831	5	AA332205	Peptide #	904	5	20.8	150	3	AG36567	Arabidops
832	4	ABB23789	Protein #	905	5	20.8	150	4	AG31651	Novel hum
833	4	AA171924	Human bon	906	5	20.8	150	8	ADL05811	M. catarr
834	4	AA193669	Human bra	907	5	20.8	150	8	ABO58682	Human gen
835	4	ABG53607	Human liv	908	5	20.8	151	2	AY20106	B. burgdo
836	5	ABG41738	Human pep	909	5	20.8	151	5	ABP29660	Streptoco
837	7	ABO60903	Klebsiell	910	5	20.8	151	5	ABP25611	Streptoco
838	5	ABP29336	Streptoco	911	5	20.8	151	6	ABU00970	S. pneumo
839	4	AAU59789	Propionib	912	5	20.8	151	6	ADA35142	Acinetoba
840	4	AAU18333	Human end	913	5	20.8	151	6	ADK99925	Streptoco
841	6	ABM56308	Propionib	914	5	20.8	151	8	ADM92108	S. pneumon
842	7	ADH88549	Enterococ	915	5	20.8	151	9	ADM42569	Human his
843	4	ABG68828	Drosophil	916	5	20.8	151	9	ADM42562	Human his
844	4	AGG78794	Human myo	917	5	20.8	152	3	AGG16405	Arabidops
845	4	AAO07135	Human pol	918	5	20.8	152	3	AGG16329	Arabidops
846	3	AAO22337	Arabidops	919	5	20.8	152	4	ABG64818	Drosophil
847	5	ABP25806	Streptoco	920	5	20.8	152	7	ADC75026	Soluble A
848	8	ADH89511	Streptoco	921	5	20.8	153	4	ABG63555	Drosophil
849	8	ADV82927	Streptoco	922	5	20.8	153	4	AAW34297	Peptide #
850	8	ADV80764	Streptoco	923	5	20.8	153	4	AAW74161	Human bon
851	6	ABU58165	Soybean s	924	5	20.8	153	4	AAW78750	Human cal
852	6	ABG05986	Novel hum	925	5	20.8	153	4	ABG55944	Human liv
853	7	ADP60242	Human con	926	5	20.8	153	5	ABG44094	Human pep
854	3	AGS58005	Arabidops	927	5	20.8	153	8	ADU02769	Novel hum
855	3	AGG16331	Arabidops	928	5	20.8	153	8	ADV89841	Streptoco
856	5	ABU51077	Halobac	929	5	20.8	153	8	ADV81094	Streptoco
857	8	ADQ97797	Mouse can	930	5	20.8	153	8	ADV83231	Streptoco
858	3	AGG16330	Arabidops	931	5	20.8	154	8	ADX72268	Plant ful
859	9	ABE38671	L. pneumo	932	5	20.8	155	2	AAV41230	H. pylori
860	3	AGS57501	Arabidops	933	5	20.8	155	4	ABB70923	Drosophil
861	3	AGS57501	Arabidops	934	5	20.8	155	4	ABG94629	Human pro
862	9	AEA19972	Novel hum	935	5	20.8	155	4	AGG81811	S. epider
863	3	ABE16371	Eucalyptu	936	5	20.8	155	8	ADT49815	Human CAM
864	3	AGS73364	Arabidops	937	5	20.8	156	2	AAW20891	H. pylori
865	3	AGG61488	Arabidops	938	5	20.8	156	3	AGG09402	Arabidops
866	7	ADD41547	Diphenol	939	5	20.8	156	3	AGS58800	Arabidops
867	9	ADY64668	S. manson	940	5	20.8	157	3	AGG23969	Arabidops
868	6	ABO15030	Human NOV	941	5	20.8	157	4	AAO01883	Human pol
869	6	AO29686	Human fat	942	5	20.8	158	4	ABG60559	Drosophil
870	7	ADB65335	Human pro	943	5	20.8	158	8	ABG68146	C. annuop
871	8	ADG97800	Human can	944	5	20.8	160	3	AA161538	Bacteriop
872	3	AG49727	Arabidops	945	5	20.8	160	4	AA165338	Bacteriop
873	3	AGG36206	Arabidops	946	5	20.8	160	9	AA165338	Bacteriop
874	4	ABB70473	Drosophil	947	5	20.8	160	9	AA165338	Bacteriop
875	4	ABF07896	Human ORP	948	5	20.8	161	4	AAU01103	Gene 41 H
876	5	ABG24087	Arabidops	949	5	20.8	161	6	ABR81867	Human int
877	5	AGG24087	Arabidops	949	5	20.8	161	9	AD236442	Human int
878	3	AGG32336	Arabidops	950	5	20.8	162	4	ABG68542	Arabidops
879	3	AGG32336	Arabidops	951	5	20.8	162	4	ABG68542	Arabidops
880	4	ABB71001	Drosophil	952	5	20.8	163	6	ABU27002	Protein e
881	2	AAV35239	Chlamydia	953	5	20.8	163	7	ADC00906	Enteroha
882	4	AG47273	Arabidops	954	5	20.8	164	7	ADF07977	Bacterial
883	4	AAU19297	Human G p	955	5	20.8	164	9	ADY66280	S. manson
884	4	ABG14559	Novel hum	956	5	20.8	166	3	AGG37352	Arabidops
885	7	AD121616	Novel hum	957	5	20.8	166	5	ABG55545	Lactococ
886	3	AGG32631	Eucalyptu	958	5	20.8	166	7	ADD30590	Plant yie
887	3	AGG47272	Arabidops	959	5	20.8	166	8	ADI44059	Plant tra
888	3	AGG11795	Arabidops	960	5	20.8	166	8	AD161341	A. thalia
889	8	ADT55945	Plant pol	961	5	20.8	166	8	ADO02289	Thalecres
890	4	AA18157	Peptide #	962	5	20.8	167	3	AGG36566	Arabidops
891	4	ABB37189	Peptide #	963	5	20.8	167	4	AGG36566	Arabidops
892	4	AA18157	Peptide #	964	5	20.8	167	4	AGG36566	Arabidops
893	4	ABR31951	Peptide #	965	5	20.8	167	4	AGG36566	Arabidops
894	4	ABR22492	Protein #	966	5	20.8	167	9	ABM94510	M. xanthu
895	4	AAW70318	Human bon	967	5	20.8	168	2	AAW74963	Human sec
896	4	AAW57900	Human bra	968	5	20.8	168	3	AGG40230	Human sec
897	4	ABG52018	Human liv	969	5	20.8	168	3	AGG10710	Arabidops
898	4	AAW05781	Peptide #	970	5	20.8	168	3	AGG10710	Arabidops
899	5	ABG39964	Human pep	971	5	20.8	168	6	ABO34617	Region of
900	2	AA20150	B. burgdo	972	5	20.8	168	8	ADH74280	Human sec

974 5 20.8 169 3 AAG36205 Arabidops  
975 5 20.8 170 3 AAG37351 Arabidops  
976 5 20.8 170 5 ABP73269 Candida a  
977 5 20.8 171 3 AAB40227 Gene 36 h  
978 5 20.8 171 3 AAB40228 Human sec  
979 5 20.8 171 3 AAG40004 Arabidops  
980 5 20.8 171 3 AAG36565 Arabidops  
981 5 20.8 171 3 AAG36565 Arabidops  
982 5 20.8 172 3 AAG17218 Arabidops  
983 5 20.8 172 3 AAG10709 Arabidops  
984 5 20.8 172 3 AAG47688 Arabidops  
985 5 20.8 172 8 ADX87709 Plant ful  
986 5 20.8 174 6 AAE33453 Mouse i-E  
987 5 20.8 175 3 AAG20202 Arabidops  
988 5 20.8 175 4 AAU23698 Novel hum  
989 5 20.8 176 5 ABB55408 Lactococc  
990 5 20.8 176 5 ABB54197 Lactococc  
991 5 20.8 177 2 AAY50043 Pseudomon  
992 5 20.8 177 3 AAG58004 Arabidops  
993 5 20.8 177 3 AAG36404 Arabidops  
994 5 20.8 177 5 ABP27025 Streptoco  
995 5 20.8 177 6 ABU41559 Protein e  
996 5 20.8 178 5 ABP28585 Streptoco  
997 5 20.8 178 6 ABU46406 Protein e  
998 5 20.8 178 9 ADX57001 Streptoco  
999 5 20.8 178 9 ADX57003 Streptoco  
1000 5 20.8 178 9 ADX57005 Streptoco

ALIGNMENTS

RESULT 1  
AAG01570  
ID AAG01570 standard; protein; 95 AA.  
AC AAG01570;  
XX  
DT 06-OCT-2000 (first entry)  
XX  
DE Human secreted protein, SEQ ID NO: 5651.  
XX  
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
KW Gene therapy; chromosome mapping.  
XX  
OS Homo sapiens.  
XX  
PN EP1033401-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 21-FEB-2000; 2000EP-00200610.  
XX  
PR 26-FEB-1999; 99US-0122487P.  
XX  
PA (GEST ) GENSET.  
XX  
PI Dumas Milne Edwards J, Duclert A, Giordano J;  
XX  
DR WPI; 2000-500381/45.  
DR N-PSDB; AAC01576.  
XX  
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for  
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.  
XX  
PS Claim 13; SEQ ID NO 5651; 71pp + Sequence Listing; English.  
XX  
CC The present sequence is a polypeptide encoded by one of a large number of  
CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were  
CC prepared from total human RNAs or polyA+ RNAs derived from 30 different  
CC tissues. EST sequences usually correspond mainly to the 3' untranslated  
CC region (UTR) of the mRNA because they are often obtained from oligo-dT

CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA  
CC sequences derived from the 5' ends of mRNAs and even in those cases where  
CC longer cDNA sequences have been obtained, the full 5' UTR is rarely  
CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can  
CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs  
CC are also used in diagnostic, forensic, gene therapy and chromosome  
CC mapping procedures. They are used to obtain upstream regulatory sequences  
CC and to design expression and secretion vectors  
XX  
SQ Sequence 95 AA;  
Query Match 100.0%; Score 24; DB 3; Length 95;  
Best Local Similarity 100.0%; Pred. No. 5.1e-17;  
Matches 24; Conservative - 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 LRFDSTQKSIPEQETNNNSSFYT 24  
Db 35 LRFDSTQKSIPEQETNNNSSFYT 58  
RESULT 2  
AAG76051  
ID AAG76051 standard; protein; 209 AA.  
XX  
AC AAG76051;  
XX  
DT 03-SEP-2001 (first entry)  
XX  
DE Human colon cancer antigen protein SEQ ID NO:6815.  
XX  
KW Human; colon cancer; colon cancer antigen; diagnosis; detection;  
KW colorectal carcinoma; chromosome 12.  
XX  
OS Homo sapiens.  
XX  
PN WO200122920-A2.  
XX  
PD 05-APR-2001.  
XX  
PF 28-SEP-2000; 2000WO-US026524.  
XX  
PR 29-SEP-1999; 99US-0157137P.  
PR 03-NOV-1999; 99US-0163280P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Ruben SM, Barash SC, Birse CE, Rosen CA;  
XX  
DR WPI; 2001-235357/24.  
DR N-PSDB; AAH35456.  
XX  
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,  
PT useful for preventing, diagnosing and/or treating colorectal cancers.  
XX  
PS Claim 11; Page 8267-8270; 9803pp; English.  
XX  
CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon  
CC cancer-associated nucleic acid molecules (N) and proteins (P), where the  
CC proteins are collectively known as colon cancer antigens. The colon  
CC cancer antigens have cytostatic activity and can be used in gene therapy  
CC and vaccine production. N and P may be used in the prevention, diagnosis  
CC and treatment of diseases associated with inappropriate P expression. For  
CC example, N and P may be used to treat disorders associated with decreased  
CC expression by rectifying mutations or deletions in a patient's genome  
CC that affect the activity of P by expressing inactive proteins or to  
CC supplement the patients own production of P. Additionally, N may be used  
CC to produce the colon cancer-associated Ps, by inserting the nucleic acids  
CC into a host cell and culturing the cell to express the proteins. N and P  
CC can be used in the prevention, diagnosis and treatment of colorectal  
CC carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent  
CC sequences used in the exemplification of the present invention. N.B.  
CC Pages 666 to 682 and page 7053 of the sequence listing were missing at  
CC time of publication, meaning no sequences are present for SEQ ID NO:1027

```
CC to 1052, 7921 and 7922
XX Sequence 209 AA;
SQ Sequence 209 AA;

Query Match      100.0%; Score 24; DB 4; Length 209;
Best Local Similarity 100.0%; Pred. No. 9.8e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSTKSIFFEQTNNNNSSFT 24
Db 73 LRFDSTKSIFFEQTNNNNSSFT 96

RESULT 3
ID AAR86834 standard; protein; 227 AA.
XX AAR86834;
AC AAR86834;
XX 12-JUL-1996 (first entry)
XX Human CD9 sequence.
XX
XX CD9 antigen; stimulated T cell; antibody; ligand; proliferation;
XX monoclonal antibody; ES5.2D8; 27 kD accessory protein; epitope;
XX immune response; cancer; infectious disease; growth factor.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Modified-site 51
FT /note= "Potential N-linked glycosylation site"
FT Modified-site 52
FT /note= "Potential N-linked glycosylation site"
FT Domain 111..194
FT /note= "Extracellular domain"
FT Domain 195..220
FT /note= "Transmembrane domain"
FT Domain 221..227
FT /note= "Cytoplasmic domain"
XX
XX WO9533823-A1.
XX
XX 14-DEC-1995.
XX
XX 01-DEC-1994; 94WO-US013782.
XX
XX 03-JUN-1994; 94US-00253751.
XX 03-JUN-1994; 94US-00253964.
XX
XX (USNA ) US SEC OF NAVY.
XX (UNMI ) UNIV MICHIGAN.
XX (REPK ) REPLIGEN CORP.
XX (DAND ) DANA FARBER CANCER INST INC.
XX
XX June CH, Thompson CB, Nabel G, Gray GS, Rennert PD, Freeman GJ;
XX WPI; 1996-040230/04.
XX
XX Selectively inducing CD8 positive T cell proliferation - by activating
XX the T cells and stimulating CD9 cell surface ligand, useful for
XX immuno:therapy of, e.g. cancer.
XX
XX Example 10; Page 38-39; 79pp; English.
XX
XX This sequence represents CD9 from the surface of stimulated T cells. The
XX antigen at residues 31-37 of human CD9 (see AAR86832) is bound by an
XX antibody or other ligand to stimulate the T cell population to
XX proliferate and expand leading to a 100- to 10000-fold increase in cell
XX number compared to the original population. The antigenic sequence fits
XX the generic sequence given in AAR86827. This epitope is recognised by the
XX monoclonal antibody (MAb) ES5.2D8. CD9 is a 27 kD accessory protein found
XX on activated T cells. The epitope was recognised by screening a phase
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CC display library. Selective proliferation of an antigen-specific T cell
CC population is useful in cases where the immune response is to be up
CC regulated, e.g. in the treatment of cancer or infectious diseases. By
CC causing proliferation of the T cell population by stimulating T cell
CC epitope removes the need for exogenous growth factors or accessory cells
XX
SQ Sequence 227 AA;

Query Match      100.0%; Score 24; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSTKSIFFEQTNNNNSSFT 24
Db 34 LRFDSTKSIFFEQTNNNNSSFT 57

RESULT 4
ID ABB78366 standard; protein; 227 AA.
XX ABB78366;
AC ABB78366;
XX 16-DEC-2002 (first entry)
XX Amino acid sequence of CD9.
XX
XX T cell; T cell proliferation; infectious disease; cancer; immunotherapy;
XX immunotherapy; CD9.
XX
XX Homo sapiens.
XX
XX US2002115214-A1.
XX 22-AUG-2002.
XX
XX 26-JAN-1996; 96US-00592711.
XX
XX 23-NOV-1988; 88US-00275433.
XX 07-APR-1992; 92US-00864805.
XX 07-APR-1992; 92US-00864807.
XX 07-APR-1992; 92US-00864866.
XX 04-JUN-1993; 93US-00073223.
XX 03-JUN-1994; 94US-00253964.
XX 10-MAR-1995; 95US-00403253.
XX 04-MAY-1995; 95US-00435816.
XX
XX (JUNE/) JUNE C H.
XX (THOM/) THOMPSON C B.
XX (NABEL/) NABEL G J.
XX (GRAY/) GRAY G S.
XX (RENN/) RENNERT P D.
XX
XX June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;
XX WPI; 2002-712476/77.
XX
XX Inducing a population of T cells to proliferate, by activating population
XX of T cells and stimulating an accessory molecule on the surface of the T
XX cells with a ligand which binds the accessory molecule.
XX
XX Example 10; Page 25; 88pp; English.
XX
XX The specification describes method for inducing a population of T cells
XX to proliferate. The method involves activating population of T cells,
XX stimulating an accessory molecule on T cell surface with a ligand
XX protein) which binds the molecule, to induce proliferation of T cells,
XX monitoring proliferation of T cells in response to continuing exposure to
XX the ligand, and reactivating and restimulating T cells when rate of
XX proliferation has decreased to induce further proliferation of the cells.
XX The method is useful for inducing proliferation of T cells, for use in
XX treatment of infectious disease, cancer and immunotherapy. The method
XX allows for the expansion of a population of T cells in numbers sufficient
```

CC to reconstitute an individuals's total CD4+ or CD8+ T cell population.  
 CC The resulting T cell population can be genetically transduced and used  
 CC for immunotherapy or can be used in methods of in vitro analyses of  
 CC infectious agents. A population of tumour-infiltrating lymphocytes can be  
 CC obtained from an individual afflicted with cancer and the T cells  
 CC stimulated to proliferate to sufficient numbers. The resulting T cell  
 CC population can be genetically transduced to express tumour necrosis  
 CC factor (TNF) or other factor and restored to the individual. CD4+ T cells  
 CC expanded by this method are useful in the treatment of HIV infection in  
 CC an individual. The present sequence represents CD9, an antigen present on  
 CC the surface of activated T cells  
 XX  
 SQ Sequence 227 AA;

Query Match 100.0%; Score 24; DB 5; Length 227;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-16;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSQTKSIFQETNNNSFYT 24  
 |||||  
 Db 34 LRFDSQTKSIFQETNNNSFYT 57

RESULT 5

ID AAE14636 standard; protein; 227 AA.

AC AAE14636;

DT 16-JUL-2002 (first entry)

DE Human CD9 antigen.

XX T cell; CD3; accessory molecule; CD28; cancer; infectious disease;  
 KW immunotherapy; human immunodeficiency virus; HIV infection; cytokine;  
 KW human; CD9 antigen.

OS Homo sapiens.

PN US6352694-B1.

PD 05-MAR-2002.

PF 10-MAR-1995; 95US-00403253.

PR 03-JUN-1994; 94US-00253964.

PA (GENY ) GENETICS INST INC.

PA (UNMI ) UNIV MICHIGAN.

XX June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;

XX WPI; 2002-314696/35.

XX Inducing T cell population to proliferate, useful in cancer therapy,  
 PT comprises activating T cells by contacting T cells in vitro with  
 PT immobilized anti-CD3 antibody and stimulating accessory molecule on T  
 PT cell surface.

PS Example 10; Col 42; 71pp; English.

XX The invention relates to a method of inducing T cell population to  
 CC proliferate for use in therapy comprising activating T cells by  
 CC contacting T cells in vitro with anti-CD3 antibody which is immobilised  
 CC on solid phase surface, and stimulating accessory molecule on T cell  
 CC surface in vitro with anti-CD28 antibody, or stimulatory form of natural  
 CC ligand for CD28 such as B7-1 or B7-2. The method is useful for inducing a  
 CC population of T cells to proliferate in sufficient numbers for use in  
 CC therapy e.g., for treating cancer or an infectious disease. The method  
 CC can be used to selectively expand the population of CD28<sup>+</sup>, CD4<sup>+</sup>, CD8<sup>+</sup>,  
 CC CD28RA<sup>+</sup> or CD28RO<sup>+</sup> T cells for immunotherapy. The T cell population  
 CC resulting by the method can be genetically transduced and used for  
 CC immunotherapy or can be used for in vitro analysis of infectious agents

CC such as human immunodeficiency virus (HIV). Proliferation of a population  
 CC of CD4+ T cells obtained from an individual infected with HIV can be  
 CC achieved and the cells rendered resistant to HIV infection. Following the  
 CC expansion of the T cells to sufficient numbers, the expanded T cells are  
 CC restored to the individual. Also CD4<sup>+</sup> T cells expanded by the above  
 CC mentioned is useful for treating HIV infection in an individual. A  
 CC population of tumour-infiltrating lymphocytes can be obtained from an  
 CC individual afflicted with cancer and the T cells stimulated to  
 CC proliferate to sufficient numbers and restored to the individual. The  
 CC supernatants from cultures of T cells expanded from above mentioned  
 CC method are useful as a rich source of cytokines and can be used to  
 CC sustain T cells in vivo or ex vivo. Stimulating and expanding a  
 CC population of antigen specific T cells are useful in therapeutic  
 CC conditions where it is desirable to upregulate an immune response. The T  
 CC cell proliferation occurs in the absence of exogenous growth factors or  
 CC accessory cells. The present sequence is human CD9 antigen which is  
 CC expressed on surface of activated T cells  
 XX  
 SQ Sequence 227 AA;

Query Match 100.0%; Score 24; DB 5; Length 227;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-16;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSQTKSIFQETNNNSFYT 24  
 |||||  
 Db 34 LRFDSQTKSIFQETNNNSFYT 57

RESULT 6

ABU05057

ID ABU05057 standard; protein; 227 AA.

AC ABU05057;

DT 29-JAN-2003 (first entry)

XX Human expressed protein tag (EPT) #1723.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
 KW protease; protease inhibitor; transporter; cytoskeletal protein;  
 KW receptor; transcription factor; cancer; MHC;  
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

OS Homo sapiens.

PN WO200278524-A2.

XX 10-OCT-2002.

PF 28-MAR-2002; 2002WO-US009671.

PR 28-MAR-2001; 2001US-0279495P.

PR 21-MAY-2001; 2001US-0292544P.

PR 08-AUG-2001; 2001US-0310801P.

PR 01-OCT-2001; 2001US-0326370P.

PR 04-DEC-2001; 2001US-0336780P.

PR 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCOs INC.

XX Chicx RM, Tomlinson AJ, Urban RG;

XX WPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
 PT cytoskeletal proteins, receptors or transcription factors), useful for  
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
 PT leukemia.

PS Example 2; SEQ ID NO 1723; 134pp; English.

CC The invention describes a purified polypeptide, which comprises a  
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
 CC transporter, cytoskeletal protein, receptor or transcription factor. The  
 CC polypeptide is useful as an immunogenic composition for eliciting in a  
 CC mammal an immunogenic response directed against any of the purified  
 CC polypeptide. The purified polypeptide, or the antibody that binds to this  
 CC polypeptide, is useful for treating cancer. The polypeptide is also  
 CC useful for identifying compounds that binds to a naturally processed  
 CC class I or class II MHC-binding polypeptide. The polypeptides and  
 CC polynucleotides are particularly useful for treating or preventing  
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
 CC lymphoma or leukaemia. These are also useful for screening agents for  
 CC treating the above mentioned diseases. This sequence represents an  
 CC expressed protein tag (EPT) isolated from human tissue for translational  
 CC profiling. Note: This sequence does not appear in the printed  
 CC specification but was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 227 AA;

Query Match 100.0%; Score 24; DB 6; Length 227;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-16;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSQTKSIFPEQETNNNSFYT 24  
 |||||  
 Db 34 LRFDSQTKSIFPEQETNNNSFYT 57

RESULT 7  
 ABU05060  
 ID ABU05060 standard; protein; 227 AA.

AC ABU05060;

DT 29-JAN-2003 (first entry)

DE Human expressed protein tag (EPT) #1726.

KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
 KW protease; protease inhibitor; transporter; cytoskeletal protein;  
 KW receptor; transcription factor; cancer; MHC;  
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

OS Homo sapiens.

XX WO200278524-A2.

PN 10-OCT-2002.

PD 28-MAR-2002; 2002WO-US009671.

PF 28-MAR-2001; 2001US-0279495P.

PR 21-MAY-2001; 2001US-0292544P.

PR 08-AUG-2001; 2001US-0310801P.

PR 01-OCT-2001; 2001US-0326370P.

PR 04-DEC-2001; 2001US-0336780P.

XX (ZYCO-) ZYCOS INC.

XX Chicx RM, Tomlinson AJ, Urban RG;

XX WPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
 PT cytoskeletal proteins, receptors or transcription factors), useful for  
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
 PT leukemia.

PS Example 2; SEQ ID NO 1726; 134pp; English.

XX

CC The invention describes a purified polypeptide, which comprises a  
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
 CC transporter, cytoskeletal protein, receptor or transcription factor. The  
 CC polypeptide is useful as an immunogenic composition for eliciting in a  
 CC mammal an immunogenic response directed against any of the purified  
 CC polypeptide. The purified polypeptide, or the antibody that binds to this  
 CC polypeptide, is useful for treating cancer. The polypeptide is also  
 CC useful for identifying compounds that binds to a naturally processed  
 CC class I or class II MHC-binding polypeptide. The polypeptides and  
 CC polynucleotides are particularly useful for treating or preventing  
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
 CC lymphoma or leukaemia. These are also useful for screening agents for  
 CC treating the above mentioned diseases. This sequence represents an  
 CC expressed protein tag (EPT) isolated from human tissue for translational  
 CC profiling. Note: This sequence does not appear in the printed  
 CC specification but was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 227 AA;

Query Match 100.0%; Score 24; DB 6; Length 227;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-16;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSQTKSIFPEQETNNNSFYT 24  
 |||||  
 Db 34 LRFDSQTKSIFPEQETNNNSFYT 57

RESULT 8  
 ABW00436

ID ABW00436 standard; protein; 227 AA.

AC ABW00436;

DT 15-JAN-2004 (first entry)

DE Human CD9 antigenic protein.

KW HIV infection; human immunodeficiency virus; therapy; antigen; human.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Domain 111..194 /note= "Extracellular domain"

FT Domain 195..220 /note= "Transmembrane domain"

FT Domain 221..227 /note= "Cytoplasmic domain"

XX US2003099643-A1.

XX 29-MAY-2003.

XX 08-JUL-1999; 99US-00350202.

XX 23-NOV-1988; 88US-00275433.

PR 22-NOV-1989; 89WO-US005304.

PR 07-APR-1992; 92US-00864805.

PR 07-APR-1992; 92US-00864807.

PR 07-APR-1992; 92US-00864866.

PR 04-JUN-1993; 93US-00073223.

PR 03-JUN-1994; 94US-00253694.

PR 10-MAR-1995; 95US-00403253.

XX (JUNE/) JUNE C H.

PA (THOM/) THOMPSON C B.

PA (NABEL/) NABEL G J.

PA (GRAY/) GRAY G S.

PA (RENN/) RENNERT P D.

PI June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;



XX WPI; 2003-801206/75.  
XX Treating HIV infection in individual by isolating T cells from  
PT leukocytes, contacting T cells with anti-CD3 antibody for T cell  
PT proliferation, separating antibody from T cells, monitoring proliferation  
PT of T cells.  
XX Example 10; Page 23; Opp; English.  
XX The present invention relates to a novel method of treating human  
CC immunodeficiency virus (HIV) infection in an individual. The method  
CC involves isolating population of CD4 T cells from leukocytes, contacting  
CC population of CD4+ T cells with an anti-CD3 antibody for stimulating T  
CC cell proliferation, separating antibody from T cells, monitoring  
CC proliferation of T cells, restimulating T cells with antibody and  
CC restoring T cells to individual. The present sequence is human CD9  
CC antigenic protein. This sequence is used to illustrate the method of the  
CC invention  
XX Sequence 227 AA;  
SQ  
Query Match 100.0%; Score 24; DB 7; Length 227;  
Best Local Similarity 100.0%; Pred. No. 1.1e-16;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LRFDSTQKSIPEQETNNNSFYT 24  
DB 34 LRFDSTQKSIPEQETNNNSFYT 57  
RESULT 9  
ADK69862  
ID ADK69862 standard; protein; 227 AA.  
XX ADK69862;  
XX 06-MAY-2004 (first entry)  
XX Human CD9 protein.  
XX CD28-associated signal; immunotherapy; infectious disease; cancer;  
XX leukopheresis; human.  
XX Homo sapiens.  
XX US6534055-B1.  
XX 18-MAR-2003.  
XX 04-MAY-1995; 95US-00435816.  
XX 07-APR-1992; 92US-00864805.  
XX 07-APR-1992; 92US-00864807.  
XX 07-APR-1992; 92US-00864866.  
XX 04-JUN-1993; 93US-00073223.  
XX 03-JUN-1994; 94US-00253964.  
XX 10-MAR-1995; 95US-00403253.  
XX (GEMY ) GENETICS INST INC.  
XX June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;  
XX WPI; 2003-531074/50.  
XX Expanding T cell populations, useful for preparing renewable sources of T  
XX cells (e.g. CD4+) for immunotherapy or diagnostics, by stimulating a CD28  
PT -associated signal on the surface of the cells with an anti-CD28  
PT antibody, B7-1 or B7-2.  
XX Example 10; SEQ ID NO 6; 82pp; English.  
XX The invention relates to a method for expanding a population of T cells

CC to about 100-100000-fold over the original T cell population, or to about  
CC 10 log 1 0 to 12 log 1 2. The method comprises stimulating a CD28-  
CC associated signal on the surface of the T cells with agent comprising an  
CC anti-CD28 antibody, B7-1 or B7-2. The method is useful for inducing a  
CC population of T cells (e.g. CD4+, CD28+, CD8+, CD28RA+ or CD28RO+ T  
CC cells) to proliferate. The method is particularly useful for preparing a  
CC renewable source of CD4+ T cells. The expanded T cell population can be  
CC genetically transduced, and used for immunotherapy to treat a variety of  
CC human diseases (e.g. infectious diseases or cancer), or used in  
CC diagnostic protocols. T cells were obtained from leukopheresis of a  
CC normal donor, and purified with FICOLL density gradient centrifugation,  
CC followed by magnetic immunobead sorting. The present sequence is CD9 used  
CC in the exemplification of the invention.  
XX Sequence 227 AA;  
SQ  
Query Match 100.0%; Score 24; DB 7; Length 227;  
Best Local Similarity 100.0%; Pred. No. 1.1e-16;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LRFDSTQKSIPEQETNNNSFYT 24  
DB 34 LRFDSTQKSIPEQETNNNSFYT 57  
RESULT 10  
ADI19366  
ID ADI19366 standard; protein; 227 AA.  
XX ADI19366;  
XX 15-APR-2004 (first entry)  
XX Human CD9 protein.  
XX T cell; immunotherapy; therapy; HIV infection; cancer;  
XX infectious disease; cytostatic; antimicrobial; human.  
XX Homo sapiens.  
XX US2004001829-A1.  
XX 01-JAN-2004.  
XX 17-MAR-2003; 2003US-00390330.  
XX 23-NOV-1988; 88US-00275433.  
XX 22-NOV-1989; 89WO-US005304.  
XX 07-APR-1992; 92US-00864805.  
XX 07-APR-1992; 92US-00864807.  
XX 07-APR-1992; 92US-00864866.  
XX 04-JUN-1993; 93US-00073223.  
XX 03-JUN-1994; 94US-00253964.  
XX 10-MAR-1995; 95US-00403253.  
XX 04-MAY-1995; 95US-00435816.  
XX (JUNE/) JUNE C H.  
XX (THOM/) THOMPSON C B.  
XX (NABEL/) NABEL G J.  
XX (GRAY/) GRAY G S.  
XX (RENN/) RENNERT P D.  
XX June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;  
XX WPI; 2004-061648/06.  
XX Inducing a population of T cells to proliferate, for immunotherapy or  
XX treating HIV infection, cancer or infectious disease, comprises  
PT activating a population of T cells and stimulating an accessory molecule  
PT on the surface of the T cells.  
XX Example 10; SEQ ID NO 6; 80pp; English.  
XX



CC The invention relates to a method for inducing a population of T cells to  
CC proliferate. The method comprising activating a population of T cells,  
CC and stimulating an accessory molecule on the surface of the T cells with  
CC a ligand that binds the accessory molecule. The invention is useful for  
CC immunotherapy, for treating HIV infection, cancer or infectious disease,  
CC or in diagnostic applications. The present sequence is human CD9 protein.  
SQ Sequence 227 AA;

Query Match 100.0%; Score 24; DB 8; Length 227;  
Best Local Similarity 100.0%; Pred. No. 1.1e-16;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSQTSIFQETNNNNSSFT 24  
|||  
DB 34 LRFDSQTSIFQETNNNNSSFT 57  
|||

RESULT 11  
AEA89005  
ID AEA89005 standard; protein; 227 AA.  
XX  
AC AEA89005;  
XX  
DT 25-AUG-2005 (first entry)  
XX  
DE Human CD9 antigenic protein, SEQ ID NO: 6.  
XX  
KW Cell therapy; immune stimulation; immunotherapy; diagnosis;  
KW infectious disease; antimicrobial; infection; cancer; cytostatic;  
KW neoplasm; CD9; antigen.  
XX  
OS Homo sapiens.  
XX  
PN US6905681-B1.  
XX  
PD 14-JUN-2005.  
XX  
PF 08-JUL-1999; 99US-00349915.  
XX  
PR 03-JUN-1994; 94US-00253964.  
PR 10-MAR-1995; 95US-00403253.  
XX  
(GEMY ) GENETICS INST INC.  
PA (UNMI ) UNIV MICHIGAN.  
PA (USNA ) US SEC OF NAVY.  
XX  
PI June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;  
XX WPI; 2005-46477/47.  
XX  
DR Ex vivo proliferation of T cell population for use in therapy, involves  
XX contacting population of T cells with surface having anti-CD3 antibody  
XX and anti-CD28 antibody for activating T cells and stimulating activated T  
XX cells, respectively.

PS Example 10; SEQ ID NO 6; 76pp; English.  
XX  
XX The present invention relates to a method of including ex vivo  
CC proliferation of a population of T cells to sufficient numbers for use in  
CC therapy. The method involves contacting population of T cells with  
CC surface having anti-CD3 antibody and anti-CD28 antibody for activating T  
CC cells and stimulating activated T cells, respectively. The invention is  
CC useful for treating cancer and infectious disease and also useful in cell  
CC therapy. The present sequence is the human CD9 antigenic protein. This  
CC sequence is bound by an ES5.2D8 monoclonal antibody, which is to be used  
CC to stimulate a CD8+ T cell population.  
XX  
SQ Sequence 227 AA;

Query Match 100.0%; Score 24; DB 9; Length 227;  
Best Local Similarity 100.0%; Pred. No. 1.1e-16;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSQTSIFQETNNNNSSFT 24  
|||  
DB 34 LRFDSQTSIFQETNNNNSSFT 57  
|||

RESULT 12  
ABB44581  
ID ABB44581 standard; protein; 228 AA.  
XX  
AC ABB44581;  
XX  
DT 25-JAN-2002 (first entry)  
XX  
DE Human wound healing related polypeptide SEQ ID NO 38.  
XX  
KW Human; mouse; vulnery; dermatological; skin disorder; wound healing;  
KW gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN CA2325226-A1.  
XX  
PD 17-MAY-2001.  
XX  
PF 16-NOV-2000; 2000CA-02325226.  
XX  
PR 17-NOV-1999; 99DE-01055349.  
PR 17-DEC-1999; 99US-0172511P.  
PR 20-JUN-2000; 2000DE-01030149.  
XX  
(SWIT-) SWITCH BIOTECH AG.  
XX  
PI Regenbogen J, Wolf E, Goppelt A, Werner S, Halle J;  
XX WPI; 2001-433142/47.  
XX  
DR Use of novel polypeptide or its variant or nucleic acid encoding the  
XX polypeptide for diagnosing and/or preventing and/or treating skin  
XX disorders and/or treatment in wound healing or for identifying active  
XX substances.

PS Disclosure; Page 193-194; 265pp; English.  
XX  
XX The invention relates to the use of a polypeptide (ABB44544-ABB44601,  
XX ABB44606-ABB44623) or its variant or encoding nucleic acid (ABA81990-  
XX ABA81995, ABA82016-ABA82032) with vulnery and/or dermatological  
XX activity for the diagnosis, prevention and treatment of skin disorders  
XX and treatment in wound healing or for the identification of  
XX pharmacologically active substances. The nucleic acids are useful in gene  
XX therapy. Note: The printed sequence listing for this specification was  
XX incomplete, terminating part way through SEQ ID NO 106. The remaining  
XX data was obtained from EPO data for an equivalent patent (Epl114862)  
XX Sequence 228 AA;

Query Match 100.0%; Score 24; DB 4; Length 228;  
Best Local Similarity 100.0%; Pred. No. 1.1e-16;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSQTSIFQETNNNNSSFT 24  
|||  
DB 35 LRFDSQTSIFQETNNNNSSFT 58  
|||

RESULT 13  
ABU05059  
ID ABU05059 standard; protein; 228 AA.  
XX  
AC ABU05059;  
XX  
DT 29-JAN-2003 (first entry)  
XX

```
DE Human expressed protein tag (BPT) #1725.
XX
XX Translational profiling; expressed protein tag; BPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
XX WO200278524-A2.
XX
XX 10-OCT-2002.
XX
XX 28-MAR-2002; 2002WO-US009671.
XX
XX 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
XX (ZYCO-) ZYCOS INC.
XX
XX Chicx RM, Tomlinson AJ, Urban RG;
XX
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1725; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor.
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (BPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 228 AA;

Query Match 100.0%; Score 24; DB 6; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSTQKSIPEQETNNNSSFT 24
DB 35 LRFDSTQKSIPEQETNNNSSFT 58

RESULT 14
ABU05052
ID ABU05052 standard; protein; 228 AA.
XX
XX ABU05052;
AC
XX
XX 29-JAN-2003 (first entry)
DT
XX
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```
DE Human expressed protein tag (BPT) #1718.
XX
XX Translational profiling; expressed protein tag; BPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
XX WO200278524-A2.
XX
XX 10-OCT-2002.
XX
XX 28-MAR-2002; 2002WO-US009671.
XX
XX 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
XX (ZYCO-) ZYCOS INC.
XX
XX Chicx RM, Tomlinson AJ, Urban RG;
XX
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1718; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor.
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (BPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 228 AA;

Query Match 100.0%; Score 24; DB 6; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSTQKSIPEQETNNNSSFT 24
DB 35 LRFDSTQKSIPEQETNNNSSFT 58

RESULT 15
ABU05048
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XX
XX ABU05048;
AC
XX
XX 29-JAN-2003 (first entry)
DT
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DE Human expressed protein tag (EPT) #1714.  
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
XX Homo sapiens.  
XX OS  
XX PN WO200278524-A2.  
XX PD 10-OCT-2002.  
XX PF 28-MAR-2002; 2002WO-US009671.  
XX PR 28-MAR-2001; 2001US-0279495P.  
PR 21-MAY-2001; 2001US-0292544P.  
PR 08-AUG-2001; 2001US-0310801P.  
PR 01-OCT-2001; 2001US-0326370P.  
PR 04-DEC-2001; 2001US-0336780P.  
PR 20-FEB-2002; 2002US-0358985P.  
XX (ZYCO-) ZYCO INC.  
XX Chicx RM, Tomlinson AJ, Urban RG;  
XX WPI; 2003-040607/03.  
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.  
XX Example 2; SEQ ID NO 1714; 134pp; English.  
XX The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX Sequence 228 AA;  
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Query Match 100.0%; Score 24; DB 6; Length 228;  
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DB 35 LRPDSQTKSIFQEQTNNNSSPYT 58  
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Search completed: January 20, 2006, 17:42:00  
Job time : 69.0769 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2006, 17:38:26 ; Search time 8.76923 Seconds  
(without alignments)  
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Searched: 572060 seqs, 82675679 residues

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Minimum DB seq length: 0

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Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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168	5	20.8	88	2	US-09-333-809-105	Sequence 105, App	241	5	20.8	138	2	US-09-270-767-42296	Sequence 42296, A
169	5	20.8	88	2	US-09-746-311B-169	Sequence 169, App	242	5	20.8	139	2	US-09-615-192A-297	Sequence 297, App
170	5	20.8	88	2	US-09-746-311B-299	Sequence 299, App	243	5	20.8	139	2	US-09-270-767-37514	Sequence 37514, A
171	5	20.8	88	2	US-09-746-311B-297	Sequence 297, App	244	5	20.8	139	2	US-09-270-767-52731	Sequence 52731, A
172	5	20.8	88	2	US-09-746-311B-302	Sequence 302, App	245	5	20.8	140	2	US-09-270-767-31947	Sequence 31947, A
173	5	20.8	89	2	US-09-333-809-107	Sequence 107, App	246	5	20.8	140	2	US-09-270-767-47164	Sequence 47164, A
												US-09-248-796A-23981	Sequence 23981, A

247	5	20.8	140	2	US-10-104-047-3489	Sequence 3489, Ap	320	5	20.8	188	2	US-09-134-000C-4373	Sequence 4373, Ap
248	5	20.8	141	2	US-09-248-796A-20650	Sequence 20650, A	321	5	20.8	188	2	US-09-746-311B-294	Sequence 294, Ap
249	5	20.8	142	2	US-09-270-767-34825	Sequence 34825, A	322	5	20.8	188	2	US-09-893-737-15	Sequence 16, Appl
250	5	20.8	143	2	US-09-270-767-50042	Sequence 50042, A	323	5	20.8	189	2	US-09-248-796A-19441	Sequence 19441, A
251	5	20.8	144	2	US-09-198-452A-657	Sequence 657, App	324	5	20.8	190	2	US-09-615-192A-301	Sequence 301, App
252	5	20.8	144	2	US-09-270-767-46661	Sequence 46661, A	325	5	20.8	190	2	US-09-270-767-58731	Sequence 58731, A
253	5	20.8	144	2	US-09-248-796A-21043	Sequence 21043, A	326	5	20.8	190	2	US-09-248-796A-20502	Sequence 20502, A
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256	5	20.8	146	2	US-09-248-796A-28095	Sequence 28095, A	329	5	20.8	191	2	US-09-270-767-51964	Sequence 51964, A
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259	5	20.8	147	2	US-09-270-767-54135	Sequence 54135, A	332	5	20.8	192	2	US-09-248-796A-27575	Sequence 27575, A
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262	5	20.8	150	2	US-09-540-236-3497	Sequence 3497, Ap	335	5	20.8	196	2	US-09-270-767-61292	Sequence 61292, A
263	5	20.8	150	2	US-09-438-185A-621	Sequence 621, App	336	5	20.8	196	2	US-09-248-796A-17562	Sequence 17562, A
264	5	20.8	151	2	US-09-328-352-6429	Sequence 6429, Ap	337	5	20.8	198	2	US-09-252-991A-25186	Sequence 25186, A
265	5	20.8	151	2	US-09-830-230A-667	Sequence 667, App	338	5	20.8	199	2	US-09-543-681A-4701	Sequence 4701, Ap
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267	5	20.8	155	2	US-09-085-761A-25	Sequence 25, Appl	340	5	20.8	199	2	US-09-248-796A-14467	Sequence 14467, A
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271	5	20.8	155	2	US-09-248-796A-18789	Sequence 18789, A	344	5	20.8	201	6	5171840-11	Patent No. 5171840
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273	5	20.8	157	2	US-09-270-767-40195	Sequence 40195, A	346	5	20.8	202	2	US-09-270-767-34966	Sequence 34966, A
274	5	20.8	157	2	US-09-270-767-55161	Sequence 55161, A	347	5	20.8	202	2	US-09-270-767-50183	Sequence 50183, A
275	5	20.8	157	2	US-09-270-767-55411	Sequence 55411, A	348	5	20.8	202	1	US-08-729-152-8	Sequence 8, Appl
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278	5	20.8	159	2	US-09-248-796A-27510	Sequence 27510, A	351	5	20.8	208	2	US-08-956-171E-5202	Sequence 5202, Ap
279	5	20.8	160	2	US-09-902-540-13876	Sequence 13876, A	352	5	20.8	208	2	US-09-134-000C-3698	Sequence 3698, Ap
280	5	20.8	161	2	US-09-270-767-34267	Sequence 34267, A	353	5	20.8	208	2	US-08-781-986A-5202	Sequence 5202, Ap
281	5	20.8	161	2	US-09-270-767-43484	Sequence 43484, A	354	5	20.8	208	2	US-09-248-796A-26815	Sequence 26815, A
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283	5	20.8	162	2	US-09-270-767-39335	Sequence 39335, A	356	5	20.8	209	2	US-09-248-796A-15963	Sequence 15963, A
284	5	20.8	162	2	US-09-270-767-54552	Sequence 54552, A	357	5	20.8	209	2	US-09-248-796A-28163	Sequence 28163, A
285	5	20.8	162	2	US-09-248-796A-28017	Sequence 28017, A	358	5	20.8	209	2	US-09-746-311B-172	Sequence 172, App
286	5	20.8	164	2	US-09-543-681A-8262	Sequence 8262, Ap	359	5	20.8	209	2	US-09-949-016-10830	Sequence 10830, A
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288	5	20.8	165	2	US-09-270-767-49911	Sequence 49911, A	361	5	20.8	210	2	US-09-134-001C-3671	Sequence 3671, Ap
289	5	20.8	165	2	US-09-248-796A-16738	Sequence 16738, A	362	5	20.8	212	2	US-09-328-352-7678	Sequence 7678, Ap
290	5	20.8	166	2	US-09-270-767-39721	Sequence 39721, A	363	5	20.8	212	2	US-09-107-433-4196	Sequence 4196, Ap
291	5	20.8	166	2	US-09-270-767-41330	Sequence 41330, A	364	5	20.8	213	2	US-09-248-796A-14823	Sequence 14823, A
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294	5	20.8	166	2	US-09-248-796A-23059	Sequence 23059, A	367	5	20.8	214	2	US-09-903-540-13849	Sequence 13849, A
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296	5	20.8	167	2	US-09-710-279-986	Sequence 986, App	369	5	20.8	216	2	US-09-270-767-57457	Sequence 57457, A
297	5	20.8	167	2	US-09-710-279-2128	Sequence 2128, Ap	370	5	20.8	217	2	US-09-270-767-31877	Sequence 31877, A
298	5	20.8	167	2	US-09-902-540-13709	Sequence 13709, A	371	5	20.8	217	2	US-09-270-767-47094	Sequence 47094, A
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305	5	20.8	174	2	US-09-248-796A-15154	Sequence 15154, A	378	5	20.8	226	2	US-09-270-767-44368	Sequence 44368, A
306	5	20.8	174	2	US-09-746-311B-173	Sequence 173, App	379	5	20.8	226	2	US-09-248-796A-20804	Sequence 20804, A
307	5	20.8	174	2	US-09-858-580-23	Sequence 23, Appl	380	5	20.8	226	2	US-09-248-796A-26342	Sequence 26342, A
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312	5	20.8	179	2	US-09-438-185A-990	Sequence 990, App	385	5	20.8	230	2	US-09-333-809-221	Sequence 221, App
313	5	20.8	180	2	US-09-583-110-4398	Sequence 110-4398	386	5	20.8	230	2	US-09-333-809-222	Sequence 222, App
314	5	20.8	181	2	US-09-270-767-61846	Sequence 61846, A	387	5	20.8	230	2	US-09-333-809-228	Sequence 228, App
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317	5	20.8	185	2	US-09-602-787A-2	Sequence 2, Appl	390	5	20.8	230	2	US-09-746-311B-371	Sequence 371, App
318	5	20.8	186	2	US-09-248-796A-18477	Sequence 18477, A	391	5	20.8	230	2	US-09-746-311B-377	Sequence 377, App
319	5	20.8	188	2	US-09-252-991A-31741	Sequence 31741, A	392	5	20.8	230	2	US-09-640-211A-1926	Sequence 1926, Ap

393	5	20.8	232	2	US-09-543-681A-5424	Sequence 5424, Ap	466	5	20.8	275	2	US-09-85A-133-584	Sequence 584, App
394	5	20.8	232	2	US-09-248-796A-16788	Sequence 16788, A	467	5	20.8	277	2	US-09-107-532A-7213	Sequence 7213, Ap
395	5	20.8	234	2	US-09-270-767-43381	Sequence 43381, A	468	5	20.8	277	2	US-09-759-143-906	Sequence 906, App
396	5	20.8	235	2	US-09-583-110-3490	Sequence 3490, Ap	469	5	20.8	277	2	US-10-012-896-906	Sequence 906, App
397	5	20.8	235	2	US-09-248-796A-24725	Sequence 24725, A	470	5	20.8	278	2	US-09-270-767-41910	Sequence 41910, A
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399	5	20.8	237	2	US-08-470-535-14	Sequence 14, Appl	472	5	20.8	278	2	US-09-710-279-2700	Sequence 2700, Ap
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403	5	20.8	237	2	US-09-746-311B-359	Sequence 359, App	476	5	20.8	284	2	US-09-270-767-51791	Sequence 51791, A
404	5	20.8	238	2	US-09-489-039A-12131	Sequence 12131, A	477	5	20.8	288	2	US-09-248-796A-16676	Sequence 16676, A
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412	5	20.8	243	2	US-09-248-796A-15919	Sequence 15919, A	485	5	20.8	295	2	US-09-248-796A-14635	Sequence 14635, A
413	5	20.8	243	2	US-09-900-345A-22	Sequence 22, Appl	486	5	20.8	296	1	US-08-261-662-2	Sequence 2, Appl
414	5	20.8	243	2	US-09-900-345A-24	Sequence 24, Appl	487	5	20.8	296	4	PCT-US95-07752-2	Sequence 2, Appl
415	5	20.8	244	2	US-09-328-352-7894	Sequence 7894, Ap	488	5	20.8	298	2	US-09-248-796A-27737	Sequence 27737, A
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417	5	20.8	245	2	US-09-270-767-36519	Sequence 36519, A	490	5	20.8	299	2	US-09-710-279-1768	Sequence 1768, Ap
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421	5	20.8	246	2	US-09-888-655-2	Sequence 2, Appl	494	5	20.8	303	2	US-09-248-796A-19122	Sequence 19122, A
422	5	20.8	246	2	US-09-710-279-900	Sequence 900, App	495	5	20.8	305	2	US-09-248-796A-14506	Sequence 14506, A
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424	5	20.8	246	2	US-09-888-501-2	Sequence 2, Appl	497	5	20.8	306	2	US-09-538-092-519	Sequence 519, App
425	5	20.8	248	2	US-09-270-767-42758	Sequence 42758, A	498	5	20.8	307	2	US-09-134-001C-3792	Sequence 3792, Ap
426	5	20.8	248	2	US-09-270-767-44243	Sequence 44243, A	499	5	20.8	307	2	US-09-583-110-3427	Sequence 3427, Ap
427	5	20.8	249	2	US-09-248-796A-15815	Sequence 15815, A	500	5	20.8	308	2	US-08-508-761B-35	Sequence 35, Appl
428	5	20.8	251	2	US-09-248-796A-17563	Sequence 17563, A	501	5	20.8	308	2	US-09-252-991A-31991	Sequence 31991, A
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433	5	20.8	253	2	US-09-270-767-47163	Sequence 47163, A	506	5	20.8	311	2	US-09-248-796A-25849	Sequence 25849, A
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435	5	20.8	254	4	PCT-US95-02689-20	Sequence 20, Appl	508	5	20.8	313	2	US-09-107-433-5045	Sequence 5045, Ap
436	5	20.8	255	2	US-09-248-796A-18387	Sequence 18387, A	509	5	20.8	315	2	US-09-313-942-16	Sequence 16, Appl
437	5	20.8	255	2	US-09-640-211A-2261	Sequence 2261, Ap	510	5	20.8	315	2	US-09-248-796A-17439	Sequence 17439, A
438	5	20.8	258	2	US-09-270-767-34189	Sequence 34189, A	511	5	20.8	315	2	US-10-282-162-16	Sequence 16, Appl
439	5	20.8	258	2	US-09-270-767-49406	Sequence 49406, A	512	5	20.8	316	2	US-09-248-796A-18293	Sequence 18293, A
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442	5	20.8	260	2	US-09-248-796A-24025	Sequence 24025, A	515	5	20.8	321	2	US-09-582-660-5	Sequence 5, Appl
443	5	20.8	261	2	US-09-248-796A-19121	Sequence 19121, A	516	5	20.8	323	6	5171840-6	Patent No. 5171840
444	5	20.8	262	2	US-09-248-796A-25774	Sequence 25774, A	517	5	20.8	323	6	5480796-6	Patent No. 5480796
445	5	20.8	263	2	US-09-543-681A-17789	Sequence 17789, Ap	518	5	20.8	324	2	US-09-248-796A-21777	Sequence 21777, A
446	5	20.8	263	2	US-09-248-796A-14154	Sequence 14154, A	519	5	20.8	325	2	US-09-711-164-358	Sequence 358, App
447	5	20.8	263	2	US-09-248-796A-15305	Sequence 15305, A	520	5	20.8	325	2	US-09-270-767-41440	Sequence 41440, A
448	5	20.8	263	2	US-09-248-796A-19569	Sequence 19569, A	521	5	20.8	325	2	US-09-248-796A-19440	Sequence 19440, A
449	5	20.8	264	1	US-08-484-905-120	Sequence 120, App	522	5	20.8	326	1	US-08-997-080-43	Sequence 43, Appl
450	5	20.8	264	2	US-08-481-985B-120	Sequence 120, App	523	5	20.8	326	1	US-08-997-362-43	Sequence 43, Appl
451	5	20.8	264	2	US-08-370-476-120	Sequence 120, App	524	5	20.8	326	2	US-08-873-970-43	Sequence 43, Appl
452	5	20.8	266	2	US-09-144-776B-14	Sequence 14, Appl	525	5	20.8	326	2	US-09-095-855-43	Sequence 43, Appl
453	5	20.8	266	2	US-08-882-431B-14	Sequence 14, Appl	526	5	20.8	326	2	US-08-705-347A-43	Sequence 43, Appl
454	5	20.8	266	2	US-09-746-311B-165	Sequence 165, App	527	5	20.8	326	2	US-09-324-542-43	Sequence 43, Appl
455	5	20.8	266	2	US-09-746-311B-166	Sequence 166, App	528	5	20.8	326	2	US-09-205-426-43	Sequence 43, Appl
456	5	20.8	266	2	US-09-746-311B-295	Sequence 295, App	529	5	20.8	326	2	US-09-200-663-43	Sequence 43, Appl
457	5	20.8	266	2	US-09-746-311B-296	Sequence 296, App	530	5	20.8	326	2	US-09-10-194-125-4	Sequence 4, Appl
458	5	20.8	266	2	US-09-746-311B-334	Sequence 334, App	531	5	20.8	328	2	US-09-300-672-2	Sequence 2, Appl
459	5	20.8	269	2	US-09-270-767-44704	Sequence 44704, A	532	5	20.8	329	2	US-09-489-039A-14082	Sequence 14082, A
460	5	20.8	269	2	US-09-248-796A-22276	Sequence 22276, A	533	5	20.8	331	2	US-09-248-796A-18701	Sequence 18701, A
461	5	20.8	271	2	US-09-543-681A-6644	Sequence 6644, Ap	534	5	20.8	332	1	US-08-118-270-53	Sequence 53, Appl
462	5	20.8	273	2	US-09-270-767-42116	Sequence 42116, A	535	5	20.8	332	2	US-09-248-796A-15783	Sequence 15783, A
463	5	20.8	274	2	US-09-270-767-62098	Sequence 62098, A	536	5	20.8	332	2	US-09-248-796A-20189	Sequence 20189, A
464	5	20.8	274	2	US-09-248-796A-17624	Sequence 17624, A	537	5	20.8	332	4	PCT-US93-08528-53	Sequence 53, Appl
465	5	20.8	275	2	US-09-248-796A-27507	Sequence 27507, A	538	5	20.8	335	2	US-09-252-991A-31961	Sequence 31961, A



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540	5	20.8	336	2	US-09-248-796A-17941	Sequence 17941, A	613	5	20.8	384	2	US-09-534-185-2	Sequence 2, Appli
541	5	20.8	337	2	US-09-841-786-7	Sequence 7, Appli	614	5	20.8	384	2	US-09-270-767-47918	Sequence 47918, A
542	5	20.8	338	2	US-09-543-681A-6965	Sequence 6965, Ap	615	5	20.8	384	2	US-09-248-796A-20580	Sequence 20580, A
543	5	20.8	339	2	US-09-270-767-60870	Sequence 60870, A	616	5	20.8	386	6	517840-5	Patent No. 517840
544	5	20.8	339	2	US-09-248-796A-15032	Sequence 15032, A	617	5	20.8	386	6	5480796-5	Patent No. 5480796
545	5	20.8	339	2	US-09-248-796A-16100	Sequence 16100, A	618	5	20.8	389	2	US-09-270-767-44335	Sequence 44335, A
546	5	20.8	339	2	US-09-248-796A-20595	Sequence 20595, A	619	5	20.8	389	2	US-09-248-796A-15248	Sequence 15248, A
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548	5	20.8	340	1	US-08-107-676-3	Sequence 3, Appli	621	5	20.8	392	2	US-09-248-796A-21883	Sequence 21883, A
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550	5	20.8	340	1	US-08-997-080-37	Sequence 37, Appli	623	5	20.8	393	2	US-09-248-796A-18493	Sequence 18493, A
551	5	20.8	340	1	US-08-997-362-37	Sequence 37, Appli	624	5	20.8	393	2	US-09-248-796A-26699	Sequence 26699, A
552	5	20.8	340	2	US-08-873-970-37	Sequence 37, Appli	625	5	20.8	394	2	US-09-248-796A-19661	Sequence 19661, A
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554	5	20.8	340	2	US-08-705-347A-37	Sequence 37, Appli	627	5	20.8	395	2	US-09-538-092-857	Sequence 857, App
555	5	20.8	340	2	US-09-324-542-37	Sequence 37, Appli	628	5	20.8	396	1	US-07-841-646-5	Sequence 5, Appli
556	5	20.8	340	2	US-09-205-426-37	Sequence 37, Appli	629	5	20.8	396	1	US-07-901-703-15	Sequence 15, Appli
557	5	20.8	340	2	US-09-200-643-37	Sequence 37, Appli	630	5	20.8	396	1	US-08-147-023-5	Sequence 5, Appli
558	5	20.8	340	2	US-09-107-532A-3720	Sequence 3720, Ap	631	5	20.8	396	1	US-08-447-570-5	Sequence 5, Appli
559	5	20.8	340	2	US-09-295-820-3	Sequence 3, Appli	632	5	20.8	396	1	US-08-459-346-10	Sequence 10, Appli
560	5	20.8	340	2	US-09-295-820-31	Sequence 31, Appli	633	5	20.8	396	1	US-08-449-700-5	Sequence 5, Appli
561	5	20.8	341	2	US-09-248-796A-26889	Sequence 26889, A	634	5	20.8	396	1	US-07-989-847-2	Sequence 5, Appli
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563	5	20.8	344	6	5480796-7	Patent No. 5480796	636	5	20.8	396	1	US-08-889-419-10	Sequence 10, Appli
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565	5	20.8	349	2	US-09-248-796A-17015	Sequence 17015, A	638	5	20.8	396	2	US-08-469-411-2	Sequence 2, Appli
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572	5	20.8	355	2	US-09-270-767-45275	Sequence 2, Appli	645	5	20.8	396	2	US-09-248-796A-18742	Sequence 18742, A
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575	5	20.8	359	2	US-09-248-796A-15017	Sequence 15017, A	648	5	20.8	396	4	PCT-US93-05446-15	Sequence 15, Appli
576	5	20.8	360	2	US-09-313-942-15	Sequence 15, Appli	649	5	20.8	396	4	PCT-US93-07189-10	Sequence 10, Appli
577	5	20.8	360	2	US-09-248-796A-27270	Sequence 27270, A	650	5	20.8	396	6	5166058-4	Patent No. 5166058
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580	5	20.8	361	2	US-09-362-842-14	Sequence 14, Appli	653	5	20.8	400	6	5168050-5	Patent No. 5168050
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582	5	20.8	361	2	US-09-248-796A-20099	Sequence 20099, A	655	5	20.8	402	2	US-09-248-796A-18910	Sequence 18910, A
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586	5	20.8	362	2	US-09-270-767-45770	Sequence 45770, A	659	5	20.8	406	1	US-07-973-431B-1	Sequence 1, Appli
587	5	20.8	364	2	US-09-051-755-14	Sequence 14, Appli	660	5	20.8	409	2	US-09-270-767-44594	Sequence 44594, A
588	5	20.8	369	2	US-09-487-558B-468	Sequence 59756, A	661	5	20.8	409	2	US-09-248-796A-16363	Sequence 16363, A
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590	5	20.8	370	2	US-09-248-796A-21722	Sequence 21722, A	663	5	20.8	411	1	US-08-362-670B-28	Sequence 92, Appli
591	5	20.8	370	2	US-09-685-296-39	Sequence 39, Appli	664	5	20.8	411	1	US-08-333-676C-28	Sequence 28, Appli
592	5	20.8	370	2	US-09-574-141A-56	Sequence 56, Appli	665	5	20.8	411	2	US-08-808-324-28	Sequence 28, Appli
593	5	20.8	371	2	US-09-568-189A-56	Sequence 56, Appli	666	5	20.8	411	2	US-09-945-182-28	Sequence 28, Appli
594	5	20.8	371	2	US-09-270-767-46033	Sequence 46033, A	667	5	20.8	411	2	PCT-US94-14030A-18500	Sequence 18500, A
595	5	20.8	371	6	5168050-3	Patent No. 5168050	668	5	20.8	411	4	PCT-US94-14030A-28	Sequence 28, Appli
596	5	20.8	372	2	US-09-538-092-1035	Sequence 1035, Ap	669	5	20.8	412	2	US-09-248-796A-16539	Sequence 16539, A
597	5	20.8	372	2	US-09-543-681A-5137	Sequence 5137, Ap	670	5	20.8	413	2	US-08-942-572-2	Sequence 2, Appli
598	5	20.8	373	2	US-09-248-796A-14832	Sequence 14832, A	671	5	20.8	413	2	US-09-614-069-13	Sequence 13, Appli
599	5	20.8	373	2	US-09-538-092-683	Sequence 683, App	672	5	20.8	413	2	US-09-821-803A-7	Sequence 7, Appli
600	5	20.8	374	2	US-09-270-767-43192	Sequence 43192, A	673	5	20.8	413	2	US-09-821-803A-8	Sequence 8, Appli
601	5	20.8	374	2	US-09-248-796A-16020	Sequence 16020, A	674	5	20.8	413	2	US-09-248-796A-15624	Sequence 15624, A
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688	5	20.8	428	2	US-08-477-346-29	Sequence 29, Appl	761	5	20.8	499	2	US-09-993-777-69	Sequence 69, Appl
689	5	20.8	428	2	US-08-473-089-29	Sequence 29, Appl	762	5	20.8	499	4	PCT-US96-03916-8	Sequence 8, Appl
690	5	20.8	428	2	US-08-487-072A-29	Sequence 29, Appl	763	5	20.8	499	4	PCT-US96-03916-69	Sequence 69, Appl
691	5	20.8	429	2	US-09-438-185A-497	Sequence 497, App	764	5	20.8	508	1	US-07-891-942G-10	Sequence 10, Appl
692	5	20.8	431	2	US-09-107-532A-7056	Sequence 7056, Ap	765	5	20.8	508	2	US-09-248-796A-20809	Sequence 20809, A
693	5	20.8	431	2	US-09-489-039A-12670	Sequence 12670, A	766	5	20.8	508	2	US-09-639-207-1	Sequence 1, Appl
694	5	20.8	432	2	US-09-118-319-2	Sequence 2, Appl	767	5	20.8	509	2	US-09-252-991A-22513	Sequence 22513, A
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696	5	20.8	434	2	US-09-248-796A-16502	Sequence 16502, A	769	5	20.8	510	2	US-09-270-767-44374	Sequence 44374, A
697	5	20.8	435	2	US-09-248-796A-15070	Sequence 15070, A	770	5	20.8	510	2	US-09-248-796A-18513	Sequence 18513, A
698	5	20.8	437	2	US-08-713-556F-40	Sequence 40, Appl	771	5	20.8	512	2	US-09-142-108C-6	Sequence 6, Appl
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700	5	20.8	440	2	US-10-104-047-3856	Sequence 3856, Ap	773	5	20.8	513	1	US-08-464-272-2	Sequence 2, Appl
701	5	20.8	442	2	US-09-248-796A-17027	Sequence 17027, A	774	5	20.8	513	2	US-08-464-514-2	Sequence 2, Appl
702	5	20.8	444	1	US-07-881-075-3	Sequence 3, Appl	775	5	20.8	513	2	US-08-486-403-2	Sequence 2, Appl
703	5	20.8	444	1	US-08-120-827-3	Sequence 3, Appl	776	5	20.8	513	2	US-09-248-796A-25078	Sequence 25078, A
704	5	20.8	444	1	US-08-478-675-3	Sequence 3, Appl	777	5	20.8	514	2	US-09-679-686B-22	Sequence 22, Appl
705	5	20.8	445	2	US-09-270-767-46024	Sequence 46024, A	778	5	20.8	515	2	US-09-270-767-45839	Sequence 45839, A
706	5	20.8	445	2	US-09-248-796A-15251	Sequence 15251, A	779	5	20.8	517	2	US-09-248-796A-20437	Sequence 20437, A
707	5	20.8	448	1	US-08-231-342-23	Sequence 23, Appl	780	5	20.8	518	2	US-09-881-578A-4	Sequence 4, Appl
708	5	20.8	448	2	US-09-270-767-32701	Sequence 32701, A	781	5	20.8	518	2	US-09-424-978B-24	Sequence 24, Appl
709	5	20.8	448	2	US-09-639-576-8	Sequence 8, Appl	782	5	20.8	518	2	US-09-976-594-287	Sequence 287, App
710	5	20.8	450	2	US-09-248-796A-15183	Sequence 15183, A	783	5	20.8	520	2	US-09-919-039-143	Sequence 143, App
711	5	20.8	451	2	US-09-248-796A-15356	Sequence 15356, A	784	5	20.8	518	2	US-09-248-796A-19845	Sequence 19845, A
712	5	20.8	454	2	US-09-717-364A-23	Sequence 23, Appl	785	5	20.8	519	2	US-09-248-796A-14534	Sequence 14534, A
713	5	20.8	454	2	US-09-270-767-45646	Sequence 45646, A	786	5	20.8	523	2	US-09-910-174B-11	Sequence 11, Appl
714	5	20.8	460	2	US-09-270-767-60881	Sequence 60881, A	787	5	20.8	523	2	US-09-620-461-11	Sequence 11, Appl
715	5	20.8	461	2	US-09-248-796A-23597	Sequence 23597, A	788	5	20.8	524	2	US-09-248-796A-20256	Sequence 20256, A
716	5	20.8	463	2	US-09-082-310-1	Sequence 1, Appl	789	5	20.8	525	2	US-09-976-594-64	Sequence 64, Appl
717	5	20.8	463	2	US-09-575-205-1	Sequence 1, Appl	790	5	20.8	525	2	US-09-919-039-62	Sequence 62, Appl
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719	5	20.8	464	2	US-09-426-072-2	Sequence 2, Appl	792	5	20.8	527	2	US-09-910-174B-10	Sequence 10, Appl
720	5	20.8	468	2	US-08-795-473B-5	Sequence 5, Appl	793	5	20.8	527	2	US-09-620-461-10	Sequence 10, Appl
721	5	20.8	468	2	US-09-439-856-5	Sequence 5, Appl	794	5	20.8	529	1	US-07-891-942G-8	Sequence 8, Appl
722	5	20.8	468	2	US-09-949-016-5959	Sequence 5959, Ap	795	5	20.8	529	1	US-08-370-909-19	Sequence 19, Appl
723	5	20.8	468	6	5171840-2	Sequence 5171840	796	5	20.8	529	1	US-08-504-048-8	Sequence 8, Appl
724	5	20.8	468	6	5480796-2	Patent No. 5480796	797	5	20.8	529	1	US-09-341-982-1	Sequence 1, Appl
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726	5	20.8	472	2	US-09-004-838-40	Sequence 40, Appl	799	5	20.8	529	2	US-09-620-461-13	Sequence 13, Appl
727	5	20.8	472	2	US-09-004-838-48	Sequence 48, Appl	800	5	20.8	529	2	US-09-169-717E-39	Sequence 39, Appl
728	5	20.8	472	2	US-09-004-838-103	Sequence 103, App	801	5	20.8	529	2	US-10-011-436-4	Sequence 4, Appl
729	5	20.8	472	2	US-09-538-092-312	Sequence 312, App	802	5	20.8	529	2	US-08-533-895A-39	Sequence 39, Appl
730	5	20.8	473	2	US-09-107-433-4669	Sequence 4669, Ap	803	5	20.8	532	2	US-09-826-509-521	Sequence 521, App
731	5	20.8	475	2	US-09-248-796A-17531	Sequence 17531, A	804	5	20.8	532	2	US-09-487-558B-162	Sequence 162, App
732	5	20.8	478	2	US-09-004-838-105	Sequence 105, App	805	5	20.8	535	2	US-09-269-731-4	Sequence 4, Appl
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ALIGNMENTS

RESULT 1
US-09-513-999C-5651
; Sequence 5651, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
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; SOFTWARE: Patent.pm
; SEQ ID NO 5651
; LENGTH: 95
; TYPE: PPT
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US-09-513-999C-5651
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Best Local Similarity 100.0%; Pred. No. 2.4e-17;
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RESULT 2
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; Sequence 1, Application US/08254493
; Patent No. 5439886
; GENERAL INFORMATION:
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; APPLICANT: SENOO, MASAHARU
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND
; TITLE OF INVENTION: PRODUCTION THEREOF
; NUMBER OF SEQUENCES: 7

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Sequence 13928, A
Sequence 282, App
Sequence 11143, A

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ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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INFORMATION FOR SEQ ID NO: 1:
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STRANDEDNESS: single
TOPOLOGY: linear
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; GENERAL INFORMATION:
; APPLICANT: June, Carl H.
; APPLICANT: Thompson, Craig B.
; APPLICANT: Nabel, Gary J.
; APPLICANT: Gray, Gary S.
; APPLICANT: Rennert, Paul D.
; APPLICANT: Freeman, Gordon J.
; TITLE OF INVENTION: METHODS FOR SELECTIVELY STIMULATING
; TITLE OF INVENTION: PROLIFERATION OF T-CELLS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
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STREET: 60 STATE STREET, SUITE 510
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STATE: MA
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COUNTRY: USA  
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COMPUTER READABLE FORM:  
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OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII TEXT  
CURRENT APPLICATION DATA:  
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APPLICATION NUMBER: US 08/200,947  
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FILING DATE: 7 APR 1992  
APPLICATION NUMBER: 08/218,155  
FILING DATE: 25 MAR 1994  
APPLICATION NUMBER: US 07/864,807  
FILING DATE: 7 APR 1992  
APPLICATION NUMBER: US 07/902,467  
FILING DATE: 16 JUNE 1992  
APPLICATION NUMBER: US 07/275,433  
FILING DATE: 23 NOV 1988  
ATTORNEY/AGENT INFORMATION:  
NAME: MANDRAGOURAS, AMY E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: RPI-002CPB  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 227 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-253-751-6

Query Match 100.0%; Score 24; DB 1; Length 227;  
Best Local Similarity 100.0%; Pred. No. 5.2e-17;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LRFDSQTKSIFQEQTNNNSSFYT 24  
|||||  
Db 34 LRFDSQTKSIFQEQTNNNSSFYT 57  
|||||

RESULT 4  
US-08-453-925-6  
Sequence 6, Application US/08453925  
Patent No. 583223  
GENERAL INFORMATION:  
APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.  
APPLICANT: Gray, Gary S., Rennert, Paul D., Freeman, Gordon J.  
TITLE OF INVENTION: METHODS FOR SELECTIVELY STIMULATING  
PROLIFERATION OF T-CELLS  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 STATE STREET, SUITE 510  
CITY: BOSTON  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII TEXT  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/453,925  
FILING DATE: 30 MAY 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/253,751  
FILING DATE: 3 JUNE 1994  
APPLICATION NUMBER: US 08/073,223  
FILING DATE: 4 JUNE 1993  
APPLICATION NUMBER: US 08/200,947  
FILING DATE: 23 FEB 1994  
APPLICATION NUMBER: US 07/864,805  
FILING DATE: 7 APR 1992  
APPLICATION NUMBER: US 08/247,505  
FILING DATE: 23 MAY 1994  
APPLICATION NUMBER: US 07/864,866  
FILING DATE: 7 APR 1992  
APPLICATION NUMBER: 08/218,155  
FILING DATE: 25 MAR 1994  
APPLICATION NUMBER: US 07/864,807  
FILING DATE: 7 APR 1992  
APPLICATION NUMBER: US 07/902,467  
FILING DATE: 16 JUNE 1992  
APPLICATION NUMBER: US 07/275,433  
FILING DATE: 23 NOV 1988  
ATTORNEY/AGENT INFORMATION:  
NAME: MANDRAGOURAS, AMY E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: RPI-002CPB  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 227 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-453-925-6

Query Match 100.0%; Score 24; DB 1; Length 227;  
Best Local Similarity 100.0%; Pred. No. 5.2e-17;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LRFDSQTKSIFQEQTNNNSSFYT 24  
|||||  
Db 34 LRFDSQTKSIFQEQTNNNSSFYT 57  
|||||

RESULT 5  
US-08-403-253A-6  
Sequence 6, Application US/08403253A  
Patent No. 6352694  
GENERAL INFORMATION:  
APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.  
APPLICANT: Gray, Gary S., Rennert, Paul D.  
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/403,253A

;; FILING DATE: March 10, 1995  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/253,964  
;; FILING DATE: 3 JUNE 1994  
;; APPLICATION NUMBER: US 08/073,223  
;; FILING DATE: 4 JUNE 1993  
;; APPLICATION NUMBER: US 08/200,947  
;; FILING DATE: 23 FEB 1994  
;; APPLICATION NUMBER: US 07/864,805  
;; FILING DATE: 7 APR 1992  
;; APPLICATION NUMBER: US 08/247,505  
;; FILING DATE: 25 MAR 1994  
;; APPLICATION NUMBER: US 07/864,807  
;; FILING DATE: 7 APR 1992  
;; APPLICATION NUMBER: US 07/902,467  
;; FILING DATE: 16 JUNE 1992  
;; APPLICATION NUMBER: US 07/275,433  
;; FILING DATE: 23 NOV 1988  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Mandragouras, Amy E.  
;; REGISTRATION NUMBER: 36,207  
;; REFERENCE/DOCKET NUMBER: RPI-002CP2  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617) 227-7400  
;; TELEFAX: (617) 742-4214  
;; INFORMATION FOR SEQ ID NO: 6:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 227 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-403-253A-6

Query Match 100.0%; Score 24; DB 2; Length 227;  
Best Local Similarity 100.0%; Pred. No. 5.2e-17;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LRFDSTKSIPEQETNNNSFYT 24  
Db 34 LRFDSTKSIPEQETNNNSFYT 57

## RESULT 6

US-08-435-816A-6  
; Sequence 6, Application US/08435816A  
; Patent No. 6534055  
; GENERAL INFORMATION:  
; APPLICANT: June, Carl H.  
; APPLICANT: Thompson, Craig B.  
; APPLICANT: Nabel, Gary J.  
; APPLICANT: Gray, Gary S.  
; APPLICANT: Rennert, Paul D.  
; TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street, Suite 510  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/435,816A

;; FILING DATE: May 4, 1995  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/403,253  
;; FILING DATE: 10 MARCH 1995  
;; APPLICATION NUMBER: US 08/253,964  
;; FILING DATE: 3 JUNE 1994  
;; APPLICATION NUMBER: US 08/073,223  
;; FILING DATE: 4 JUNE 1993  
;; APPLICATION NUMBER: US 08/200,947  
;; FILING DATE: 23 FEB 1994  
;; APPLICATION NUMBER: US 07/864,805  
;; FILING DATE: 7 APR 1992  
;; APPLICATION NUMBER: US 08/247,505  
;; FILING DATE: 23 MAY 1994  
;; APPLICATION NUMBER: US 07/864,866  
;; FILING DATE: 7 APR 1992  
;; APPLICATION NUMBER: US 08/218,155  
;; FILING DATE: 25 MAR 1994  
;; APPLICATION NUMBER: US 07/864,807  
;; FILING DATE: 7 APR 1992  
;; APPLICATION NUMBER: US 07/902,467  
;; FILING DATE: 16 JUNE 1992  
;; APPLICATION NUMBER: US 07/275,433  
;; FILING DATE: 23 NOV 1988  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Mandragouras, Amy E.  
;; REGISTRATION NUMBER: 36,207  
;; REFERENCE/DOCKET NUMBER: RPI-002CP3  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617) 227-7400  
;; TELEFAX: (617) 227-5941  
;; INFORMATION FOR SEQ ID NO: 6:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 227 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-435-816A-6

Query Match 100.0%; Score 24; DB 2; Length 227;  
Best Local Similarity 100.0%; Pred. No. 5.2e-17;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LRFDSTKSIPEQETNNNSFYT 24  
Db 34 LRFDSTKSIPEQETNNNSFYT 57

## RESULT 7

US-09-350-202-6  
; Sequence 6, Application US/09350202  
; Patent No. 6887466  
; GENERAL INFORMATION:  
; APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.  
; APPLICANT: Gray, Gary S., Rennert, Paul D.  
; TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/350,202  
; FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/403,253  
FILING DATE: March 10, 1995  
APPLICATION NUMBER: US 08/253,964  
FILING DATE: 3 JUNE 1994  
APPLICATION NUMBER: US 08/073,223  
FILING DATE: 4 JUNE 1993  
APPLICATION NUMBER: US 08/200,947  
FILING DATE: 23 FEB 1994  
APPLICATION NUMBER: US 07/864,805  
FILING DATE: 7 APR 1992  
APPLICATION NUMBER: US 08/247,505  
FILING DATE: 23 MAY 1994  
APPLICATION NUMBER: US 07/864,866  
FILING DATE: 7 APR 1992  
APPLICATION NUMBER: US 08/218,155  
FILING DATE: 25 MAR 1994  
APPLICATION NUMBER: US 07/864,807  
FILING DATE: 7 APR 1992  
APPLICATION NUMBER: US 07/902,467  
FILING DATE: 16 JUNE 1992  
APPLICATION NUMBER: US 07/275,433  
FILING DATE: 23 NOV 1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: RPI-002CP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 742-4214  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 227 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-350-202-6

Query Match 100.0%; Score 24; DB 2; Length 227;  
Best Local Similarity 100.0%; Pred. No. 5.2e-17;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSQTKSIFQEQTNNNSPYT 24  
Db 34 LRFDSQTKSIFQEQTNNNSPYT 57

RESULT 8  
US-08-592-711-6  
Sequence 6, Application US/08592711  
Patent No. 6905680  
GENERAL INFORMATION:

APPLICANT: June, Carl H.  
APPLICANT: Thompson, Craig B.  
APPLICANT: Nabel, Gary J.  
APPLICANT: Gray, Gary S.  
APPLICANT: Remert, Paul D.

TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells

NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/592,711  
FILING DATE: 26-JAN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/435,816  
FILING DATE: 4-MAY-1995  
APPLICATION NUMBER: US 08/403,253  
FILING DATE: 10-MARCH-1995  
APPLICATION NUMBER: US 08/253,964  
FILING DATE: 3-JUNE-1994  
APPLICATION NUMBER: US 08/073,223  
FILING DATE: 4-JUNE-1993  
APPLICATION NUMBER: US 08/200,947  
FILING DATE: 23-FEB-1994  
APPLICATION NUMBER: US 07/864,805  
FILING DATE: 7-APR-1992  
APPLICATION NUMBER: US 08/247,505  
FILING DATE: 23-MAY-1994  
APPLICATION NUMBER: US 07/864,866  
FILING DATE: 7-APR-1992  
APPLICATION NUMBER: US 08/218,155  
FILING DATE: 25-MAR-1994  
APPLICATION NUMBER: US 07/864,807  
FILING DATE: 7-APR-1992  
APPLICATION NUMBER: US 07/902,467  
FILING DATE: 16-JUNE-1992  
APPLICATION NUMBER: US 07/275,433  
FILING DATE: 23-NOV-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: RPI-002CP4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 227 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-592-711-6

Query Match 100.0%; Score 24; DB 2; Length 227;  
Best Local Similarity 100.0%; Pred. No. 5.2e-17;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSQTKSIFQEQTNNNSPYT 24  
Db 34 LRFDSQTKSIFQEQTNNNSPYT 57

RESULT 9

US-09-349-915B-6  
Sequence 6, Application US/09349915B  
Patent No. 6905681  
GENERAL INFORMATION:

APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.

TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells

NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HALE AND DORR LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25



;  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/349,915B  
; FILING DATE: 01-AUG-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/403,253  
; FILING DATE: March 10, 1995  
; APPLICATION NUMBER: US 08/253,964  
; FILING DATE: 3 JUNE 1994  
; APPLICATION NUMBER: US 08/073,223  
; FILING DATE: 4 JUNE 1993  
; APPLICATION NUMBER: US 08/200,947  
; FILING DATE: 23 FEB 1994  
; APPLICATION NUMBER: US 07/864,805  
; FILING DATE: 7 APR 1992  
; APPLICATION NUMBER: US 08/247,505  
; FILING DATE: 23 MAY 1994  
; APPLICATION NUMBER: US 07/864,866  
; FILING DATE: 7 APR 1992  
; APPLICATION NUMBER: US 08/218,155  
; FILING DATE: 25 MAR 1994  
; APPLICATION NUMBER: US 07/864,807  
; FILING DATE: 7 APR 1992  
; APPLICATION NUMBER: US 07/902,467  
; FILING DATE: 16 JUNE 1992  
; APPLICATION NUMBER: US 07/275,433  
; FILING DATE: 23 NOV 1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Superko, Colleen  
; REGISTRATION NUMBER: 39,850  
; REFERENCE/DOCKET NUMBER: 36119-125 (US10)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 526-6564  
; TELEFAX: (617) 526-5000  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-349-915B-6

Query Match 100.0%; Score 24; DB 2; Length 227;  
Best Local Similarity 100.0%; Pred. No. 5.2e-17;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LRFDSQTKSIFQEQTNNNSFYT 24  
Db 34 LRFDSQTKSIFQEQTNNNSFYT 57

RESULT 10  
US-08-408-222B-1  
; Sequence 1, Application US/08408222B  
; Patent No. 5776727  
; GENERAL INFORMATION:  
; APPLICANT: Ikeyama, Shuichi  
; APPLICANT: Koyama, Masaru  
; APPLICANT: Miyake, Masayuki  
; APPLICANT: Senoo, Masaharu  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: DIKE, Bronstein, Roberts & Cushman  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/254,493

;  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/408,222B  
; FILING DATE: 22-MAR-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/254,493  
; FILING DATE: 06-JUN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP-079996-1991  
; FILING DATE: 12-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP-085396-1991  
; FILING DATE: 14-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP-022321-1992  
; FILING DATE: 07-FEB-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Resnick, David S.  
; REGISTRATION NUMBER: 34,235  
; REFERENCE/DOCKET NUMBER: 41777-DIV  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-523-3400  
; TELEFAX: 617-523-6440  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 228 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHEetical: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
US-08-408-222B-1

Query Match 100.0%; Score 24; DB 1; Length 228;  
Best Local Similarity 100.0%; Pred. No. 5.3e-17;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LRFDSQTKSIFQEQTNNNSFYT 24  
Db 35 LRFDSQTKSIFQEQTNNNSFYT 58

RESULT 11  
US-08-254-493-7  
; Sequence 7, Application US/08254493  
; Patent No. 5439886  
; GENERAL INFORMATION:  
; APPLICANT: IKEYAMA, SHUICHI  
; APPLICANT: KOYAMA, MASARU  
; APPLICANT: MIYAKE, MASAYUKI  
; APPLICANT: SENOO, MASAHARU  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DAVID G. CONLIN, DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
; STREET: 130 WATER STREET  
; CITY: BOSTON  
; STATE: MASSACHUSETTS  
; COUNTRY: US  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/254,493



;; FILING DATE: 435  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/865552  
;; FILING DATE: 09-APR-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: JP 0799996-1991  
;; FILING DATE: 12-APR-1991  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: JP 085396-1991  
;; FILING DATE: 17-APR-1991  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: JP 022321-1992  
;; FILING DATE: 07-FEB-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: RESNICK, DAVID S.  
;; REGISTRATION NUMBER: 34235  
;; REFERENCE/DOCKET NUMBER: 41777  
;; TELEPHONE: (617) 523-3400  
;; TELEFAX: (617) 523-6440  
;; TELEX: 200291 STRE UR  
;; INFORMATION FOR SEQ ID NO: 7:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 26 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-254-493-7

Query Match 95.8%; Score 23; DB 1; Length 26;  
Best Local Similarity 100.0%; Pred. No. 7.8e-17;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RFDSTKSIFFEQETNNNSFFYT 24  
Db 1 RFDSTKSIFFEQETNNNSFFYT 23

RESULT 12  
US-08-408-222B-7  
; Sequence 7, Application US/08408222B  
; Patent No. 5776727  
; GENERAL INFORMATION:  
; APPLICANT: Ikeyama, Shuichi  
; APPLICANT: Koyama, Masaru  
; APPLICANT: Miyake, Masaharu  
; APPLICANT: Senoo, Masaharu  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dike, Bronstein, Roberts & Cushman  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/408,222B  
; FILING DATE: 22-MAR-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/254,493  
; FILING DATE: 06-JUN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP-0799996-1991  
; FILING DATE: 12-APR-1991

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: JP-085396-1991  
;; FILING DATE: 14-APR-1991  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: JP-022321-1992  
;; FILING DATE: 07-FEB-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Resnick, David S.  
;; REGISTRATION NUMBER: 34,235  
;; REFERENCE/DOCKET NUMBER: 41777-DIV  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 617-523-3400  
;; TELEFAX: 617-523-6440  
;; INFORMATION FOR SEQ ID NO: 7:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 26 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; US-08-408-222B-7

Query Match 95.8%; Score 23; DB 1; Length 26;  
Best Local Similarity 100.0%; Pred. No. 7.8e-17;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RFDSTKSIFFEQETNNNSFFYT 24  
Db 1 RFDSTKSIFFEQETNNNSFFYT 23

RESULT 13  
US-09-270-767-41112  
; Sequence 41112, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 41112  
; LENGTH: 153  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
; FEATURE:  
; OTHER INFORMATION: Xaa means any amino acid  
US-09-270-767-41112

Query Match 29.2%; Score 7; DB 2; Length 153;  
Best Local Similarity 100.0%; Pred. No. 6.1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 56328, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
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; TYPE: PRT
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Query Match          29.2%; Score 7; DB 2; Length 153;
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RESULT 15
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; Sequence 4, Application US/08642846
; Patent No. 5856151
; GENERAL INFORMATION:
; APPLICANT: HOSTETTER, MARGARET K.
; APPLICANT: GALE, CHERYL A.
; APPLICANT: BENDEL, CATHERINE M.
; APPLICANT: TAO, NIAN-JUN
; APPLICANT: KENDRICK, KATHLEEN
; TITLE OF INVENTION: CANDIDA ALBICANS GENE, INTEGRIN-LIKE
; TITLE OF INVENTION: PROTEIN, ANTIBODIES, AND METHODS OF USE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MUETING, RAASCH, GERHARDT & SCHWAPPACH, P.A.
; STREET: 119 NORTH FOURTH STREET, SUITE 203
; CITY: MINNEAPOLIS
; STATE: MINNESOTA
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/642,846
; FILING DATE: 03-MAY-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: MUETING, ANN M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 110,00280101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1217
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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172	6	25.0	426	6	US-11-097-143-28551	Sequence 28551, A	245	6	25.0	706	5	US-10-840-060-172	Sequence 172, App
173	6	25.0	437	6	US-11-097-143-15138	Sequence 15138, A	246	6	25.0	706	6	US-11-097-143-5748	Sequence 5748, Ap

247	6	25.0	713	6	US-11-097-143-42672	Sequence 42672, A	320	6	25.0	1423	6	US-11-097-143-42390	Sequence 42390, A
248	6	25.0	720	4	US-10-369-493-12449	Sequence 12449, A	321	6	25.0	1447	5	US-10-745-237-76	Sequence 76, Appl
249	6	25.0	722	4	US-10-282-122A-51562	Sequence 51562, A	322	6	25.0	1464	6	US-11-097-143-10389	Sequence 10389, A
250	6	25.0	730	3	US-09-801-368-126	Sequence 126, Appl	323	6	25.0	1476	5	US-10-732-923-8767	Sequence 8767, Ap
251	6	25.0	732	3	US-09-994-485-8	Sequence 8, Appl	324	6	25.0	1476	6	US-11-097-143-2910	Sequence 2910, Ap
252	6	25.0	732	3	US-09-832-292-12	Sequence 12, Appl	325	6	25.0	1487	4	US-10-437-963-161300	Sequence 161300,
253	6	25.0	732	6	US-11-097-143-23142	Sequence 23142, A	326	6	25.0	1501	3	US-09-924-154-17	Sequence 17, Appl
254	6	25.0	742	5	US-10-741-849-7274	Sequence 7274, Ap	327	6	25.0	1504	4	US-10-369-493-2471	Sequence 2471, Ap
255	6	25.0	752	6	US-10-732-923-6886	Sequence 6886, Ap	328	6	25.0	1520	4	US-10-369-493-5596	Sequence 5596, Ap
256	6	25.0	761	6	US-11-097-143-41475	Sequence 41475, A	329	6	25.0	1526	4	US-10-369-493-5597	Sequence 5597, Ap
257	6	25.0	764	4	US-10-032-585-7597	Sequence 7597, Ap	330	6	25.0	1526	5	US-10-471-758-2	Sequence 2, Appl
258	6	25.0	765	6	US-11-097-143-37089	Sequence 37089, A	331	6	25.0	1531	3	US-09-876-883-347	Sequence 347, App
259	6	25.0	790	6	US-11-097-143-9105	Sequence 9105, Ap	332	6	25.0	1531	3	US-09-998-598-2593	Sequence 2593, A
260	6	25.0	814	6	US-11-097-143-31314	Sequence 31314, A	333	6	25.0	1531	4	US-10-171-311-222	Sequence 222, App
261	6	25.0	844	6	US-11-097-143-23046	Sequence 23046, A	334	6	25.0	1531	4	US-10-301-822-211	Sequence 211, App
262	6	25.0	848	4	US-10-369-493-18353	Sequence 18353, A	335	6	25.0	1531	4	US-10-435-695-46	Sequence 46, Appl
263	6	25.0	849	5	US-10-780-507-101	Sequence 101, Appl	336	6	25.0	1531	5	US-10-723-860-2100	Sequence 2100, Ap
264	6	25.0	856	3	US-09-949-029-66	Sequence 66, Appl	337	6	25.0	1531	5	US-10-645-756-42	Sequence 42, Appl
265	6	25.0	856	6	US-11-097-143-9741	Sequence 9741, Ap	338	6	25.0	1531	5	US-10-756-149-5261	Sequence 5261, Ap
266	6	25.0	856	6	US-11-097-143-33216	Sequence 33216, A	339	6	25.0	1531	5	US-10-745-237-268	Sequence 268, App
267	6	25.0	865	5	US-10-477-173-1036	Sequence 1036, Ap	340	6	25.0	1568	5	US-10-712-533A-12	Sequence 12, Appl
268	6	25.0	916	4	US-10-263-929-146	Sequence 146, Appl	341	6	25.0	1572	4	US-10-225-567A-344	Sequence 344, App
269	6	25.0	916	6	US-11-097-143-17637	Sequence 17637, Ap	342	6	25.0	1572	5	US-10-781-581-183	Sequence 183, App
270	6	25.0	920	6	US-11-097-143-12861	Sequence 12861, A	343	6	25.0	1573	4	US-10-292-798-870	Sequence 870, App
271	6	25.0	921	4	US-10-389-566-1850	Sequence 1850, Ap	344	6	25.0	1584	5	US-10-732-923-13548	Sequence 13548, A
272	6	25.0	921	5	US-10-477-173-1035	Sequence 1035, Ap	345	6	25.0	1613	4	US-10-464-368-83	Sequence 83, Appl
273	6	25.0	922	4	US-10-389-566-1848	Sequence 1848, Ap	346	6	25.0	1613	4	US-10-464-368-84	Sequence 84, Appl
274	6	25.0	924	4	US-10-389-566-1849	Sequence 1849, Ap	347	6	25.0	1613	5	US-10-477-238A-811	Sequence 811, App
275	6	25.0	924	4	US-10-389-566-1851	Sequence 1851, Ap	348	6	25.0	1613	5	US-10-680-287A-811	Sequence 811, App
276	6	25.0	938	6	US-11-097-143-8478	Sequence 8478, Ap	349	6	25.0	1613	5	US-10-477-173-764	Sequence 764, App
277	6	25.0	941	4	US-10-032-585-7930	Sequence 7930, Ap	350	6	25.0	1621	4	US-10-296-115-1161	Sequence 1161, Ap
278	6	25.0	941	5	US-10-450-763-56160	Sequence 56160, A	351	6	25.0	1626	4	US-10-408-765A-3017	Sequence 3017, Ap
279	6	25.0	943	6	US-11-097-143-13047	Sequence 13047, A	352	6	25.0	1626	5	US-10-745-237-270	Sequence 270, App
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281	6	25.0	950	6	US-11-097-143-40605	Sequence 40605, A	354	6	25.0	1664	3	US-09-964-858-1	Sequence 1, Appl
282	6	25.0	960	5	US-10-840-060-259	Sequence 259, Appl	355	6	25.0	1665	6	US-11-097-143-18822	Sequence 18822, A
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284	6	25.0	960	4	US-11-097-143-2094	Sequence 2094, Ap	357	6	25.0	1778	6	US-11-097-143-7035	Sequence 7035, Ap
285	6	25.0	968	4	US-10-263-929-158	Sequence 158, Appl	358	6	25.0	1805	6	US-11-097-143-22578	Sequence 22578, A
286	6	25.0	998	6	US-11-097-143-8061	Sequence 8061, Ap	359	6	25.0	1810	5	US-10-505-486-128	Sequence 128, App
287	6	25.0	1001	4	US-10-282-122A-58746	Sequence 58746, A	360	6	25.0	1874	4	US-10-424-599-248103	Sequence 248103,
288	6	25.0	1046	6	US-11-097-143-4713	Sequence 4713, Ap	361	6	25.0	1893	6	US-11-097-143-6279	Sequence 6279, Ap
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290	6	25.0	1070	5	US-10-732-923-6885	Sequence 6885, Ap	363	6	25.0	1980	6	US-11-097-143-29559	Sequence 29559, A
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294	6	25.0	1111	4	US-10-370-685-117	Sequence 117, Appl	367	6	25.0	2130	5	US-10-732-923-15030	Sequence 15030, A
295	6	25.0	1111	4	US-10-369-493-1413	Sequence 1413, Ap	368	6	25.0	2150	4	US-10-135-322-17	Sequence 17, Appl
296	6	25.0	1138	4	US-10-782-020-11	Sequence 11, Appl	369	6	25.0	2167	3	US-09-801-368-56	Sequence 56, Appl
297	6	25.0	1138	4	US-10-782-141-15	Sequence 15, Appl	370	6	25.0	2167	4	US-10-369-493-1773	Sequence 1773, Ap
298	6	25.0	1138	4	US-10-782-096-16	Sequence 16, Appl	371	6	25.0	2175	6	US-11-097-143-23886	Sequence 23886, A
299	6	25.0	1138	4	US-10-782-570-12	Sequence 12, Appl	372	6	25.0	2240	6	US-11-097-143-11742	Sequence 11742, A
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305	6	25.0	1173	6	US-11-097-143-11327	Sequence 11327, A	378	6	25.0	3190	5	US-10-732-923-18448	Sequence 18448, A
306	6	25.0	1194	6	US-11-097-143-5730	Sequence 5730, Ap	379	6	25.0	3275	5	US-10-840-060-90	Sequence 90, Appl
307	6	25.0	1195	5	US-10-732-923-4353	Sequence 4353, Ap	380	6	25.0	3275	6	US-11-097-143-38103	Sequence 38103, A
308	6	25.0	1195	6	US-11-097-143-17874	Sequence 17874, A	381	6	25.0	3276	5	US-10-732-923-18447	Sequence 18447, A
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310	6	25.0	1228	5	US-10-732-923-22378	Sequence 22378, A	383	6	25.0	3356	6	US-11-097-143-23232	Sequence 23232, A
311	6	25.0	1228	5	US-10-732-923-22466	Sequence 22466, A	384	6	25.0	3614	6	US-11-097-143-14784	Sequence 14784, A
312	6	25.0	1234	4	US-10-369-493-3432	Sequence 3432, Ap	385	6	25.0	6761	5	US-10-732-923-15035	Sequence 15035, A
313	6	25.0	1235	5	US-10-732-923-8669	Sequence 8669, Ap	386	5	20.8	9	3	US-09-935-384-41	Sequence 41, Appl
314	6	25.0	1244	4	US-10-369-493-1425	Sequence 1425, Ap	387	5	20.8	9	3	US-09-935-384-131	Sequence 131, App
315	6	25.0	1262	6	US-11-097-143-39309	Sequence 39309, A	388	5	20.8	9	3	US-09-935-384-229	Sequence 229, App
316	6	25.0	1266	4	US-10-320-797-3352	Sequence 3352, Ap	389	5	20.8	9	3	US-09-935-384-310	Sequence 310, App
317	6	25.0	1286	4	US-10-006-780-2	Sequence 2, Appl	390	5	20.8	9	3	US-09-935-384-419	Sequence 419, App
318	6	25.0	1402	4	US-10-369-493-5502	Sequence 5502, Ap	391	5	20.8	9	3	US-09-935-384-529	Sequence 529, App
319	6	25.0	1403	4	US-10-108-605-93	Sequence 93, Appl	392	5	20.8	9	3	US-09-935-384-616	Sequence 616, App

393	5	20.8	9	5	US-10-808-187-1154	Sequence 1154, Ap	466	5	20.8	58	4	US-10-424-599-224443	Sequence 224443,
394	5	20.8	9	5	US-10-705-459-307	Sequence 307, App	467	5	20.8	58	4	US-10-425-115-243522	Sequence 243522,
395	5	20.8	10	3	US-10-807-807-1134	Sequence 1134, Ap	468	5	20.8	59	4	US-10-424-599-174968	Sequence 174968,
396	5	20.8	10	3	US-09-935-384-368	Sequence 368, App	469	5	20.8	59	4	US-10-424-599-193462	Sequence 193462,
397	5	20.8	12	3	US-09-935-384-661	Sequence 661, App	470	5	20.8	59	4	US-10-437-963-138122	Sequence 138122,
398	5	20.8	12	3	US-09-982-173-186	Sequence 186, App	471	5	20.8	60	4	US-10-424-599-239679	Sequence 239679,
399	5	20.8	12	3	US-09-982-173-245	Sequence 245, App	472	5	20.8	60	4	US-10-424-599-245557	Sequence 245557,
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401	5	20.8	16	4	US-10-239-313A-590	Sequence 590, App	474	5	20.8	61	4	US-10-425-115-280841	Sequence 280841,
402	5	20.8	16	4	US-10-312-732A-18	Sequence 18, Appl	475	5	20.8	62	4	US-10-425-115-280841	Sequence 280841,
403	5	20.8	18	4	US-10-225-567A-1150	Sequence 1150, Ap	476	5	20.8	63	4	US-10-424-599-254465	Sequence 254465,
404	5	20.8	18	4	US-10-225-567A-1588	Sequence 1588, Ap	477	5	20.8	63	4	US-10-424-599-252715	Sequence 252715,
405	5	20.8	21	3	US-09-962-756-501	Sequence 501, App	478	5	20.8	64	4	US-10-425-115-340966	Sequence 340966,
406	5	20.8	21	4	US-10-253-471-501	Sequence 501, App	479	5	20.8	64	4	US-10-425-115-366085	Sequence 366085,
407	5	20.8	21	4	US-10-253-493-501	Sequence 501, App	480	5	20.8	65	4	US-10-424-599-216258	Sequence 216258,
408	5	20.8	23	3	US-09-967-869A-501	Sequence 1, Appl	481	5	20.8	65	4	US-10-425-115-209526	Sequence 209526,
409	5	20.8	23	6	US-11-045-828-1	Sequence 1, Appl	482	5	20.8	65	4	US-10-425-115-246319	Sequence 246319,
410	5	20.8	25	4	US-10-416-249-377	Sequence 377, App	483	5	20.8	65	4	US-10-425-115-267115	Sequence 267115,
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412	5	20.8	30	3	US-09-864-761-42566	Sequence 42566, A	485	5	20.8	66	4	US-10-424-599-180651	Sequence 180651,
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414	5	20.8	30	4	US-10-296-734-1022	Sequence 1022, Ap	487	5	20.8	66	4	US-10-437-963-203810	Sequence 203810,
415	5	20.8	30	4	US-10-296-734-1024	Sequence 1024, Ap	488	5	20.8	66	4	US-10-425-115-188731	Sequence 188731,
416	5	20.8	31	5	US-10-742-469-121	Sequence 121, App	489	5	20.8	66	4	US-10-425-115-230429	Sequence 230429,
417	5	20.8	32	4	US-10-425-115-263987	Sequence 263987, A	490	5	20.8	66	4	US-10-425-115-295616	Sequence 295616,
418	5	20.8	32	5	US-10-742-469-198	Sequence 198, App	491	5	20.8	66	5	US-10-734-049A-227	Sequence 227, App
419	5	20.8	35	4	US-10-425-114-54234	Sequence 54234, A	492	5	20.8	67	4	US-10-424-599-153314	Sequence 153314,
420	5	20.8	36	3	US-09-994-595-128	Sequence 128, App	493	5	20.8	67	4	US-10-424-599-166051	Sequence 166051,
421	5	20.8	37	4	US-10-289-228-34	Sequence 34, Appl	494	5	20.8	67	4	US-10-424-599-262490	Sequence 262490,
422	5	20.8	37	4	US-10-373-592-34	Sequence 34, Appl	495	5	20.8	67	4	US-10-416-800-43	Sequence 43, Appl
423	5	20.8	37	4	US-10-373-592-93	Sequence 93, Appl	496	5	20.8	67	4	US-10-416-800-51	Sequence 51, Appl
424	5	20.8	37	4	US-10-431-596-34	Sequence 34, Appl	497	5	20.8	67	4	US-10-437-963-156391	Sequence 156391,
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426	5	20.8	41	3	US-09-864-761-44443	Sequence 44443, A	499	5	20.8	68	4	US-10-425-115-274211	Sequence 274211,
427	5	20.8	41	5	US-10-450-763-49964	Sequence 49964, A	500	5	20.8	68	4	US-10-424-599-171534	Sequence 171534,
428	5	20.8	42	3	US-09-764-860-351	Sequence 351, App	501	5	20.8	68	4	US-10-424-599-198750	Sequence 198750,
429	5	20.8	42	4	US-10-074-095-351	Sequence 351, App	502	5	20.8	68	4	US-10-416-800-37	Sequence 37, Appl
430	5	20.8	42	4	US-10-212-872-351	Sequence 351, App	503	5	20.8	69	4	US-10-424-599-221673	Sequence 221673,
431	5	20.8	44	4	US-10-424-599-187438	Sequence 187438, A	504	5	20.8	69	4	US-10-424-599-232914	Sequence 232914,
432	5	20.8	44	4	US-10-724-972A-5486	Sequence 5486, Ap	505	5	20.8	69	4	US-10-416-800-1	Sequence 1, Appl
433	5	20.8	46	3	US-09-864-761-37857	Sequence 37857, A	506	5	20.8	69	4	US-10-416-800-32	Sequence 32, Appl
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438	5	20.8	49	4	US-10-239-423-22	Sequence 22, Appl	511	5	20.8	70	4	US-10-424-599-235907	Sequence 235907,
439	5	20.8	51	4	US-10-424-599-254039	Sequence 254039, A	512	5	20.8	70	4	US-10-424-599-279449	Sequence 279449,
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441	5	20.8	51	6	US-11-097-143-34218	Sequence 34218, A	514	5	20.8	72	4	US-10-424-599-253301	Sequence 253301,
442	5	20.8	52	4	US-10-218-102-350	Sequence 350, App	515	5	20.8	72	4	US-10-424-599-254522	Sequence 254522,
443	5	20.8	52	4	US-10-424-599-186362	Sequence 186362, A	516	5	20.8	72	4	US-10-416-800-49	Sequence 49, Appl
444	5	20.8	52	4	US-10-424-599-282154	Sequence 282154, A	517	5	20.8	72	4	US-10-425-115-313944	Sequence 313944,
445	5	20.8	52	4	US-10-716-293-12	Sequence 12, Appl	518	5	20.8	73	3	US-09-925-302-543	Sequence 543, App
446	5	20.8	52	4	US-10-716-293-14	Sequence 14, Appl	519	5	20.8	73	3	US-09-864-761-47535	Sequence 47535, A
447	5	20.8	53	4	US-10-424-599-174380	Sequence 174380, A	520	5	20.8	73	3	US-09-925-302-543	Sequence 543, App
448	5	20.8	53	4	US-10-424-599-180369	Sequence 180369, A	521	5	20.8	73	4	US-10-424-599-162722	Sequence 162722,
449	5	20.8	54	4	US-10-424-599-233625	Sequence 233625, A	522	5	20.8	73	4	US-10-424-599-233066	Sequence 233066,
450	5	20.8	54	4	US-10-424-599-279281	Sequence 279281, A	523	5	20.8	74	4	US-10-424-599-279629	Sequence 279629,
451	5	20.8	54	4	US-10-724-972A-7061	Sequence 7061, Ap	524	5	20.8	74	4	US-10-425-115-244533	Sequence 244533,
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543	5	20.8	78	4	US-10-319-763-225	Sequence 225, App	616	5	20.8	93	4	US-10-425-115-361668	Sequence 361668,
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577	5	20.8	87	4	US-10-424-599-189970	Sequence 189970,	650	5	20.8	104	4	US-10-474-776-712	Sequence 712, App
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581	5	20.8	87	4	US-10-437-963-178636	Sequence 178636,	654	5	20.8	105	3	US-09-935-384-776	Sequence 776, App
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## ALIGNMENTS

RESULT 1  
US-10-106-698-6825  
; Sequence 6825, Application US/10106698  
; Publication No. US20030109690A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide  
; FILE REFERENCE: PA005P1  
; CURRENT APPLICATION NUMBER: US/10/106,698  
; CURRENT FILING DATE: 2002-03-27  
; PRIOR APPLICATION NUMBER: PCT/US00/26524  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: US 60/157,137  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: US 60/163,280  
; PRIOR FILING DATE: 1999-11-03  
; NUMBER OF SEQ ID NOS: 8564  
; SOFTWARE: PatentIn Ver. 3.0  
; SEQ ID NO 6825  
; LENGTH: 209  
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: MISC\_FEATURE  
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; NAME/KEY: MISC\_FEATURE  
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; NAME/KEY: MISC\_FEATURE  
; LOCATION: (201)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (206)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-10-106-698-6825

Query Match 100.0%; Score 24; DB 4; Length 209;

Best Local Similarity 100.0%; Pred. No. 4.4e-17;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 73 LRFDSTKSIPEQETNNNSFYT 96  
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RESULT 2  
US-08-592-711-6  
; Sequence 6, Application US/08592711  
; Publication No. US20020115214A1  
; GENERAL INFORMATION:  
; APPLICANT: June, Carl H.  
; APPLICANT: Thompson, Craig B.  
; APPLICANT: Nabel, Gary J.  
; APPLICANT: Gray, Gary S.  
; APPLICANT: Rennett, Paul D.  
; TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/592,711  
; FILING DATE: 26-JAN-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/435,816  
; FILING DATE: 4-MAY-1995  
; APPLICATION NUMBER: US 08/403,253  
; FILING DATE: 10-MARCH-1995  
; APPLICATION NUMBER: US 08/253,964  
; FILING DATE: 3-JUNE-1994  
; APPLICATION NUMBER: US 08/073,223  
; FILING DATE: 4-JUNE-1993  
; APPLICATION NUMBER: US 08/200,947  
; FILING DATE: 23-FEB-1994  
; APPLICATION NUMBER: US 07/864,805  
; FILING DATE: 7-APR-1992  
; APPLICATION NUMBER: US 08/247,505  
; FILING DATE: 23-MAY-1994  
; APPLICATION NUMBER: US 07/864,866  
; FILING DATE: 7-APR-1992  
; APPLICATION NUMBER: US 08/218,155  
; FILING DATE: 25-MAR-1994  
; APPLICATION NUMBER: US 07/864,807  
; FILING DATE: 7-APR-1992  
; APPLICATION NUMBER: US 07/902,467  
; FILING DATE: 16-JUNE-1992  
; APPLICATION NUMBER: US 07/275,433  
; FILING DATE: 23-NOV-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mandragouras, Amy E.  
; REGISTRATION NUMBER: 36,207  
; REFERENCE/DOCKET NUMBER: RPT-002CP4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 6:  
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; TOPOLOGY: linear  
; MOLECULE TYPE: protein



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## RESULT 5

US-10-390-330-6  
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; Publication No. US20040001829A1  
; GENERAL INFORMATION:  
; APPLICANT: June, Carl H.  
; APPLICANT: Thompson, Craig B.  
; APPLICANT: Nabel, Gary J.  
; APPLICANT: Gray, Gary S.  
; APPLICANT: Remmert, Paul D.  
; TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation  
; TITLE OF INVENTION: Of T-Cells  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street, Suite 510  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/390,330  
; FILING DATE: March 17, 2003  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/435,816A  
; FILING DATE: May 4, 1995  
; CLASSIFICATION:  
; APPLICATION NUMBER: US 08/403,253  
; FILING DATE: 10 MARCH 1995  
; APPLICATION NUMBER: US 08/253,964  
; FILING DATE: 3 JUNE 1994  
; APPLICATION NUMBER: US 08/073,223  
; FILING DATE: 4 JUNE 1993  
; APPLICATION NUMBER: US 08/200,947  
; FILING DATE: 23 FEB 1994  
; APPLICATION NUMBER: US 07/864,805  
; FILING DATE: 7 APR 1992  
; APPLICATION NUMBER: US 08/247,505  
; FILING DATE: 23 MAY 1994  
; APPLICATION NUMBER: US 07/864,866  
; FILING DATE: 7 APR 1992  
; APPLICATION NUMBER: US 08/218,155  
; FILING DATE: 25 MAR 1994  
; APPLICATION NUMBER: US 07/864,807  
; FILING DATE: 7 APR 1992  
; APPLICATION NUMBER: US 07/902,467  
; FILING DATE: 16 JUNE 1992  
; APPLICATION NUMBER: US 07/275,433  
; FILING DATE: 23 NOV 1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mandregouras, Amy E.  
; REGISTRATION NUMBER: 36,207  
; REFERENCE/DOCKET NUMBER: RPI-002CP3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941

## ; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 227 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-10-390-330-6

Query Match 100.0%; Score 24; DB 4; Length 227;  
Best Local Similarity 100.0%; Pred. No. 4.7e-17;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSTKSIFFQETNNNSFYT 24  
|||||  
Db 34 LRFDSTKSIFFQETNNNSFYT 57

## RESULT 6

US-10-473-127-1723  
; Sequence 1723, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1723  
; LENGTH: 227  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1723

Query Match 100.0%; Score 24; DB 5; Length 227;  
Best Local Similarity 100.0%; Pred. No. 4.7e-17;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSTKSIFFQETNNNSFYT 24  
|||||  
Db 34 LRFDSTKSIFFQETNNNSFYT 57

## RESULT 7

US-10-473-127-1726  
; Sequence 1726, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370

```
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1726
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1726

Query Match      100.0%; Score 24; DB 5; Length 227;
Best Local Similarity 100.0%; Pred. No. 4.7e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LRFDSQTSIFEQETNNNSFYT 24
Db 34 LRFDSQTSIFEQETNNNSFYT 57

RESULT 8
US-10-156-136-39
; Sequence 39, Application US/10156136
; Publication No. US20030129696A1
; GENERAL INFORMATION:
; APPLICANT: Ni, et al.
; TITLE OF INVENTION: Polynucleotides and Polypeptides Encoding
; FILE REFERENCE: P5014R1-PCT
; CURRENT APPLICATION NUMBER: US 60/360,066
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 60/345,444
; PRIOR FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: US 60/351,885
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 60/360,066
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: US 60/362,004
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/366,869
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: US 60/366,284
; PRIOR FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: US 60/368,679
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 95
; SEQ ID NO 41
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-331-496A-41

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/156.136
FILING DATE: 29-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010.146
FILING DATE: <Unknown>
APPLICATION NUMBER: WO US98/00959
FILING DATE: 21-JAN-1998
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF354PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 228 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-156-136-39

Query Match      100.0%; Score 24; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 4.7e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 LRFDSQTSIFEQETNNNSFYT 24
Db 35 LRFDSQTSIFEQETNNNSFYT 58

RESULT 9
US-10-331-496A-41
; Sequence 41, Application US/10331496A
; Publication No. US20030228305A1
; GENERAL INFORMATION:
; APPLICANT: FRANTZ, GRETCHEN
; APPLICANT: HILLAN, KENNETH J.
; APPLICANT: PHILLIPS, HEIDI S.
; APPLICANT: POLAKIS, PAUL
; APPLICANT: SMITH, VICTORIA
; APPLICANT: SPENCER, SUSAN D.
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WU, THOMAS D.
; APPLICANT: ZHANG, ZEMIN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P5014R1-PCT
; CURRENT APPLICATION NUMBER: US/10/331,496A
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 60/345,444
; PRIOR FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: US 60/351,885
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 60/360,066
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: US 60/362,004
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/366,869
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: US 60/366,284
; PRIOR FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: US 60/368,679
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 95
; SEQ ID NO 41
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-331-496A-41

Query Match      100.0%; Score 24; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 4.7e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LRFDSQTSIFEQETNNNSFYT 24
Db 35 LRFDSQTSIFEQETNNNSFYT 58

RESULT 10
US-10-619-323-1
; Sequence 1, Application US/10619323
; Publication No. US20040136985A1
; GENERAL INFORMATION:
; APPLICANT: Jennings, Lisa K.
; APPLICANT: Longhurst, Celia M.
; APPLICANT: Cook, George A.
; APPLICANT: Bao, Jianxiong
; APPLICANT: Zhang, Chunxiang
; APPLICANT: White, Melanie M.
; APPLICANT: Crossno, Jr., Joseph T.
; APPLICANT: Lu, Yi
; TITLE OF INVENTION: METHODS OF MODIFYING BEHAVIOR OF CD9-EXPRESSING CELLS
; FILE REFERENCE: 20609/241
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; CURRENT APPLICATION NUMBER: US/10/619,323
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: 60/395,864
; PRIOR FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homosapien
US-10-619-323-1
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Query Match          100.0%; Score 24; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 4.7e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 LRFDSQTSIFEQETNNNSFYT 24
Db 35 LRFDSQTSIFEQETNNNSFYT 58
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RESULT 11
US-10-794-899-97
; Sequence 97, Application US/10794899
; Publication No. US20040146516A1
; GENERAL INFORMATION:
; APPLICANT: Utah Ventures
; TITLE OF INVENTION: Lumen-Exposed Molecules and Methods Targeted Delivery
; FILE REFERENCE: 27110-715
; CURRENT APPLICATION NUMBER: US/10/794,899
; CURRENT FILING DATE: 2004-03-05
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 97
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-794-899-97
```

```
Query Match          100.0%; Score 24; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 4.7e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 LRFDSQTSIFEQETNNNSFYT 24
Db 35 LRFDSQTSIFEQETNNNSFYT 58
```

```
RESULT 12
US-10-473-127-1714
; Sequence 1714, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR FILING DATE: 2001-05-21
; PRIOR FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2001-10-01
; PRIOR FILING DATE: 2001-12-04
; PRIOR FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2001-10-01
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 1714
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; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1714
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Query Match          100.0%; Score 24; DB 5; Length 228;
Best Local Similarity 100.0%; Pred. No. 4.7e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 LRFDSQTSIFEQETNNNSFYT 24
Db 35 LRFDSQTSIFEQETNNNSFYT 58
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RESULT 13
US-10-473-127-1715
; Sequence 1715, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1715
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1715
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```
Query Match          100.0%; Score 24; DB 5; Length 228;
Best Local Similarity 100.0%; Pred. No. 4.7e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 LRFDSQTSIFEQETNNNSFYT 24
Db 35 LRFDSQTSIFEQETNNNSFYT 58
```

```
RESULT 14
US-10-473-127-1716
; Sequence 1716, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
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; PRIOR APPLICATION NUMBER: 60/358,985  
 ; PRIOR FILING DATE: 2002-02-20  
 ; NUMBER OF SEQ ID NOS: 2041  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1716  
 ; LENGTH: 228  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-473-127-1716

Query Match 100.0%; Score 24; DB 5; Length 228;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-17;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LRPDSQTKSIFEQETNNNSSFYT 24  
 |||||  
 Db 35 LRPDSQTKSIFEQETNNNSSFYT 58

# RESULT 15

US-10-473-127-1718  
 ; Sequence 1718, Application US/10473127  
 ; Publication No. US20040236091A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Zycos Inc.  
 ; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
 ; FILE REFERENCE: 08191-026W01  
 ; CURRENT APPLICATION NUMBER: US/10/473,127  
 ; CURRENT FILING DATE: 2003-09-26  
 ; PRIOR APPLICATION NUMBER: 60/279,495  
 ; PRIOR FILING DATE: 2001-03-28  
 ; PRIOR APPLICATION NUMBER: 60/292,544  
 ; PRIOR FILING DATE: 2001-05-21  
 ; PRIOR APPLICATION NUMBER: 60/310,801  
 ; PRIOR FILING DATE: 2001-08-08  
 ; PRIOR APPLICATION NUMBER: 60/326,370  
 ; PRIOR FILING DATE: 2001-10-01  
 ; PRIOR APPLICATION NUMBER: 60/336,780  
 ; PRIOR FILING DATE: 2001-12-04  
 ; PRIOR APPLICATION NUMBER: 60/358,985  
 ; PRIOR FILING DATE: 2002-02-20  
 ; NUMBER OF SEQ ID NOS: 2041  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1718  
 ; LENGTH: 228  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-473-127-1718

Query Match 100.0%; Score 24; DB 5; Length 228;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-17;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LRPDSQTKSIFEQETNNNSSFYT 24  
 |||||  
 Db 35 LRPDSQTKSIFEQETNNNSSFYT 58

Search completed: January 20, 2006, 17:47:28  
 Job time : 38.6154 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:42:32 ; Search time 2.53846 Seconds  
(without alignments)  
95.811 Million cell updates/sec

Title: US-10-619-323-1\_COPY\_35\_58

Perfect score: 24

Sequence: 1 LRFDSTKSIPEQETNNNSFYT 24

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 70606 seqs, 1013881 residues

Word size : 0

Total number of hits satisfying chosen parameters: 70606

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Published Applications AA.New.\*

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2: /cgn2\_6/ptodata/1/pubppaa/US06\_NEW\_PUB.pep.\*

3: /cgn2\_6/ptodata/1/pubppaa/US07\_NEW\_PUB.pep.\*

4: /cgn2\_6/ptodata/1/pubppaa/PCT\_NEW\_PUB.pep.\*

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8: /cgn2\_6/ptodata/1/pubppaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	228	6	US-10-821-234-1266
2	6	25.0	131	7	US-11-052-554A-58
3	6	25.0	354	7	US-11-089-551A-4
4	6	25.0	592	6	US-10-467-962B-95
5	6	25.0	592	6	US-10-524-647-112
6	6	25.0	1531	7	US-11-087-227-24
7	6	25.0	1531	7	US-11-186-284-211
8	6	25.0	1613	7	US-11-108-528-88
9	6	25.0	1613	7	US-11-108-528-86
10	6	25.0	2053	7	US-11-013-759-9
11	5	20.8	9	7	US-11-045-024-616
12	5	20.8	10	7	US-11-045-024-770
13	5	20.8	23	6	US-10-467-657-8871
14	5	20.8	56	6	US-10-467-657-6884
15	5	20.8	78	5	US-09-978-360A-737
16	5	20.8	78	6	US-10-884-730-170
17	5	20.8	81	6	US-10-884-730-167
18	5	20.8	81	6	US-10-884-730-168
19	5	20.8	81	6	US-10-884-730-298
20	5	20.8	81	6	US-10-884-730-341
21	5	20.8	81	6	US-10-884-730-343
22	5	20.8	85	6	US-10-884-730-300
23	5	20.8	85	6	US-10-884-730-301
24	5	20.8	85	6	US-10-884-730-335
25	5	20.8	88	6	US-10-884-730-169
					Sequence 1266, Ap
					Sequence 58, Appl
					Sequence 4, Appli
					Sequence 95, Appl
					Sequence 112, App
					Sequence 211, App
					Sequence 84, Appl
					Sequence 86, Appl
					Sequence 9, Appli
					Sequence 616, App
					Sequence 770, App
					Sequence 8871, Ap
					Sequence 6884, Ap
					Sequence 737, App
					Sequence 170, App
					Sequence 167, App
					Sequence 168, App
					Sequence 181, App
					Sequence 298, App
					Sequence 341, App
					Sequence 343, App
					Sequence 300, App
					Sequence 301, App
					Sequence 335, App
					Sequence 169, App

26	5	20.8	88	6	US-10-884-730-297	Sequence 297, App
27	5	20.8	88	6	US-10-884-730-299	Sequence 299, App
28	5	20.8	88	6	US-10-884-730-302	Sequence 302, App
29	5	20.8	89	6	US-10-884-730-171	Sequence 171, App
30	5	20.8	89	6	US-10-884-730-174	Sequence 174, App
31	5	20.8	89	6	US-10-884-730-213	Sequence 213, App
32	5	20.8	89	6	US-10-884-730-340	Sequence 340, App
33	5	20.8	103	7	US-11-090-916-6	Sequence 6, Appli
34	5	20.8	111	6	US-10-884-730-338	Sequence 338, App
35	5	20.8	112	6	US-10-884-730-136	Sequence 136, App
36	5	20.8	114	6	US-10-467-657-5012	Sequence 5012, Ap
37	5	20.8	148	7	US-11-052-554A-359	Sequence 359, App
38	5	20.8	155	6	US-10-793-626-716	Sequence 716, App
39	5	20.8	167	6	US-10-793-626-808	Sequence 808, App
40	5	20.8	167	6	US-10-793-626-986	Sequence 986, App
41	5	20.8	167	6	US-10-793-626-2128	Sequence 2128, Ap
42	5	20.8	174	6	US-10-884-730-173	Sequence 173, App
43	5	20.8	188	6	US-10-884-730-294	Sequence 294, App
44	5	20.8	209	6	US-10-884-730-172	Sequence 172, App
45	5	20.8	230	6	US-10-884-730-370	Sequence 370, App
46	5	20.8	230	6	US-10-884-730-371	Sequence 371, App
47	5	20.8	230	6	US-10-884-730-377	Sequence 377, App
48	5	20.8	237	6	US-10-884-730-359	Sequence 359, App
49	5	20.8	246	6	US-10-793-626-900	Sequence 900, App
50	5	20.8	246	6	US-10-793-626-1956	Sequence 1956, Ap
51	5	20.8	259	6	US-10-512-184-34	Sequence 34, Appl
52	5	20.8	266	6	US-10-884-730-165	Sequence 165, App
53	5	20.8	266	6	US-10-884-730-166	Sequence 166, App
54	5	20.8	266	6	US-10-884-730-296	Sequence 296, App
55	5	20.8	266	6	US-10-884-730-334	Sequence 334, App
56	5	20.8	266	6	US-10-884-730-334	Sequence 334, App
57	5	20.8	275	7	US-11-000-463-868	Sequence 868, App
58	5	20.8	278	6	US-10-793-626-2700	Sequence 2700, Ap
59	5	20.8	287	6	US-10-467-657-5866	Sequence 5866, Ap
60	5	20.8	291	7	US-11-000-463-396	Sequence 396, App
61	5	20.8	299	6	US-10-793-626-1192	Sequence 1192, Ap
62	5	20.8	299	6	US-10-793-626-1768	Sequence 1768, Ap
63	5	20.8	300	6	US-10-667-295-117	Sequence 117, App
64	5	20.8	302	6	US-10-667-295-116	Sequence 116, App
65	5	20.8	314	6	US-10-467-657-5094	Sequence 5094, Ap
66	5	20.8	316	6	US-10-667-295-115	Sequence 115, App
67	5	20.8	371	6	US-10-512-184-71	Sequence 71, Appl
68	5	20.8	382	7	US-11-069-185-8	Sequence 8, Appli
69	5	20.8	390	6	US-10-821-234-1273	Sequence 1273, Ap
70	5	20.8	396	7	US-11-051-568-5	Sequence 5, Appli
71	5	20.8	399	6	US-10-821-234-1163	Sequence 1163, Ap
72	5	20.8	406	6	US-10-821-234-1521	Sequence 1521, Ap
73	5	20.8	410	6	US-10-821-234-952	Sequence 952, App
74	5	20.8	415	6	US-10-467-657-10	Sequence 10, Appl
75	5	20.8	415	6	US-10-467-657-5468	Sequence 5468, Ap
76	5	20.8	428	6	US-10-485-517-371	Sequence 371, App
77	5	20.8	433	6	US-10-793-626-1332	Sequence 1332, Ap
78	5	20.8	434	6	US-10-667-295-141	Sequence 141, App
79	5	20.8	476	7	US-11-024-959-385	Sequence 385, App
80	5	20.8	477	7	US-11-089-551A-34	Sequence 34, Appl
81	5	20.8	486	7	US-11-067-425A-82	Sequence 82, Appl
82	5	20.8	506	6	US-10-667-295-140	Sequence 140, App
83	5	20.8	510	6	US-10-467-657-3260	Sequence 3260, Ap
84	5	20.8	526	6	US-10-667-295-139	Sequence 139, App
85	5	20.8	527	7	US-11-113-424-81	Sequence 81, Appl
86	5	20.8	529	7	US-11-113-424-82	Sequence 82, Appl
87	5	20.8	529	7	US-11-033-039-487	Sequence 487, App
88	5	20.8	529	7	US-11-155-288-1	Sequence 1, Appli
89	5	20.8	532	7	US-11-127-877-42	Sequence 42, Appl
90	5	20.8	587	7	US-11-024-959-412	Sequence 412, App
91	5	20.8	626	6	US-10-512-184-49	Sequence 49, Appl
92	5	20.8	655	7	US-11-184-860-1	Sequence 1, Appli
93	5	20.8	655	7	US-11-124-368A-296	Sequence 296, App
94	5	20.8	655	7	US-11-124-368A-297	Sequence 297, App
95	5	20.8	685	6	US-10-490-824-5	Sequence 5, Appli
96	5	20.8	693	7	US-11-196-475-68	Sequence 68, Appl
97	5	20.8	710	7	US-11-089-551A-33	Sequence 33, Appl
98	5	20.8	718	7	US-11-147-109-6	Sequence 6, Appli

99	5	20.8	750	7	US-11-089-551A-32	Sequence 32, Appl	172	4	16.7	78	6	US-10-884-730-242	Sequence 242, App
100	5	20.8	758	7	US-11-089-551A-31	Sequence 31, Appl	173	4	16.7	78	6	US-10-884-730-254	Sequence 254, App
101	5	20.8	766	6	US-10-793-626-2578	Sequence 2578, Ap	174	4	16.7	78	6	US-10-884-730-290	Sequence 290, App
102	5	20.8	852	6	US-10-645-441-15	Sequence 15, Appl	175	4	16.7	79	6	US-10-884-730-55	Sequence 55, Appl
103	5	20.8	852	7	US-11-050-804-6	Sequence 6, Appl	176	4	16.7	79	6	US-10-884-730-127	Sequence 127, App
104	5	20.8	964	7	US-11-089-551A-30	Sequence 30, Appl	177	4	16.7	79	6	US-10-884-730-128	Sequence 128, App
105	5	20.8	1034	7	US-11-103-957-11	Sequence 11, Appl	178	4	16.7	79	6	US-10-884-730-131	Sequence 131, App
106	5	20.8	1038	7	US-11-107-028-1	Sequence 1, Appl	179	4	16.7	79	6	US-10-884-730-279	Sequence 279, App
107	5	20.8	1075	7	US-11-089-551A-23	Sequence 23, Appl	180	4	16.7	80	6	US-10-884-730-24	Sequence 24, Appl
108	5	20.8	1268	7	US-11-052-554A-1	Sequence 1, Appl	181	4	16.7	80	6	US-10-884-730-61	Sequence 61, Appl
109	5	20.8	1448	6	US-10-485-517-212	Sequence 212, App	182	4	16.7	80	6	US-10-884-730-68	Sequence 68, Appl
110	5	20.8	1476	6	US-10-647-956A-4	Sequence 4, Appl	183	4	16.7	80	6	US-10-884-730-70	Sequence 70, Appl
111	5	20.8	1614	7	US-11-108-528-82	Sequence 82, Appl	184	4	16.7	80	6	US-10-884-730-96	Sequence 96, Appl
112	5	20.8	1615	7	US-11-108-528-80	Sequence 80, Appl	185	4	16.7	80	6	US-10-884-730-101	Sequence 101, App
113	5	20.8	2101	6	US-10-857-780-23	Sequence 80, Appl	186	4	16.7	80	6	US-10-884-730-142	Sequence 142, App
114	5	20.8	2399	7	US-11-052-554A-92	Sequence 92, Appl	187	4	16.7	80	6	US-10-884-730-147	Sequence 147, App
115	5	20.8	5335	6	US-10-995-561-776	Sequence 776, App	188	4	16.7	80	6	US-10-884-730-224	Sequence 224, App
116	5	20.8	6893	7	US-11-205-109-14	Sequence 14, Appl	189	4	16.7	80	6	US-10-884-730-245	Sequence 245, App
117	4	16.7	6	US-10-615-668-23	Sequence 23, Appl	190	4	16.7	80	6	US-10-884-730-249	Sequence 249, App	
118	4	16.7	7	US-11-096-706-96	Sequence 96, Appl	191	4	16.7	80	6	US-10-884-730-250	Sequence 250, App	
119	4	16.7	10	US-11-041-893-31	Sequence 31, Appl	192	4	16.7	80	6	US-10-884-730-288	Sequence 288, App	
120	4	16.7	11	US-10-914-842A-12	Sequence 12, Appl	193	4	16.7	80	6	US-10-884-730-314	Sequence 314, App	
121	4	16.7	12	US-11-069-834-14	Sequence 14, Appl	194	4	16.7	80	6	US-10-884-730-314	Sequence 314, App	
122	4	16.7	12	US-11-069-834-16	Sequence 16, Appl	195	4	16.7	80	6	US-10-467-657-618	Sequence 618, App	
123	4	16.7	12	US-11-069-834-18	Sequence 18, Appl	196	4	16.7	80	6	US-10-884-730-3	Sequence 3, Appl	
124	4	16.7	12	US-11-069-834-34	Sequence 34, Appl	197	4	16.7	81	6	US-10-884-730-28	Sequence 28, Appl	
125	4	16.7	15	US-10-467-657-8838	Sequence 8838, Ap	198	4	16.7	81	6	US-10-884-730-62	Sequence 62, Appl	
126	4	16.7	15	US-11-045-024-13116	Sequence 13116, A	199	4	16.7	81	6	US-10-884-730-80	Sequence 80, Appl	
127	4	16.7	18	US-11-033-039-1242	Sequence 1242, Ap	200	4	16.7	81	6	US-10-884-730-81	Sequence 81, Appl	
128	4	16.7	18	US-11-033-039-1308	Sequence 1308, Ap	201	4	16.7	81	6	US-10-884-730-93	Sequence 93, Appl	
129	4	16.7	19	US-10-503-575-312	Sequence 312, App	202	4	16.7	81	6	US-10-884-730-105	Sequence 105, App	
130	4	16.7	20	US-10-509-917-4	Sequence 4, Appl	203	4	16.7	81	6	US-10-884-730-148	Sequence 148, App	
131	4	16.7	20	US-11-022-562-134	Sequence 134, App	204	4	16.7	81	6	US-10-884-730-162	Sequence 162, App	
132	4	16.7	20	US-11-022-562-135	Sequence 135, App	205	4	16.7	81	6	US-10-884-730-212	Sequence 212, App	
133	4	16.7	25	US-11-006-119-8	Sequence 8, Appl	206	4	16.7	81	6	US-10-884-730-217	Sequence 217, App	
134	4	16.7	27	US-11-097-749-1	Sequence 1, Appl	207	4	16.7	81	6	US-10-884-730-230	Sequence 230, App	
135	4	16.7	34	US-10-467-657-3966	Sequence 3966, Ap	208	4	16.7	81	6	US-10-884-730-257	Sequence 257, App	
136	4	16.7	34	US-10-467-657-8991	Sequence 8991, Ap	209	4	16.7	81	6	US-10-884-730-275	Sequence 275, App	
137	4	16.7	35	US-10-957-351-165	Sequence 165, App	210	4	16.7	81	6	US-10-884-730-303	Sequence 303, App	
138	4	16.7	39	US-10-467-657-2820	Sequence 2820, Ap	211	4	16.7	81	6	US-10-884-730-304	Sequence 304, App	
139	4	16.7	43	US-10-957-887B-155	Sequence 155, App	212	4	16.7	81	6	US-10-884-730-308	Sequence 308, App	
140	4	16.7	44	US-10-957-887B-157	Sequence 157, App	213	4	16.7	81	6	US-10-884-730-313	Sequence 313, App	
141	4	16.7	47	US-10-467-657-6650	Sequence 6650, Ap	214	4	16.7	81	6	US-10-884-730-315	Sequence 315, App	
142	4	16.7	48	US-11-019-711-40	Sequence 40, Appl	215	4	16.7	81	6	US-10-884-730-324	Sequence 324, App	
143	4	16.7	50	US-10-729-121-39	Sequence 39, Appl	216	4	16.7	81	6	US-10-884-730-344	Sequence 344, App	
144	4	16.7	51	US-11-146-523-5	Sequence 5, Appl	217	4	16.7	82	6	US-10-884-730-51	Sequence 51, Appl	
145	4	16.7	52	US-10-914-165-21	Sequence 21, Appl	218	4	16.7	82	6	US-10-884-730-58	Sequence 58, Appl	
146	4	16.7	53	US-10-467-657-2716	Sequence 2716, Ap	219	4	16.7	82	6	US-10-884-730-82	Sequence 82, Appl	
147	4	16.7	56	US-11-000-463-768	Sequence 768, App	220	4	16.7	82	6	US-10-884-730-143	Sequence 143, App	
148	4	16.7	59	US-11-134-241-14	Sequence 14, Appl	221	4	16.7	82	6	US-10-884-730-144	Sequence 144, App	
149	4	16.7	61	US-10-467-657-1506	Sequence 1506, Ap	222	4	16.7	82	6	US-10-884-730-195	Sequence 195, App	
150	4	16.7	61	US-10-467-657-2012	Sequence 2012, Ap	223	4	16.7	82	6	US-10-884-730-204	Sequence 204, App	
151	4	16.7	70	US-10-467-657-6924	Sequence 6924, Ap	224	4	16.7	82	6	US-10-884-730-207	Sequence 207, App	
152	4	16.7	71	US-10-821-234-1252	Sequence 1252, Ap	225	4	16.7	82	6	US-10-884-730-244	Sequence 244, App	
153	4	16.7	72	US-11-176-868-15	Sequence 15, Appl	226	4	16.7	82	6	US-10-884-730-280	Sequence 280, App	
154	4	16.7	73	US-10-884-730-52	Sequence 52, Appl	227	4	16.7	82	6	US-10-884-730-283	Sequence 283, App	
155	4	16.7	73	US-10-884-730-53	Sequence 53, Appl	228	4	16.7	82	6	US-10-467-657-1462	Sequence 1462, Ap	
156	4	16.7	73	US-10-884-730-56	Sequence 56, Appl	229	4	16.7	82	6	US-10-467-657-9177	Sequence 9177, Ap	
157	4	16.7	73	US-10-884-730-130	Sequence 130, App	230	4	16.7	83	6	US-10-884-730-57	Sequence 57, Appl	
158	4	16.7	73	US-10-884-730-132	Sequence 132, App	231	4	16.7	83	6	US-10-884-730-145	Sequence 145, App	
159	4	16.7	73	US-10-884-730-274	Sequence 274, App	232	4	16.7	83	6	US-10-884-730-337	Sequence 337, App	
160	4	16.7	74	US-10-884-730-45	Sequence 45, Appl	233	4	16.7	83	6	US-10-746-959C-2	Sequence 2, Appl	
161	4	16.7	74	US-10-884-730-50	Sequence 50, Appl	234	4	16.7	83	7	US-11-000-463-434	Sequence 434, App	
162	4	16.7	74	US-10-884-730-241	Sequence 241, App	235	4	16.7	83	7	US-11-000-463-906	Sequence 906, App	
163	4	16.7	74	US-10-467-657-6160	Sequence 6160, Ap	236	4	16.7	84	6	US-10-884-730-46	Sequence 46, Appl	
164	4	16.7	75	US-10-884-730-192	Sequence 192, App	237	4	16.7	84	6	US-10-884-730-103	Sequence 103, App	
165	4	16.7	76	US-10-884-730-90	Sequence 90, Appl	238	4	16.7	84	6	US-10-884-730-194	Sequence 194, App	
166	4	16.7	76	US-10-884-730-183	Sequence 183, App	239	4	16.7	84	6	US-10-884-730-209	Sequence 209, App	
167	4	16.7	77	US-10-884-730-129	Sequence 129, App	240	4	16.7	84	6	US-10-884-730-259	Sequence 259, App	
168	4	16.7	78	US-10-884-730-49	Sequence 49, Appl	241	4	16.7	84	6	US-10-884-730-260	Sequence 260, App	
169	4	16.7	78	US-10-884-730-54	Sequence 54, Appl	242	4	16.7	84	6	US-10-884-730-316	Sequence 316, App	
170	4	16.7	78	US-10-884-730-236	Sequence 236, App	243	4	16.7	84	6	US-10-884-730-325	Sequence 325, App	
171	4	16.7	78	US-10-884-730-240	Sequence 240, App	244	4	16.7	84	7	US-11-123-896-386	Sequence 386, App	

245	4	16.7	85	6	US-10-884-730-14	Sequence 14, Appl	318	4	16.7	89	6	US-10-884-730-26	Sequence 26, Appl
246	4	16.7	85	6	US-10-884-730-83	Sequence 83, Appl	319	4	16.7	89	6	US-10-884-730-27	Sequence 27, Appl
247	4	16.7	85	6	US-10-884-730-107	Sequence 107, Appl	320	4	16.7	89	6	US-10-884-730-29	Sequence 29, Appl
248	4	16.7	85	6	US-10-884-730-125	Sequence 125, Appl	321	4	16.7	89	6	US-10-884-730-30	Sequence 30, Appl
249	4	16.7	85	6	US-10-884-730-141	Sequence 141, Appl	322	4	16.7	89	6	US-10-884-730-31	Sequence 31, Appl
250	4	16.7	85	6	US-10-884-730-186	Sequence 186, Appl	323	4	16.7	89	6	US-10-884-730-34	Sequence 34, Appl
251	4	16.7	85	6	US-10-884-730-187	Sequence 187, Appl	324	4	16.7	89	6	US-10-884-730-37	Sequence 37, Appl
252	4	16.7	85	6	US-10-884-730-243	Sequence 243, Appl	325	4	16.7	89	6	US-10-884-730-59	Sequence 59, Appl
253	4	16.7	85	6	US-10-884-730-277	Sequence 277, Appl	326	4	16.7	89	6	US-10-884-730-60	Sequence 60, Appl
254	4	16.7	85	6	US-10-884-730-286	Sequence 286, Appl	327	4	16.7	89	6	US-10-884-730-64	Sequence 64, Appl
255	4	16.7	85	6	US-10-884-730-347	Sequence 347, Appl	328	4	16.7	89	6	US-10-884-730-65	Sequence 65, Appl
256	4	16.7	85	6	US-10-884-730-347	Sequence 18, Appl	329	4	16.7	89	6	US-10-884-730-66	Sequence 66, Appl
257	4	16.7	85	6	US-10-884-730-21	Sequence 21, Appl	330	4	16.7	89	6	US-10-884-730-67	Sequence 67, Appl
258	4	16.7	86	6	US-10-884-730-63	Sequence 63, Appl	331	4	16.7	89	6	US-10-884-730-72	Sequence 72, Appl
259	4	16.7	86	6	US-10-884-730-71	Sequence 71, Appl	332	4	16.7	89	6	US-10-884-730-73	Sequence 73, Appl
260	4	16.7	86	6	US-10-884-730-87	Sequence 87, Appl	333	4	16.7	89	6	US-10-884-730-74	Sequence 74, Appl
261	4	16.7	86	6	US-10-884-730-95	Sequence 95, Appl	334	4	16.7	89	6	US-10-884-730-78	Sequence 78, Appl
262	4	16.7	86	6	US-10-884-730-99	Sequence 99, Appl	335	4	16.7	89	6	US-10-884-730-91	Sequence 91, Appl
263	4	16.7	86	6	US-10-884-730-102	Sequence 102, Appl	336	4	16.7	89	6	US-10-884-730-92	Sequence 92, Appl
264	4	16.7	86	6	US-10-884-730-155	Sequence 155, Appl	337	4	16.7	89	6	US-10-884-730-97	Sequence 97, Appl
265	4	16.7	86	6	US-10-884-730-157	Sequence 157, Appl	338	4	16.7	89	6	US-10-884-730-98	Sequence 98, Appl
266	4	16.7	86	6	US-10-884-730-191	Sequence 191, Appl	339	4	16.7	89	6	US-10-884-730-100	Sequence 100, Appl
267	4	16.7	86	6	US-10-884-730-247	Sequence 247, Appl	340	4	16.7	89	6	US-10-884-730-104	Sequence 104, Appl
268	4	16.7	86	6	US-10-884-730-262	Sequence 262, Appl	341	4	16.7	89	6	US-10-884-730-106	Sequence 106, Appl
269	4	16.7	86	6	US-10-884-730-292	Sequence 292, Appl	342	4	16.7	89	6	US-10-884-730-108	Sequence 108, Appl
270	4	16.7	87	6	US-10-884-730-11	Sequence 11, Appl	343	4	16.7	89	6	US-10-884-730-109	Sequence 109, Appl
271	4	16.7	87	6	US-10-884-730-48	Sequence 48, Appl	344	4	16.7	89	6	US-10-884-730-110	Sequence 110, Appl
272	4	16.7	87	6	US-10-884-730-126	Sequence 126, Appl	345	4	16.7	89	6	US-10-884-730-111	Sequence 111, Appl
273	4	16.7	87	6	US-10-884-730-180	Sequence 180, Appl	346	4	16.7	89	6	US-10-884-730-118	Sequence 118, Appl
274	4	16.7	87	6	US-10-884-730-219	Sequence 219, Appl	347	4	16.7	89	6	US-10-884-730-119	Sequence 119, Appl
275	4	16.7	87	6	US-10-884-730-237	Sequence 237, Appl	348	4	16.7	89	6	US-10-884-730-133	Sequence 133, Appl
276	4	16.7	87	6	US-10-884-730-238	Sequence 238, Appl	349	4	16.7	89	6	US-10-884-730-137	Sequence 137, Appl
277	4	16.7	87	6	US-10-884-730-239	Sequence 239, Appl	350	4	16.7	89	6	US-10-884-730-146	Sequence 146, Appl
278	4	16.7	87	6	US-10-884-730-278	Sequence 278, Appl	351	4	16.7	89	6	US-10-884-730-149	Sequence 149, Appl
279	4	16.7	87	6	US-10-884-730-310	Sequence 310, Appl	352	4	16.7	89	6	US-10-884-730-150	Sequence 150, Appl
280	4	16.7	87	6	US-10-884-730-312	Sequence 312, Appl	353	4	16.7	89	6	US-10-884-730-151	Sequence 151, Appl
281	4	16.7	87	6	US-10-884-730-346	Sequence 346, Appl	354	4	16.7	89	6	US-10-884-730-152	Sequence 152, Appl
282	4	16.7	87	6	US-10-884-730-32	Sequence 32, Appl	355	4	16.7	89	6	US-10-884-730-154	Sequence 154, Appl
283	4	16.7	88	6	US-10-467-657-4732	Sequence 4732, Appl	356	4	16.7	89	6	US-10-884-730-156	Sequence 156, Appl
284	4	16.7	88	6	US-10-884-730-40	Sequence 40, Appl	357	4	16.7	89	6	US-10-884-730-158	Sequence 158, Appl
285	4	16.7	88	6	US-10-884-730-43	Sequence 43, Appl	358	4	16.7	89	6	US-10-884-730-159	Sequence 159, Appl
286	4	16.7	88	6	US-10-884-730-44	Sequence 44, Appl	359	4	16.7	89	6	US-10-884-730-161	Sequence 161, Appl
287	4	16.7	88	6	US-10-884-730-75	Sequence 75, Appl	360	4	16.7	89	6	US-10-884-730-161	Sequence 161, Appl
288	4	16.7	88	6	US-10-884-730-76	Sequence 76, Appl	361	4	16.7	89	6	US-10-884-730-164	Sequence 164, Appl
289	4	16.7	88	6	US-10-884-730-112	Sequence 77, Appl	362	4	16.7	89	6	US-10-884-730-176	Sequence 176, Appl
290	4	16.7	88	6	US-10-884-730-139	Sequence 112, Appl	363	4	16.7	89	6	US-10-884-730-182	Sequence 182, Appl
291	4	16.7	88	6	US-10-884-730-139	Sequence 139, Appl	364	4	16.7	89	6	US-10-884-730-184	Sequence 184, Appl
292	4	16.7	88	6	US-10-884-730-140	Sequence 140, Appl	365	4	16.7	89	6	US-10-884-730-185	Sequence 185, Appl
293	4	16.7	88	6	US-10-884-730-163	Sequence 163, Appl	366	4	16.7	89	6	US-10-884-730-188	Sequence 188, Appl
294	4	16.7	88	6	US-10-884-730-178	Sequence 178, Appl	367	4	16.7	89	6	US-10-884-730-189	Sequence 189, Appl
295	4	16.7	88	6	US-10-884-730-199	Sequence 199, Appl	368	4	16.7	89	6	US-10-884-730-190	Sequence 190, Appl
296	4	16.7	88	6	US-10-884-730-202	Sequence 202, Appl	369	4	16.7	89	6	US-10-884-730-193	Sequence 193, Appl
297	4	16.7	88	6	US-10-884-730-203	Sequence 203, Appl	370	4	16.7	89	6	US-10-884-730-197	Sequence 197, Appl
298	4	16.7	88	6	US-10-884-730-214	Sequence 214, Appl	371	4	16.7	89	6	US-10-884-730-205	Sequence 205, Appl
299	4	16.7	88	6	US-10-884-730-228	Sequence 228, Appl	372	4	16.7	89	6	US-10-884-730-206	Sequence 206, Appl
300	4	16.7	88	6	US-10-884-730-234	Sequence 234, Appl	373	4	16.7	89	6	US-10-884-730-208	Sequence 208, Appl
301	4	16.7	88	6	US-10-884-730-235	Sequence 235, Appl	374	4	16.7	89	6	US-10-884-730-210	Sequence 210, Appl
302	4	16.7	88	6	US-10-884-730-246	Sequence 246, Appl	375	4	16.7	89	6	US-10-884-730-211	Sequence 211, Appl
303	4	16.7	88	6	US-10-884-730-264	Sequence 264, Appl	376	4	16.7	89	6	US-10-884-730-215	Sequence 215, Appl
304	4	16.7	88	6	US-10-884-730-272	Sequence 272, Appl	377	4	16.7	89	6	US-10-884-730-216	Sequence 216, Appl
305	4	16.7	88	6	US-10-884-730-271	Sequence 271, Appl	378	4	16.7	89	6	US-10-884-730-218	Sequence 218, Appl
306	4	16.7	88	6	US-10-884-730-305	Sequence 305, Appl	379	4	16.7	89	6	US-10-884-730-220	Sequence 220, Appl
307	4	16.7	88	6	US-10-884-730-309	Sequence 309, Appl	380	4	16.7	89	6	US-10-884-730-221	Sequence 221, Appl
308	4	16.7	88	7	US-11-194-890-1	Sequence 1, Appl	381	4	16.7	89	6	US-10-884-730-222	Sequence 222, Appl
309	4	16.7	89	6	US-10-884-730-6	Sequence 6, Appl	382	4	16.7	89	6	US-10-884-730-223	Sequence 223, Appl
310	4	16.7	89	6	US-10-884-730-7	Sequence 7, Appl	383	4	16.7	89	6	US-10-884-730-225	Sequence 225, Appl
311	4	16.7	89	6	US-10-884-730-8	Sequence 8, Appl	384	4	16.7	89	6	US-10-884-730-226	Sequence 226, Appl
312	4	16.7	89	6	US-10-884-730-9	Sequence 9, Appl	385	4	16.7	89	6	US-10-884-730-227	Sequence 227, Appl
313	4	16.7	89	6	US-10-884-730-15	Sequence 15, Appl	386	4	16.7	89	6	US-10-884-730-233	Sequence 233, Appl
314	4	16.7	89	6	US-10-884-730-16	Sequence 16, Appl	387	4	16.7	89	6	US-10-884-730-251	Sequence 251, Appl
315	4	16.7	89	6	US-10-884-730-17	Sequence 17, Appl	388	4	16.7	89	6	US-10-884-730-252	Sequence 252, Appl
316	4	16.7	89	6	US-10-884-730-23	Sequence 23, Appl	389	4	16.7	89	6	US-10-884-730-255	Sequence 255, Appl
317	4	16.7	89	6	US-10-884-730-25	Sequence 25, Appl	390	4	16.7	89	6	US-10-884-730-256	Sequence 256, Appl

391	4	16.7	89	6	US-10-884-730-258	Sequence 258, App	464	4	16.7	122	6	US-10-678-790-60	Sequence 60, Appl
392	4	16.7	89	6	US-10-884-730-261	Sequence 261, App	465	4	16.7	122	6	US-10-746-909-9	Sequence 9, Appl
393	4	16.7	89	6	US-10-884-730-263	Sequence 263, App	466	4	16.7	123	6	US-10-793-626-1856	Sequence 1856, Ap
394	4	16.7	89	6	US-10-884-730-265	Sequence 265, App	467	4	16.7	124	6	US-10-467-657-1092	Sequence 1092, Ap
395	4	16.7	89	6	US-10-884-730-266	Sequence 266, App	468	4	16.7	125	6	US-10-516-768-18	Sequence 18, Appl
396	4	16.7	89	6	US-10-884-730-267	Sequence 267, App	469	4	16.7	126	6	US-10-516-768-11	Sequence 11, Appl
397	4	16.7	89	6	US-10-884-730-268	Sequence 268, App	470	4	16.7	127	6	US-10-467-657-4210	Sequence 4210, Ap
398	4	16.7	89	6	US-10-884-730-269	Sequence 269, App	471	4	16.7	127	6	US-10-467-657-5246	Sequence 5246, Ap
399	4	16.7	89	6	US-10-884-730-281	Sequence 281, App	472	4	16.7	127	6	US-10-467-657-6036	Sequence 6036, Ap
400	4	16.7	89	6	US-10-884-730-282	Sequence 282, App	473	4	16.7	128	6	US-10-467-657-5268	Sequence 5268, Ap
401	4	16.7	89	6	US-10-884-730-284	Sequence 284, App	474	4	16.7	128	7	US-11-116-144-147	Sequence 147, App
402	4	16.7	89	6	US-10-884-730-293	Sequence 293, App	475	4	16.7	129	6	US-10-873-528-51	Sequence 51, Appl
403	4	16.7	89	6	US-10-884-730-311	Sequence 311, App	476	4	16.7	129	6	US-10-689-742-182	Sequence 182, App
404	4	16.7	89	6	US-10-884-730-319	Sequence 319, App	477	4	16.7	131	6	US-11-141-642-5	Sequence 5, Appl
405	4	16.7	89	6	US-10-884-730-320	Sequence 320, App	478	4	16.7	132	7	US-10-793-626-1154	Sequence 1154, Ap
406	4	16.7	89	6	US-10-884-730-321	Sequence 321, App	479	4	16.7	133	6	US-10-793-626-1924	Sequence 1924, Ap
407	4	16.7	89	6	US-10-884-730-323	Sequence 323, App	480	4	16.7	134	7	US-11-091-643-2	Sequence 2, Appl
408	4	16.7	89	6	US-10-884-730-339	Sequence 339, App	481	4	16.7	134	7	US-11-084-591-2	Sequence 2, Appl
409	4	16.7	89	6	US-10-884-730-348	Sequence 348, App	482	4	16.7	136	6	US-10-467-657-6108	Sequence 6108, Ap
410	4	16.7	89	6	US-10-467-657-4576	Sequence 4576, Ap	483	4	16.7	138	6	US-10-793-626-2302	Sequence 2302, Ap
411	4	16.7	90	6	US-10-884-730-94	Sequence 94, Appl	484	4	16.7	139	6	US-10-793-626-1154	Sequence 1154, Ap
412	4	16.7	90	6	US-10-884-730-124	Sequence 124, App	485	4	16.7	139	6	US-10-878-556A-117	Sequence 117, App
413	4	16.7	90	6	US-10-884-730-201	Sequence 201, App	486	4	16.7	142	6	US-10-667-295-74	Sequence 74, Appl
414	4	16.7	90	6	US-10-884-730-248	Sequence 248, App	487	4	16.7	143	6	US-10-821-234-1408	Sequence 1408, Ap
415	4	16.7	93	6	US-10-884-730-135	Sequence 135, App	488	4	16.7	143	6	US-10-821-234-1205	Sequence 1205, Ap
416	4	16.7	94	6	US-10-884-730-39	Sequence 39, Appl	489	4	16.7	145	6	US-10-793-626-2328	Sequence 2328, Ap
417	4	16.7	94	6	US-10-884-730-42	Sequence 42, Appl	490	4	16.7	145	6	US-10-467-657-264	Sequence 264, App
418	4	16.7	94	6	US-10-884-730-122	Sequence 122, App	491	4	16.7	145	6	US-10-467-657-3600	Sequence 3600, Ap
419	4	16.7	94	6	US-10-884-730-134	Sequence 134, App	492	4	16.7	145	6	US-10-454-437-164	Sequence 164, App
420	4	16.7	94	6	US-10-884-730-229	Sequence 229, App	493	4	16.7	147	6	US-10-467-657-9020	Sequence 9020, Ap
421	4	16.7	94	6	US-10-884-730-231	Sequence 231, App	494	4	16.7	148	6	US-10-467-657-4330	Sequence 4330, Ap
422	4	16.7	94	6	US-10-884-730-232	Sequence 232, App	495	4	16.7	148	7	US-11-134-241-8	Sequence 8, Appl
423	4	16.7	96	6	US-10-884-730-253	Sequence 253, App	496	4	16.7	148	7	US-11-134-241-10	Sequence 10, Appl
424	4	16.7	96	6	US-10-467-657-3954	Sequence 3954, Ap	497	4	16.7	149	6	US-10-995-561-584	Sequence 584, App
425	4	16.7	96	7	US-11-000-463-762	Sequence 762, App	498	4	16.7	153	7	US-10-821-234-1355	Sequence 1355, Ap
426	4	16.7	97	7	US-11-054-669-50	Sequence 50, Appl	499	4	16.7	153	7	US-11-066-480-8	Sequence 8, Appl
427	4	16.7	97	7	US-11-134-241-18	Sequence 18, Appl	500	4	16.7	156	6	US-10-667-295-125	Sequence 125, App
428	4	16.7	97	7	US-10-884-730-276	Sequence 276, App	501	4	16.7	157	6	US-10-667-295-124	Sequence 124, App
429	4	16.7	98	6	US-11-082-381-11	Sequence 11, Appl	502	4	16.7	161	7	US-11-052-554A-86	Sequence 86, Appl
430	4	16.7	99	6	US-10-467-657-472	Sequence 472, App	503	4	16.7	162	6	US-10-516-768-21	Sequence 21, Appl
431	4	16.7	100	6	US-10-884-730-13	Sequence 13, Appl	504	4	16.7	162	6	US-10-793-626-1010	Sequence 1010, Ap
432	4	16.7	101	6	US-10-884-730-89	Sequence 89, Appl	505	4	16.7	162	6	US-10-793-626-2432	Sequence 2432, Ap
433	4	16.7	101	6	US-10-884-730-117	Sequence 117, App	506	4	16.7	162	7	US-11-055-822-788	Sequence 788, App
434	4	16.7	101	6	US-10-884-730-179	Sequence 179, App	507	4	16.7	163	6	US-10-667-295-123	Sequence 123, App
435	4	16.7	101	6	US-10-884-730-181	Sequence 181, App	508	4	16.7	164	6	US-10-793-626-252	Sequence 252, App
436	4	16.7	101	6	US-10-454-437-48	Sequence 48, Appl	509	4	16.7	165	7	US-11-055-822-678	Sequence 678, App
437	4	16.7	101	7	US-11-082-381-1	Sequence 1, Appl	510	4	16.7	167	6	US-10-884-730-342	Sequence 342, App
438	4	16.7	102	6	US-10-884-730-19	Sequence 19, Appl	511	4	16.7	167	7	US-11-055-822-676	Sequence 676, App
439	4	16.7	102	6	US-10-884-730-20	Sequence 20, Appl	512	4	16.7	172	7	US-10-793-626-2838	Sequence 2838, Ap
440	4	16.7	103	6	US-10-884-730-123	Sequence 123, App	513	4	16.7	175	7	US-11-058-384-2	Sequence 2, Appl
441	4	16.7	106	6	US-10-793-626-794	Sequence 794, App	514	4	16.7	176	6	US-10-467-657-1880	Sequence 1880, Ap
442	4	16.7	106	6	US-10-793-626-2140	Sequence 2140, Ap	515	4	16.7	176	6	US-10-467-657-1282	Sequence 1282, Ap
443	4	16.7	106	6	US-10-821-234-906	Sequence 906, App	516	4	16.7	177	6	US-10-467-657-7762	Sequence 7762, Ap
444	4	16.7	107	6	US-10-678-790-61	Sequence 61, Appl	517	4	16.7	177	6	US-10-623-155-165	Sequence 165, App
445	4	16.7	108	6	US-10-884-730-198	Sequence 198, App	518	4	16.7	177	6	US-10-623-155-166	Sequence 166, App
446	4	16.7	108	6	US-10-467-657-3054	Sequence 3054, Ap	519	4	16.7	177	7	US-11-035-826-16	Sequence 16, Appl
447	4	16.7	110	6	US-10-524-647-140	Sequence 140, App	520	4	16.7	177	6	US-10-467-962B-39	Sequence 39, Appl
448	4	16.7	110	7	US-11-134-241-4	Sequence 4, Appl	521	4	16.7	179	6	US-10-884-730-84	Sequence 84, Appl
449	4	16.7	111	6	US-10-467-657-980	Sequence 980, App	522	4	16.7	179	6	US-10-746-959C-10	Sequence 10, Appl
450	4	16.7	112	6	US-10-884-730-138	Sequence 138, App	523	4	16.7	181	6	US-10-884-730-86	Sequence 86, Appl
451	4	16.7	113	7	US-11-144-248-20	Sequence 20, Appl	524	4	16.7	183	6	US-10-467-657-8825	Sequence 8825, Ap
452	4	16.7	113	7	US-11-144-222-20	Sequence 20, Appl	525	4	16.7	186	7	US-11-134-241-12	Sequence 12, Appl
453	4	16.7	114	6	US-10-884-730-196	Sequence 196, App	526	4	16.7	186	7	US-10-884-730-88	Sequence 88, Appl
454	4	16.7	117	6	US-10-793-626-378	Sequence 378, App	527	4	16.7	188	6	US-10-884-730-322	Sequence 322, App
455	4	16.7	117	6	US-10-467-657-2282	Sequence 2282, Ap	528	4	16.7	189	6	US-10-995-561-806	Sequence 806, App
456	4	16.7	118	6	US-10-821-234-1247	Sequence 1247, Ap	529	4	16.7	191	6	US-10-793-626-638	Sequence 638, App
457	4	16.7	118	7	US-11-000-463-274	Sequence 274, App	530	4	16.7	191	6	US-10-519-320-23	Sequence 23, Appl
458	4	16.7	118	7	US-11-000-463-746	Sequence 746, App	531	4	16.7	191	6	US-10-624-932-4	Sequence 4, Appl
459	4	16.7	119	6	US-10-884-730-200	Sequence 200, App	532	4	16.7	193	6	US-11-194-246-301	Sequence 301, App
460	4	16.7	120	6	US-10-884-730-153	Sequence 153, App	533	4	16.7	194	7	US-11-186-284-175	Sequence 175, App
461	4	16.7	120	6	US-10-467-657-8851	Sequence 8851, Ap	534	4	16.7	195	7	US-10-467-657-3296	Sequence 3296, Ap
462	4	16.7	121	6	US-10-793-626-3214	Sequence 3214, Ap	535	4	16.7	196	6	US-10-467-657-3296	Sequence 3296, Ap
463	4	16.7	121	6	US-10-678-790-63	Sequence 63, Appl	536	4	16.7	198	6	US-10-131-826A-550	Sequence 550, App

537	4	16.7	198	6	US-10-798-532-6	Sequence 6, Appli	610	4	16.7	244	6	US-10-793-626-566	Sequence 566, App
538	4	16.7	198	7	US-11-179-411-29	Sequence 29, Appl	611	4	16.7	246	7	US-11-124-368A-170	Sequence 170, App
539	4	16.7	198	7	US-11-175-766-29	Sequence 29, Appl	612	4	16.7	247	7	US-11-054-515-2076	Sequence 2076, Ap
540	4	16.7	198	7	US-11-052-554A-34	Sequence 34, Appl	613	4	16.7	248	6	US-10-467-557-6046	Sequence 6046, Ap
541	4	16.7	199	6	US-10-454-437-162	Sequence 162, App	614	4	16.7	249	7	US-11-054-515-1838	Sequence 1838, Ap
542	4	16.7	203	6	US-10-467-557-3492	Sequence 3492, Ap	615	4	16.7	250	7	US-11-113-837-2	Sequence 2, Appli
543	4	16.7	203	6	US-11-038-284-21	Sequence 21, Appl	616	4	16.7	252	7	US-11-054-515-1772	Sequence 1772, Ap
544	4	16.7	204	6	US-10-793-626-592	Sequence 692, App	617	4	16.7	254	7	US-11-054-515-1625	Sequence 1625, Ap
545	4	16.7	206	6	US-11-055-822-1026	Sequence 2550, Ap	618	4	16.7	255	6	US-10-467-557-6148	Sequence 6148, Ap
546	4	16.7	210	6	US-10-467-557-8728	Sequence 1026, Ap	619	4	16.7	255	6	US-10-467-557-7562	Sequence 7562, Ap
547	4	16.7	211	6	US-11-038-284-22	Sequence 8728, Ap	620	4	16.7	257	6	US-10-821-234-1484	Sequence 1484, Ap
548	4	16.7	213	7	US-11-067-425A-73	Sequence 22, Appl	621	4	16.7	258	6	US-10-995-561-583	Sequence 583, App
549	4	16.7	214	7	US-11-134-241-16	Sequence 73, Appl	622	4	16.7	260	6	US-10-055-877-163	Sequence 163, App
550	4	16.7	214	7	US-11-119-212-9	Sequence 16, Appl	623	4	16.7	261	6	US-10-467-557-4282	Sequence 4282, Ap
551	4	16.7	215	7	US-11-119-212-9	Sequence 9, Appli	624	4	16.7	262	6	US-10-884-730-289	Sequence 289, App
552	4	16.7	217	6	US-10-821-234-1568	Sequence 1568, Ap	625	4	16.7	262	6	US-10-793-626-1568	Sequence 1568, Ap
553	4	16.7	217	7	US-11-080-991-58	Sequence 58, Appl	626	4	16.7	263	6	US-10-793-626-2750	Sequence 2750, Ap
554	4	16.7	217	7	US-11-206-746-2	Sequence 2, Appli	627	4	16.7	264	6	US-10-884-730-35	Sequence 35, Appl
555	4	16.7	218	6	US-10-995-561-830	Sequence 830, App	628	4	16.7	265	7	US-11-134-241-6	Sequence 6, Appli
556	4	16.7	218	7	US-11-156-084-96	Sequence 96, Appl	629	4	16.7	266	6	US-10-884-730-1	Sequence 1, Appli
557	4	16.7	219	6	US-10-793-626-2526	Sequence 2526, Ap	630	4	16.7	266	6	US-10-884-730-4	Sequence 4, Appli
558	4	16.7	219	6	US-10-883-512-92	Sequence 92, Appl	631	4	16.7	266	6	US-10-884-730-33	Sequence 33, Appl
559	4	16.7	220	6	US-10-620-787-31	Sequence 31, Appl	632	4	16.7	266	6	US-10-884-730-38	Sequence 38, Appl
560	4	16.7	221	5	US-09-978-360A-436	Sequence 436, App	633	4	16.7	266	6	US-10-884-730-47	Sequence 47, Appl
561	4	16.7	221	6	US-10-467-557-3194	Sequence 3194, Ap	634	4	16.7	266	6	US-10-884-730-79	Sequence 79, Appl
562	4	16.7	221	6	US-10-620-787-30	Sequence 30, Appl	635	4	16.7	266	6	US-10-884-730-85	Sequence 85, Appl
563	4	16.7	221	7	US-11-102-978-11	Sequence 11, Appl	636	4	16.7	266	6	US-10-884-730-116	Sequence 116, App
564	4	16.7	221	7	US-11-067-425A-74	Sequence 74, Appl	637	4	16.7	266	6	US-10-884-730-121	Sequence 121, App
565	4	16.7	222	6	US-10-467-557-7990	Sequence 7990, App	638	4	16.7	266	6	US-10-884-730-270	Sequence 270, App
566	4	16.7	222	6	US-10-454-437-380	Sequence 380, App	639	4	16.7	266	6	US-10-884-730-285	Sequence 285, App
567	4	16.7	222	7	US-11-019-711-81	Sequence 81, Appl	640	4	16.7	266	6	US-10-884-730-287	Sequence 287, App
568	4	16.7	224	6	US-10-857-780-25	Sequence 25, Appl	641	4	16.7	266	6	US-10-884-730-306	Sequence 306, App
569	4	16.7	225	6	US-10-884-730-5	Sequence 5, Appli	642	4	16.7	266	6	US-10-884-730-345	Sequence 345, App
570	4	16.7	225	6	US-10-980-388-86	Sequence 86, Appl	643	4	16.7	266	6	US-10-502-972-8	Sequence 8, Appli
571	4	16.7	227	6	US-10-670-009-4	Sequence 4, Appli	644	4	16.7	266	7	US-11-000-463-381	Sequence 381, App
572	4	16.7	228	5	US-09-978-360A-475	Sequence 475, App	645	4	16.7	266	7	US-11-000-463-853	Sequence 853, App
573	4	16.7	228	6	US-10-467-557-156	Sequence 156, App	646	4	16.7	266	7	US-11-156-084-187	Sequence 187, App
574	4	16.7	229	6	US-10-467-557-1754	Sequence 1754, Ap	647	4	16.7	267	6	US-10-623-155-352	Sequence 352, App
575	4	16.7	229	6	US-10-873-528-131	Sequence 131, App	648	4	16.7	267	6	US-10-524-647-86	Sequence 86, Appl
576	4	16.7	230	6	US-10-884-730-372	Sequence 372, App	649	4	16.7	267	7	US-11-194-890-11	Sequence 11, Appl
577	4	16.7	230	6	US-10-884-730-373	Sequence 373, App	650	4	16.7	269	6	US-10-793-626-2472	Sequence 2472, Ap
578	4	16.7	230	6	US-10-884-730-374	Sequence 374, App	651	4	16.7	270	7	US-11-052-554A-315	Sequence 315, App
579	4	16.7	230	6	US-10-884-730-375	Sequence 375, App	652	4	16.7	271	7	US-11-074-176-104	Sequence 104, App
580	4	16.7	230	6	US-10-884-730-376	Sequence 376, App	653	4	16.7	272	6	US-10-793-626-1308	Sequence 1308, Ap
581	4	16.7	230	6	US-10-454-437-294	Sequence 294, App	654	4	16.7	273	5	US-09-978-360A-709	Sequence 709, App
582	4	16.7	230	6	US-10-873-528-187	Sequence 187, App	655	4	16.7	273	7	US-11-196-475-98	Sequence 98, Appl
583	4	16.7	233	6	US-10-467-557-8268	Sequence 8268, Ap	656	4	16.7	273	7	US-11-196-475-101	Sequence 101, App
584	4	16.7	234	7	US-11-052-554A-348	Sequence 348, App	657	4	16.7	274	7	US-11-196-475-86	Sequence 86, Appl
585	4	16.7	236	7	US-11-156-084-284	Sequence 2, Appli	658	4	16.7	274	7	US-11-196-475-138	Sequence 138, App
586	4	16.7	237	6	US-10-884-730-2	Sequence 10, Appl	659	4	16.7	274	7	US-11-156-062-2	Sequence 2, Appli
587	4	16.7	237	6	US-10-884-730-10	Sequence 12, Appl	660	4	16.7	274	7	US-11-156-062-4	Sequence 4, Appli
588	4	16.7	237	6	US-10-884-730-12	Sequence 22, Appl	661	4	16.7	274	7	US-11-156-062-6	Sequence 6, Appli
589	4	16.7	237	6	US-10-884-730-22	Sequence 26, Appl	662	4	16.7	274	7	US-11-156-062-8	Sequence 8, Appli
590	4	16.7	237	6	US-10-884-730-36	Sequence 36, Appl	663	4	16.7	274	7	US-11-156-062-10	Sequence 10, Appl
591	4	16.7	237	6	US-10-884-730-41	Sequence 41, Appl	664	4	16.7	274	7	US-11-156-062-12	Sequence 12, Appl
592	4	16.7	237	6	US-10-884-730-113	Sequence 113, App	665	4	16.7	274	7	US-11-156-062-14	Sequence 14, Appl
593	4	16.7	237	6	US-10-884-730-120	Sequence 120, App	666	4	16.7	274	7	US-11-156-062-16	Sequence 16, Appl
594	4	16.7	237	6	US-10-884-730-175	Sequence 175, App	667	4	16.7	274	7	US-11-156-062-18	Sequence 18, Appl
595	4	16.7	237	6	US-10-884-730-177	Sequence 177, App	668	4	16.7	274	7	US-10-467-557-1544	Sequence 1544, Ap
596	4	16.7	237	6	US-10-884-730-273	Sequence 273, App	669	4	16.7	275	6	US-11-110-977-2	Sequence 2, Appli
597	4	16.7	237	6	US-10-884-730-307	Sequence 307, App	670	4	16.7	275	7	US-11-091-100-16	Sequence 16, Appl
598	4	16.7	237	6	US-10-884-730-317	Sequence 317, App	671	4	16.7	276	7	US-11-091-100-16	Sequence 16, Appl
599	4	16.7	237	6	US-10-884-730-318	Sequence 318, App	672	4	16.7	277	6	US-10-793-626-94	Sequence 94, Appl
600	4	16.7	237	6	US-10-884-730-336	Sequence 336, App	673	4	16.7	277	7	US-11-156-084-180	Sequence 180, App
601	4	16.7	237	6	US-10-884-730-355	Sequence 355, App	674	4	16.7	277	6	US-10-883-512-105	Sequence 105, App
602	4	16.7	237	6	US-10-884-730-356	Sequence 356, App	675	4	16.7	280	6	US-10-485-517-240	Sequence 240, App
603	4	16.7	237	6	US-10-884-730-357	Sequence 357, App	676	4	16.7	280	7	US-11-170-653-66	Sequence 66, Appl
604	4	16.7	237	6	US-10-884-730-358	Sequence 358, App	677	4	16.7	284	7	US-11-089-551A-36	Sequence 36, Appl
605	4	16.7	237	6	US-10-884-730-360	Sequence 360, App	678	4	16.7	285	7	US-11-179-843-3	Sequence 3, Appli
606	4	16.7	237	6	US-10-884-730-361	Sequence 361, App	679	4	16.7	289	6	US-10-793-626-3254	Sequence 3254, Ap
607	4	16.7	237	6	US-10-884-730-362	Sequence 362, App	680	4	16.7	291	7	US-11-096-070-36	Sequence 36, Appl
608	4	16.7	238	6	US-10-467-557-1308	Sequence 1308, Ap	681	4	16.7	295	6	US-10-467-557-1604	Sequence 1604, Ap
609	4	16.7	238	7	US-11-194-890-12	Sequence 12, Appl	682	4	16.7	295	6	US-10-995-561-581	Sequence 581, App

683	4	16.7	298	7	US-11-025-834A-14	Sequence 14, Appl	756	4	16.7	346	7	US-11-118-809-8	Sequence 8, Appl
684	4	16.7	299	6	US-10-623-155-354	Sequence 354, App	757	4	16.7	347	6	US-10-793-626-462	Sequence 462, App
685	4	16.7	299	7	US-11-156-084-339	Sequence 339, App	758	4	16.7	347	6	US-10-793-626-1268	Sequence 1268, Ap
686	4	16.7	300	7	US-11-025-834A-21	Sequence 21, Appl	759	4	16.7	347	6	US-10-821-234-1136	Sequence 1136, Ap
687	4	16.7	301	7	US-11-152-569-10	Sequence 10, Appl	760	4	16.7	347	6	US-10-821-234-1379	Sequence 1379, Ap
688	4	16.7	302	7	US-11-119-212-13	Sequence 13, Appl	761	4	16.7	347	6	US-10-512-277-3	Sequence 3, Appl
689	4	16.7	302	7	US-11-119-212-25	Sequence 25, Appl	762	4	16.7	348	6	US-10-512-277-4	Sequence 4, Appl
690	4	16.7	303	6	US-10-467-962B-16	Sequence 16, Appl	763	4	16.7	348	6	US-10-667-295-121	Sequence 121, App
691	4	16.7	303	6	US-10-467-962B-45	Sequence 45, Appl	764	4	16.7	348	6	US-10-667-295-121	Sequence 1, Appl
692	4	16.7	303	6	US-10-793-626-74	Sequence 74, Appl	765	4	16.7	348	7	US-10-512-277-1	Sequence 3, Appl
693	4	16.7	303	7	US-11-134-241-2	Sequence 2, Appl	766	4	16.7	348	7	US-11-102-497-3	Sequence 11, Appl
694	4	16.7	304	6	US-11-156-084-291	Sequence 291, App	767	4	16.7	349	7	US-11-182-946-13	Sequence 13, Appl
695	4	16.7	305	6	US-10-995-561-582	Sequence 582, App	768	4	16.7	349	7	US-11-055-822-186	Sequence 186, App
696	4	16.7	306	6	US-10-793-626-382	Sequence 382, App	769	4	16.7	350	6	US-10-667-295-120	Sequence 120, App
697	4	16.7	306	6	US-10-467-657-1318	Sequence 1318, Ap	770	4	16.7	350	6	US-10-517-939-176	Sequence 176, App
698	4	16.7	308	4	US-11-156-084-304	Sequence 304, App	771	4	16.7	350	6	US-10-517-939-192	Sequence 192, App
699	4	16.7	309	6	US-10-793-626-1608	Sequence 1608, Ap	772	4	16.7	350	6	US-11-132-285-41	Sequence 41, Appl
700	4	16.7	309	7	US-11-138-642-1	Sequence 1, Appl	773	4	16.7	351	6	US-10-729-121-2	Sequence 2, Appl
701	4	16.7	309	7	US-11-138-882-1	Sequence 1, Appl	774	4	16.7	351	7	US-11-118-809-6	Sequence 6, Appl
702	4	16.7	310	6	US-10-131-826A-538	Sequence 538, App	775	4	16.7	351	7	US-11-122-849-2	Sequence 2, Appl
703	4	16.7	310	7	US-11-000-463-357	Sequence 357, App	776	4	16.7	352	7	US-11-037-243-95	Sequence 95, Appl
704	4	16.7	310	7	US-11-025-834A-13	Sequence 13, Appl	777	4	16.7	354	7	US-11-052-554A-156	Sequence 156, App
705	4	16.7	310	7	US-11-025-834A-15	Sequence 15, Appl	778	4	16.7	355	7	US-11-082-389-6	Sequence 6, Appl
706	4	16.7	310	7	US-11-156-084-301	Sequence 301, App	779	4	16.7	355	7	US-11-182-946-14	Sequence 14, Appl
707	4	16.7	311	6	US-10-467-657-3740	Sequence 3740, Ap	780	4	16.7	355	7	US-11-205-109-31	Sequence 31, Appl
708	4	16.7	311	7	US-11-000-463-345	Sequence 345, App	781	4	16.7	356	6	US-10-793-626-2054	Sequence 2054, Ap
709	4	16.7	311	7	US-11-000-463-829	Sequence 829, App	782	4	16.7	356	7	US-11-143-986-8	Sequence 8, Appl
710	4	16.7	311	7	US-11-156-084-176	Sequence 176, App	783	4	16.7	356	7	US-11-143-986-9	Sequence 9, Appl
711	4	16.7	311	7	US-11-156-084-330	Sequence 330, App	784	4	16.7	358	6	US-10-838-616-12	Sequence 12, Appl
712	4	16.7	312	6	US-10-527-500-11	Sequence 11, Appl	785	4	16.7	358	7	US-11-129-143-111	Sequence 111, App
713	4	16.7	312	7	US-11-156-084-331	Sequence 331, App	786	4	16.7	358	7	US-11-205-460-4	Sequence 4, Appl
714	4	16.7	313	7	US-11-099-691-4	Sequence 4, Appl	787	4	16.7	359	7	US-11-129-143-71	Sequence 71, Appl
715	4	16.7	314	7	US-11-143-980-56	Sequence 56, Appl	788	4	16.7	360	6	US-10-467-962B-75	Sequence 75, Appl
716	4	16.7	315	6	US-10-454-437-220	Sequence 220, App	789	4	16.7	360	6	US-10-878-556A-134	Sequence 134, App
717	4	16.7	315	7	US-11-156-084-313	Sequence 313, App	790	4	16.7	360	6	US-10-878-556A-137	Sequence 137, App
718	4	16.7	315	7	US-11-156-084-353	Sequence 353, App	791	4	16.7	360	7	US-11-186-284-115	Sequence 115, App
719	4	16.7	319	6	US-10-467-657-640	Sequence 640, App	792	4	16.7	361	7	US-11-129-143-108	Sequence 108, App
720	4	16.7	319	6	US-10-467-657-1760	Sequence 1760, Ap	793	4	16.7	362	6	US-10-821-234-1148	Sequence 1148, Ap
721	4	16.7	319	6	US-10-467-657-2324	Sequence 2324, Ap	794	4	16.7	363	6	US-10-995-561-804	Sequence 804, App
722	4	16.7	319	6	US-10-467-657-6604	Sequence 6604, Ap	795	4	16.7	363	6	US-10-055-877-14	Sequence 14, Appl
723	4	16.7	320	6	US-10-793-626-2988	Sequence 2988, Ap	796	4	16.7	363	7	US-11-055-822-1156	Sequence 1156, Ap
724	4	16.7	320	6	US-10-055-877-338	Sequence 338, App	797	4	16.7	363	7	US-11-156-084-189	Sequence 189, App
725	4	16.7	322	6	US-10-454-437-218	Sequence 218, App	798	4	16.7	363	7	US-11-156-084-347	Sequence 347, App
726	4	16.7	322	7	US-11-055-822-66	Sequence 66, Appl	799	4	16.7	365	6	US-10-821-234-1575	Sequence 1575, Ap
727	4	16.7	324	7	US-11-119-212-15	Sequence 15, Appl	800	4	16.7	365	7	US-11-024-959-403	Sequence 403, App
728	4	16.7	324	7	US-11-063-343-20	Sequence 20, Appl	801	4	16.7	366	7	US-11-000-463-457	Sequence 457, App
729	4	16.7	326	7	US-11-119-212-19	Sequence 19, Appl	802	4	16.7	369	7	US-11-024-959-485	Sequence 485, App
730	4	16.7	326	7	US-11-156-084-239	Sequence 239, App	803	4	16.7	372	7	US-11-143-986-5	Sequence 5, Appl
731	4	16.7	329	7	US-11-156-084-28	Sequence 28, Appl	804	4	16.7	372	7	US-11-143-986-6	Sequence 6, Appl
732	4	16.7	329	7	US-11-156-084-46	Sequence 46, Appl	805	4	16.7	372	7	US-11-024-959-362	Sequence 362, App
733	4	16.7	329	7	US-11-156-084-171	Sequence 171, App	806	4	16.7	374	7	US-11-000-463-453	Sequence 453, App
734	4	16.7	329	7	US-11-156-084-243	Sequence 243, App	807	4	16.7	375	6	US-10-667-295-119	Sequence 119, App
735	4	16.7	330	6	US-10-453-372-516	Sequence 516, App	808	4	16.7	375	7	US-11-139-406-3	Sequence 3, Appl
736	4	16.7	330	7	US-11-205-460-2	Sequence 2, Appl	809	4	16.7	376	6	US-10-467-657-6138	Sequence 6138, Ap
737	4	16.7	331	6	US-10-453-372-508	Sequence 508, App	810	4	16.7	377	6	US-10-793-626-3014	Sequence 3014, Ap
738	4	16.7	331	7	US-11-129-143-87	Sequence 87, Appl	811	4	16.7	377	6	US-10-821-234-1436	Sequence 1436, Ap
739	4	16.7	331	7	US-11-149-403-4	Sequence 4, Appl	812	4	16.7	378	6	US-10-485-517-410	Sequence 410, App
740	4	16.7	332	6	US-10-793-626-540	Sequence 540, App	813	4	16.7	378	6	US-10-793-626-1428	Sequence 1428, App
741	4	16.7	332	6	US-10-793-626-2562	Sequence 2562, Ap	814	4	16.7	378	6	US-10-995-561-891	Sequence 891, App
742	4	16.7	333	7	US-11-024-959-349	Sequence 349, App	815	4	16.7	378	7	US-11-152-892-7	Sequence 7, Appl
743	4	16.7	335	6	US-10-453-372-512	Sequence 512, App	816	4	16.7	379	6	US-10-793-626-2810	Sequence 2810, Ap
744	4	16.7	336	6	US-10-793-626-1858	Sequence 1858, Ap	817	4	16.7	379	7	US-11-109-156-16	Sequence 16, Appl
745	4	16.7	336	6	US-10-453-372-510	Sequence 510, App	818	4	16.7	379	7	US-11-156-062-23	Sequence 23, Appl
746	4	16.7	337	6	US-10-467-962B-97	Sequence 97, Appl	819	4	16.7	380	6	US-10-793-626-702	Sequence 702, App
747	4	16.7	337	7	US-11-102-497-5	Sequence 5, Appl	820	4	16.7	380	7	US-11-089-551A-25	Sequence 25, Appl
748	4	16.7	337	7	US-11-102-497-12	Sequence 12, Appl	821	4	16.7	381	7	US-11-194-246-340	Sequence 340, App
749	4	16.7	338	6	US-10-821-234-1565	Sequence 1565, Ap	822	4	16.7	383	7	US-11-052-554A-239	Sequence 239, App
750	4	16.7	338	7	US-11-055-822-830	Sequence 830, App	823	4	16.7	384	6	US-10-838-616-28	Sequence 28, Appl
751	4	16.7	339	7	US-11-043-542-40	Sequence 40, Appl	824	4	16.7	385	7	US-11-060-029-2	Sequence 2, Appl
752	4	16.7	344	7	US-11-083-800-10	Sequence 10, Appl	825	4	16.7	386	7	US-11-022-562-229	Sequence 229, App
753	4	16.7	344	7	US-11-108-172-1085	Sequence 1085, Ap	826	4	16.7	386	7	US-11-143-986-2	Sequence 2, Appl
754	4	16.7	345	7	US-11-100-352-4	Sequence 4, Appl	827	4	16.7	386	7	US-11-143-986-3	Sequence 3, Appl
755	4	16.7	346	7	US-11-157-930-2	Sequence 2, Appl	828	4	16.7	387	7	US-11-092-140-17	Sequence 17, Appl



829	4	16.7	388	6	US-10-527-500-17	Sequence 17, Appl	902	4	16.7	447	7	US-11-024-959-505	Sequence 505, App
830	4	16.7	388	7	US-11-046-668-7	Sequence 7, Appli	903	4	16.7	448	6	US-10-793-626-1728	Sequence 1728, Ap
831	4	16.7	388	7	US-11-082-389-220	Sequence 20, App	904	4	16.7	448	6	US-10-763-712A-69	Sequence 69, Appl
832	4	16.7	388	7	US-11-129-143-47	Sequence 47, Appl	905	4	16.7	448	6	US-10-763-712A-112	Sequence 112, App
833	4	16.7	389	7	US-11-074-176-324	Sequence 324, App	906	4	16.7	448	6	US-10-995-561-793	Sequence 793, App
834	4	16.7	389	7	US-11-060-008-11	Sequence 11, Appl	907	4	16.7	448	7	US-11-055-822-826	Sequence 826, App
835	4	16.7	393	6	US-10-485-517-316	Sequence 316, App	908	4	16.7	448	7	US-11-052-554A-230	Sequence 230, App
836	4	16.7	394	6	US-10-793-626-300	Sequence 300, App	909	4	16.7	449	6	US-10-763-712A-73	Sequence 73, Appl
837	4	16.7	395	6	US-10-838-616-26	Sequence 26, Appl	910	4	16.7	451	6	US-10-793-626-2908	Sequence 2908, Ap
838	4	16.7	397	6	US-10-793-626-644	Sequence 644, App	911	4	16.7	451	6	US-10-821-234-1491	Sequence 1491, Ap
839	4	16.7	397	7	US-11-022-562-223	Sequence 223, App	912	4	16.7	451	6	US-10-641-678-56	Sequence 56, Appl
840	4	16.7	398	6	US-10-392-234A-4	Sequence 4, Appli	913	4	16.7	451	6	US-10-641-678-57	Sequence 57, Appl
841	4	16.7	398	6	US-10-517-939-210	Sequence 210, App	914	4	16.7	452	6	US-11-024-959-451	Sequence 451, App
842	4	16.7	398	7	US-11-046-668-9	Sequence 9, Appli	915	4	16.7	453	6	US-10-793-626-3260	Sequence 3260, Ap
843	4	16.7	398	7	US-11-052-554A-252	Sequence 252, App	916	4	16.7	453	6	US-11-082-389-198	Sequence 198, App
844	4	16.7	399	6	US-10-392-234A-10	Sequence 10, Appl	917	4	16.7	453	7	US-11-052-554A-224	Sequence 224, App
845	4	16.7	399	6	US-10-821-234-1031	Sequence 1031, Ap	918	4	16.7	454	7	US-11-089-551A-35	Sequence 35, Appl
846	4	16.7	400	6	US-10-454-437-306	Sequence 306, App	919	4	16.7	454	7	US-11-196-475-160	Sequence 160, App
847	4	16.7	401	6	US-10-641-678-33	Sequence 33, Appl	920	4	16.7	455	6	US-10-793-626-718	Sequence 718, App
848	4	16.7	401	6	US-10-838-616-18	Sequence 18, Appl	921	4	16.7	455	6	US-10-880-881-4	Sequence 4, Appli
849	4	16.7	401	7	US-11-097-749-3	Sequence 3, Appli	922	4	16.7	458	7	US-11-069-642-3	Sequence 3, Appli
850	4	16.7	401	7	US-11-134-795-28	Sequence 28, Appl	923	4	16.7	459	7	US-11-200-486-2	Sequence 2, Appli
851	4	16.7	401	7	US-11-052-554A-66	Sequence 66, Appl	924	4	16.7	459	6	US-10-467-657-2360	Sequence 2360, Ap
852	4	16.7	402	7	US-11-052-554A-184	Sequence 184, App	925	4	16.7	466	7	US-11-074-176-58	Sequence 58, Appl
853	4	16.7	403	6	US-10-528-031-7	Sequence 7, Appli	926	4	16.7	466	7	US-11-127-877-41	Sequence 41, Appl
854	4	16.7	404	6	US-10-667-295-112	Sequence 112, App	927	4	16.7	467	6	US-10-519-238-2	Sequence 2, Appli
855	4	16.7	404	6	US-10-793-626-398	Sequence 398, App	928	4	16.7	467	7	US-11-000-463-452	Sequence 452, App
856	4	16.7	405	7	US-11-089-551A-29	Sequence 29, Appl	929	4	16.7	467	7	US-11-000-463-924	Sequence 924, App
857	4	16.7	405	7	US-11-089-551A-50	Sequence 50, Appl	930	4	16.7	467	6	US-10-957-569-28	Sequence 28, Appl
858	4	16.7	406	7	US-11-074-176-92	Sequence 92, Appl	931	4	16.7	468	6	US-10-957-569-28	Sequence 28, Appl
859	4	16.7	410	6	US-10-513-759-14	Sequence 14, Appl	932	4	16.7	468	6	US-10-793-626-1648	Sequence 1648, Ap
860	4	16.7	411	7	US-11-119-212-17	Sequence 17, Appl	933	4	16.7	469	6	US-10-063-703-58	Sequence 58, Appl
861	4	16.7	412	7	US-11-074-176-24	Sequence 24, Appl	934	4	16.7	469	6	US-11-102-240-58	Sequence 58, Appl
862	4	16.7	412	7	US-11-168-874-12	Sequence 12, Appl	935	4	16.7	469	7	US-11-024-959-398	Sequence 398, App
863	4	16.7	413	7	US-11-060-029-4	Sequence 4, Appli	936	4	16.7	471	7	US-11-156-084-23	Sequence 23, Appl
864	4	16.7	413	7	US-11-119-212-21	Sequence 21, Appl	937	4	16.7	472	6	US-10-793-626-658	Sequence 658, App
865	4	16.7	414	6	US-10-995-561-803	Sequence 803, App	938	4	16.7	472	6	US-10-793-626-1902	Sequence 1902, Ap
866	4	16.7	415	6	US-10-793-626-1406	Sequence 1406, Ap	939	4	16.7	480	6	US-10-793-626-2852	Sequence 2852, Ap
867	4	16.7	416	6	US-10-793-626-196	Sequence 196, App	940	4	16.7	480	6	US-10-793-626-2986	Sequence 2986, Ap
868	4	16.7	417	6	US-10-613-744-2	Sequence 2, Appli	941	4	16.7	480	7	US-11-080-991-76	Sequence 76, Appl
869	4	16.7	419	6	US-10-793-626-2516	Sequence 2516, App	942	4	16.7	480	7	US-11-132-142-6	Sequence 6, Appli
870	4	16.7	420	6	US-10-520-820-14	Sequence 14, Appl	943	4	16.7	483	7	US-11-037-829A-5	Sequence 5, Appli
871	4	16.7	421	6	US-10-793-626-144	Sequence 144, App	944	4	16.7	484	6	US-10-467-657-6816	Sequence 6816, Ap
872	4	16.7	422	6	US-10-467-657-212	Sequence 212, App	945	4	16.7	485	6	US-10-485-517-136	Sequence 136, App
873	4	16.7	422	6	US-10-467-657-6516	Sequence 6516, Ap	946	4	16.7	486	6	US-10-821-234-1063	Sequence 1063, Ap
874	4	16.7	422	6	US-10-873-528-25	Sequence 25, Appl	947	4	16.7	489	6	US-10-793-626-3088	Sequence 3088, Ap
875	4	16.7	422	6	US-10-873-528-77	Sequence 77, Appl	948	4	16.7	489	6	US-10-793-626-3178	Sequence 3178, Ap
876	4	16.7	423	6	US-10-995-561-794	Sequence 794, App	949	4	16.7	491	6	US-10-793-626-2808	Sequence 2808, Ap
877	4	16.7	423	6	US-10-995-561-795	Sequence 795, App	950	4	16.7	491	7	US-11-069-642-137	Sequence 137, App
878	4	16.7	423	6	US-10-454-437-304	Sequence 304, App	951	4	16.7	491	7	US-11-212-443-191	Sequence 191, App
879	4	16.7	423	7	US-11-156-084-22	Sequence 22, Appl	952	4	16.7	499	6	US-10-793-626-1558	Sequence 1558, Ap
880	4	16.7	424	6	US-10-485-517-264	Sequence 264, App	953	4	16.7	500	6	US-10-957-569-18	Sequence 18, Appl
881	4	16.7	424	6	US-10-485-517-281	Sequence 281, App	954	4	16.7	501	7	US-11-167-856-22	Sequence 22, Appl
882	4	16.7	424	6	US-10-880-881-6	Sequence 6, Appli	955	4	16.7	504	6	US-10-507-928-6	Sequence 6, Appli
883	4	16.7	425	6	US-10-821-234-990	Sequence 990, App	956	4	16.7	504	7	US-11-029-465-6	Sequence 6, Appli
884	4	16.7	430	6	US-10-793-626-130	Sequence 130, App	957	4	16.7	505	6	US-10-507-928-8	Sequence 8, Appli
885	4	16.7	430	6	US-10-467-657-2346	Sequence 2346, Ap	958	4	16.7	505	7	US-11-029-465-8	Sequence 8, Appli
886	4	16.7	430	7	US-11-126-313-35	Sequence 35, Appl	959	4	16.7	507	7	US-11-033-039-96	Sequence 96, Appl
887	4	16.7	430	7	US-11-126-313-36	Sequence 36, Appl	960	4	16.7	510	6	US-10-485-517-320	Sequence 320, App
888	4	16.7	431	7	US-11-169-013-2	Sequence 2, Appli	961	4	16.7	510	7	US-11-093-814-1	Sequence 1, Appli
889	4	16.7	436	6	US-10-131-826A-404	Sequence 404, App	962	4	16.7	512	6	US-10-467-657-4870	Sequence 4870, Ap
890	4	16.7	437	6	US-10-821-234-1608	Sequence 1608, Ap	963	4	16.7	513	6	US-10-131-826A-152	Sequence 152, App
891	4	16.7	438	6	US-10-821-234-1051	Sequence 1051, Ap	964	4	16.7	513	6	US-10-485-517-233	Sequence 233, App
892	4	16.7	438	7	US-11-074-176-152	Sequence 152, App	965	4	16.7	513	6	US-10-995-561-566	Sequence 566, App
893	4	16.7	439	7	US-11-034-869-16	Sequence 16, Appl	966	4	16.7	514	6	US-10-840-688-2	Sequence 2, Appli
894	4	16.7	439	7	US-11-093-814-2	Sequence 2, Appli	967	4	16.7	514	6	US-10-840-688-3	Sequence 3, Appli
895	4	16.7	446	6	US-10-667-295-111	Sequence 111, App	968	4	16.7	514	6	US-10-840-688-4	Sequence 4, Appli
896	4	16.7	446	6	US-11-108-172-1121	Sequence 1121, Ap	969	4	16.7	514	6	US-10-840-688-5	Sequence 5, Appli
897	4	16.7	447	6	US-10-467-657-364	Sequence 364, App	970	4	16.7	514	6	US-10-840-688-6	Sequence 6, Appli
898	4	16.7	447	6	US-10-467-657-4034	Sequence 4034, Ap	971	4	16.7	514	6	US-10-840-688-7	Sequence 7, Appli
899	4	16.7	447	6	US-10-467-657-7050	Sequence 7050, Ap	972	4	16.7	514	6	US-10-840-688-8	Sequence 8, Appli
900	4	16.7	447	7	US-11-196-475-162	Sequence 162, App	973	4	16.7	514	6	US-10-840-688-9	Sequence 9, Appli
901	4	16.7	447	7	US-11-024-959-452	Sequence 452, App	974	4	16.7	514	6	US-10-840-688-10	Sequence 10, Appl

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975 4 16.7 514 6 US-10-840-688-11 Sequence 11, Appl
976 4 16.7 514 6 US-10-840-688-12 Sequence 12, Appl
977 4 16.7 514 6 US-10-840-688-13 Sequence 13, Appl
978 4 16.7 514 6 US-10-840-688-21 Sequence 21, Appl
979 4 16.7 518 6 US-10-821-234-1165 Sequence 1165, Ap
980 4 16.7 521 7 US-11-105-268-58 Sequence 58, Appl
981 4 16.7 522 6 US-10-793-626-604 Sequence 604, App
982 4 16.7 522 6 US-10-517-939-286 Sequence 286, App
983 4 16.7 523 6 US-10-453-372-1006 Sequence 1006, App
984 4 16.7 523 6 US-10-453-372-1008 Sequence 1008, Ap
985 4 16.7 524 6 US-10-878-556A-131 Sequence 131, App
986 4 16.7 525 6 US-10-878-556A-171 Sequence 171, App
987 4 16.7 527 7 US-11-120-543-18 Sequence 18, Appl
988 4 16.7 528 6 US-10-467-657-1042 Sequence 1042, Ap
989 4 16.7 529 6 US-10-632-150-44 Sequence 44, Appl
990 4 16.7 529 7 US-11-073-457-44 Sequence 44, Appl
991 4 16.7 529 7 US-11-073-460-44 Sequence 44, Appl
992 4 16.7 531 7 US-11-096-070-4 Sequence 4, Appli
993 4 16.7 532 6 US-10-793-626-546 Sequence 546, App
994 4 16.7 533 7 US-11-145-035-15 Sequence 15, Appl
995 4 16.7 534 7 US-11-089-551A-52 Sequence 52, Appl
996 4 16.7 537 6 US-10-504-364-6 Sequence 6, Appli
997 4 16.7 537 6 US-10-504-364-7 Sequence 7, Appli
998 4 16.7 537 7 US-11-129-442-47 Sequence 47, Appl
999 4 16.7 540 7 US-11-045-802-35 Sequence 35, Appl
1000 4 16.7 546 6 US-10-520-820-8 Sequence 8, Appli
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## ALIGNMENTS

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RESULT 1
US-10-821-234-1266
; Sequence 1266, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1266
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1266
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Query Match 100.0%; Score 24; DB 6; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.5e-18;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 LRFDSQTKSIFEQETNNNSFFT 24
Db 35 LRFDSQTKSIFEQETNNNSFFT 58
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RESULT 2
US-11-052-554A-58
; Sequence 58, Application US/11052554A
; Publication No. US20050288866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
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; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 58
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Escherichia coli 0157:H7
US-11-052-554A-58

Query Match 25.0%; Score 6; DB 7; Length 131;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DSQTKS 9
Db 99 DSQTKS 104
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RESULT 3
US-11-089-551A-4
; Sequence 4, Application US/11089551A
; Publication No. US20050266242A1
; GENERAL INFORMATION:
; APPLICANT: Lindquist et al.
; TITLE OF INVENTION: ELECTRICAL CONDUCTORS AND DEVICES FROM PRION-LIKE PROTEINS
; FILE REFERENCE: 30554/40025A
; CURRENT APPLICATION NUMBER: US/11/089,551A
; CURRENT FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: US 60/559,286
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-11-089-551A-4

Query Match 25.0%; Score 6; DB 7; Length 354;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 NNNNS 21
Db 47 NNNNS 52
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RESULT 4
US-10-467-962B-95
; Sequence 95, Application US/10467962B
; Publication No. US20050246784A1
; GENERAL INFORMATION:
; APPLICANT: Plesch, Gunnar
; APPLICANT: Blau, Astrid
; APPLICANT: Daeschner, Klaus
; APPLICANT: Klein, Mathieu
; TITLE OF INVENTION: Identification of Herbicidally Active Substances
; FILE REFERENCE: 2000 857
; CURRENT APPLICATION NUMBER: US/10/467,962B
; CURRENT FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: PCT/EP02/01466
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn Vers. 2.0
; SEQ ID NO 95
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-467-962B-95
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Query Match 25.0%; Score 6; DB 6; Length 592;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TNNNS 20  
Db 13 TNNNS 18  
|||||

RESULT 5  
US-10-524-647-112  
; Sequence 112, Application US/10524647  
; Publication No. US20050281909A1  
; GENERAL INFORMATION:  
; APPLICANT: Flachmann, Ralf  
; APPLICANT: Sauer, Matt  
; APPLICANT: Schopfer, Christel R.  
; APPLICANT: Klebsattel, Martin  
; APPLICANT: Pfeiffer, Angelika-Maria  
; APPLICANT: Luck, Thomas  
; APPLICANT: Voeste, Dirk  
; TITLE OF INVENTION: Use of astaxanthin-containing plants or parts of plants of the  
; TITLE OF INVENTION: genus Tagetes as feedstuffs  
; FILE REFERENCE: 13173-00004-US  
; CURRENT FILING DATE: 2005-02-17  
; PRIOR APPLICATION NUMBER: US/10/524,647  
; PRIOR FILING DATE: 2003-08-18  
; PRIOR APPLICATION NUMBER: DE 102 38 980.2  
; PRIOR FILING DATE: 2002-08-20  
; PRIOR APPLICATION NUMBER: DE 102 38 978.0  
; PRIOR FILING DATE: 2002-08-20  
; PRIOR APPLICATION NUMBER: DE 102 38 979.9  
; PRIOR FILING DATE: 2002-08-20  
; PRIOR APPLICATION NUMBER: DE 102 53 112.9  
; PRIOR FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: DE 102 58 971.2  
; PRIOR FILING DATE: 2002-12-16  
; NUMBER OF SEQ ID NOS: 142  
; SOFTWARE: Patent in version 3.3  
; SEQ ID NO 112  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-10-524-647-112

Query Match 25.0%; Score 6; DB 6; Length 592;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TNNNS 20  
Db 13 TNNNS 18  
|||||

RESULT 6  
US-11-087-227-24  
; Sequence 24, Application US/11087227  
; Publication No. US20050260566A1  
; GENERAL INFORMATION:  
; APPLICANT: Fischer, Timothy J.  
; APPLICANT: Malinowski, Douglas P.  
; APPLICANT: Taylor, Adriann J.  
; APPLICANT: Parker, Margaret R.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE  
; TITLE OF INVENTION: DETECTION OF CERVICAL DISEASE  
; FILE REFERENCE: 046143/287139  
; CURRENT APPLICATION NUMBER: US/11/087,227  
; CURRENT FILING DATE: 2005-03-23  
; PRIOR APPLICATION NUMBER: 60/556,495  
; PRIOR FILING DATE: 2004-03-24  
; NUMBER OF SEQ ID NOS: 90

; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 24  
; LENGTH: 1531  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-087-227-24

Query Match 25.0%; Score 6; DB 7; Length 1531;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FDSQTK 8  
Db 373 FDSQTK 378  
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RESULT 7  
US-11-186-284-211  
; Sequence 211, Application US/11186284  
; Publication No. US20050266493A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; APPLICANT: Berger, Allison  
; APPLICANT: Guillemette, Tracy L.  
; APPLICANT: Kamatkar, Shubhangi  
; APPLICANT: Schlegel, Robert  
; APPLICANT: Monahan, John E.  
; APPLICANT: Thibodeau, Stephen N.  
; APPLICANT: Burgart, Lawrence J.  
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND  
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
; FILE REFERENCE: MEM01-029P2RNM  
; CURRENT APPLICATION NUMBER: US/11/186,284  
; CURRENT FILING DATE: 2005-07-21  
; PRIOR APPLICATION NUMBER: US/10/301,822  
; PRIOR FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 60/339,971  
; PRIOR FILING DATE: 2001-12-10  
; PRIOR APPLICATION NUMBER: US 60/361,978  
; PRIOR FILING DATE: 2002-03-05  
; PRIOR APPLICATION NUMBER: US 60/381,988  
; PRIOR FILING DATE: 2002-05-20  
; NUMBER OF SEQ ID NOS: 228  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 211  
; LENGTH: 1531  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-11-186-284-211

Query Match 25.0%; Score 6; DB 7; Length 1531;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FDSQTK 8  
Db 373 FDSQTK 378  
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RESULT 8  
US-11-108-528-84  
; Sequence 84, Application US/11108528  
; Publication No. US20050261189A1  
; GENERAL INFORMATION:  
; APPLICANT: Larsen, Glenn  
; APPLICANT: Marvin, Martha  
; APPLICANT: Li, Dean Y.  
; APPLICANT: Wang, Elizabeth  
; APPLICANT: Chen, C. M. Amy  
; APPLICANT: Shamah, Steven M.  
; TITLE OF INVENTION: METHODS OF PROMOTING CARDIAC CELL  
; TITLE OF INVENTION: PROLIFERATION

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; FILE REFERENCE: HYDR-P01-041
; CURRENT APPLICATION NUMBER: US/11/108,528
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US 60/563,137
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/598,368
; PRIOR FILING DATE: 2004-08-02
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 1613
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-108-528-84

Query Match          25.0%; Score 6; DB 7; Length 1613;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 ETNNNN 19
Db      648 ETNNNN 653

RESULT 9
US-11-108-528-86
; Sequence 86, Application US/11/108528
; Publication No. US20050261189A1
; GENERAL INFORMATION:
; APPLICANT: Larsen, Glenn
; APPLICANT: Marvin, Martha
; APPLICANT: Li, Dean Y.
; APPLICANT: Wang, Elizabeth
; APPLICANT: Chen, C. M. Amy
; APPLICANT: Shamah, Steven M.
; TITLE OF INVENTION: METHODS OF PROMOTING CARDIAC CELL
; TITLE OF INVENTION: PROLIFERATION
; FILE REFERENCE: HYDR-P01-041
; CURRENT APPLICATION NUMBER: US/11/108,528
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US 60/563,137
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/598,368
; PRIOR FILING DATE: 2004-08-02
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 1613
; TYPE: PRT
; ORGANISM: Mouse
US-11-108-528-86

Query Match          25.0%; Score 6; DB 7; Length 1613;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 ETNNNN 19
Db      648 ETNNNN 653

RESULT 10
US-11-013-759-9
; Sequence 9, Application US/11/013759
; Publication No. US20050249747A1
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Sasaki, Ken
; APPLICANT: Yang, Yan Ping
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
; TITLE OF INVENTION: PROTEIN OF MORAXELLA
; FILE REFERENCE: 1038-921MIS:jb

; FILE REFERENCE: HYDR-P01-041
; CURRENT APPLICATION NUMBER: US/11/013,759
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: US/09/361,619
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 2053
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-11-013-759-9

Query Match          25.0%; Score 6; DB 7; Length 2053;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 NNNSS 21
Db      325 NNNSS 330

RESULT 11
US-11-045-024-616
; Sequence 616, Application US/11/045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 616
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-616

Query Match          20.8%; Score 5; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 NNNNS 20
Db      3 NNNNS 7
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RESULT 12  
US-11-045-024-770  
; Sequence 770, Application US/11045024  
; Publication No. US20050271676A1  
; GENERAL INFORMATION:  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Sidney, John  
; APPLICANT: Southwood, Scott  
; APPLICANT: Livingston, Brian  
; APPLICANT: Chesnut, Robert  
; APPLICANT: Baker, Denise Marie  
; APPLICANT: Celis, Esteban  
; APPLICANT: Kubo, Ralph  
; APPLICANT: Grey, Howard M.  
; APPLICANT: Epimmune Inc.  
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
; FILE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions  
; FILE REFERENCE: 2060.0040007 US/11/045,024  
; CURRENT APPLICATION NUMBER: US/11/045,024  
; CURRENT FILING DATE: 2005-01-28  
; PRIOR APPLICATION NUMBER: US 09/412,863  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: US 08/027,146  
; PRIOR FILING DATE: 1993-03-05  
; PRIOR APPLICATION NUMBER: US 08/073,205  
; PRIOR FILING DATE: 1993-06-04  
; PRIOR APPLICATION NUMBER: US 08/103,396  
; PRIOR FILING DATE: 1993-08-06  
; PRIOR APPLICATION NUMBER: US 08/159,184  
; PRIOR FILING DATE: 1993-11-29  
; PRIOR APPLICATION NUMBER: US 08/159,339  
; PRIOR FILING DATE: 1993-11-29  
; PRIOR APPLICATION NUMBER: US 08/205,713  
; PRIOR FILING DATE: 1994-03-04  
; PRIOR APPLICATION NUMBER: US 08/347,610  
; PRIOR FILING DATE: 1994-12-01  
; NUMBER OF SEQ ID NOS: 14528  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 770  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-770

Query Match 20.8%; Score 5; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.4;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 NNNNS 20  
Db 4 NNNNS 8

RESULT 13  
US-10-467-657-8871  
; Sequence 8871, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 8871

; LENGTH: 23  
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; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-8871  
Query Match 20.8%; Score 5; DB 6; Length 23;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TKSIF 11  
Db 18 TKSIF 22

RESULT 14  
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; Sequence 6884, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 6884  
; LENGTH: 56  
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; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-6884

Query Match 20.8%; Score 5; DB 6; Length 56;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 SSFYT 24  
Db 14 SSFYT 18

RESULT 15  
US-09-978-360A-737  
; Sequence 737, Application US/09978360A  
; Publication No. US20060009633A9  
; GENERAL INFORMATION:  
; APPLICANT: Edwards, Jean-Baptiste Dumas Milne  
; APPLICANT: Duclert, Aymeric  
; APPLICANT: Bougueleret, Lydie  
; APPLICANT: Jobert, Severin  
; APPLICANT: Clusel, Catherine  
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides  
; FILE REFERENCE: 56.US4.CIP  
; CURRENT APPLICATION NUMBER: US/09/978,360A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: US 60/066,677  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: US 60/069,957  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: US 60/074,121  
; PRIOR FILING DATE: 1998-02-09  
; PRIOR APPLICATION NUMBER: US 60/081,563  
; PRIOR FILING DATE: 1998-04-13  
; PRIOR APPLICATION NUMBER: US 60/096,116  
; PRIOR FILING DATE: 1998-08-10  
; PRIOR APPLICATION NUMBER: US 60/099,273  
; PRIOR FILING DATE: -09-04

Mon Jan 23 10:12:33 2006

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; PRIOR APPLICATION NUMBER: US 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: US 09/215,435
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: PCT/IB98/02122
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: US 09/247,155
; PRIOR FILING DATE: 1999-02-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 810
; SOFTWARE: Patent.pm
; SEQ ID NO 737
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -18...-1
US-09-978-360A-737
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Query Match      20.8%; Score 5; DB 5; Length 78;
Best Local Similarity 100.0%; Pred.No. 34;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 7 TKSIF 11
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Db 48 TKSIF 52
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Job time : 4.53846 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2006, 17:35:41 ; Search time 5.53846 Seconds  
(without alignments)  
416.939 Million cell updates/sec

Title: US-10-619-323-1\_COPY\_35\_58  
Perfect score: 24  
Sequence: 1 LRFDSTKSIPEQETNNNSFYT 24

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : PIR 80:\*

1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	24	100.0	228	1 A42929	CD9 antigen - gree
3	16	66.7	226	1 S3262	CD9 antigen - rat
4	14	58.3	226	1 JX0221	CD9 antigen - bovi
5	14	58.3	226	2 I49589	antigen - mouse
6	8	33.3	680	2 H84774	probable homeodoma
7	7	29.2	279	2 A96913	ABC-type sulfate t
8	7	29.2	419	2 T18420	hypothetical prote
9	7	29.2	1274	2 S59405	probable membrane
10	6	25.0	69	1 A48180	small acid-soluble
11	6	25.0	92	2 B85911	hypothetical prote
12	6	25.0	107	2 S52508	probable membrane
13	6	25.0	131	2 B91067	hypothetical lipop
14	6	25.0	136	2 T17640	hypothetical prote
15	6	25.0	150	2 D95131	hypothetical prote
16	6	25.0	163	2 T48609	hypothetical prote
17	6	25.0	180	2 B45613	surface antigen FU
18	6	25.0	194	2 AH3405	hypothetical cytos
19	6	25.0	208	2 T46896	merozoite surface
20	6	25.0	213	2 B65019	hypothetical prote
21	6	25.0	229	2 F84685	hypothetical prote
22	6	25.0	234	2 S14469	asparagine-rich pr
23	6	25.0	241	2 T06067	hypothetical prote
24	6	25.0	257	2 G87473	transcription regu
25	6	25.0	272	2 G71618	merozoite surface
26	6	25.0	274	1 JQ0957	myb-related protei
27	6	25.0	274	2 A45632	merozoite surface
28	6	25.0	278	2 S39310	merozoite surface
29	6	25.0	280	2 T19362	hypothetical prote

30	25.0	286	2 B45632	merozoite surface
31	25.0	287	2 B39615	merozoite 45K surf
32	25.0	292	2 AG2127	hypothetical prote
33	25.0	300	2 A39112	merozoite 45K surf
34	25.0	302	2 A39615	merozoite 45K surf
35	25.0	313	2 S01303	merozoite 45K surf
36	25.0	347	2 B39112	merozoite 45K surf
37	25.0	354	2 A39609	glutathione transf
38	25.0	356	2 G84904	probable DOP zinc
39	25.0	358	2 B75081	aspartate kinase (
40	25.0	368	2 S46601	hypothetical prote
41	25.0	370	2 S59539	heat shock transcr
42	25.0	371	2 T06382	Knox protein 1 - g
43	25.0	372	2 T50014	trehalase-6-phosph
44	25.0	384	2 S45592	ERD1 protein - yea
45	25.0	390	1 B49070	ecdysone-inducible
46	25.0	398	2 D85080	KNAT1 homeobox-lik
47	25.0	416	2 S50342	hypothetical prote
48	25.0	431	2 S50977	variant-specific s
49	25.0	440	2 E71625	weakly methyltrans
50	25.0	445	2 AH1649	SLF1 protein - yea
51	25.0	447	2 S59742	hypothetical prote
52	25.0	448	2 S05355	SIN3 protein-bindi
53	25.0	459	2 S51302	hypothetical prote
54	25.0	479	2 S60924	cyclin A-type (clo
55	25.0	482	2 T02967	cyclin A-type (clo
56	25.0	483	2 T02966	cyclin A-type - c
57	25.0	483	2 T03606	Abd-B protein - fr
58	25.0	491	2 A32584	steroid 17 alpha-h
59	25.0	493	2 A34220	fork head domain p
60	25.0	508	2 S52756	hypothetical prote
61	25.0	508	2 I53018	PHD finger protein
62	25.0	508	2 S59870	phosphoprotein pho
63	25.0	533	2 H86749	hypothetical prote
64	25.0	533	2 T39025	probable homeodoma
65	25.0	538	2 S62566	DNA polymerase III
66	25.0	560	2 S41743	DNA polymerase III
67	25.0	562	2 T26279	hydroxymethylgluta
68	25.0	569	1 S70551	hypothetical prote
69	25.0	575	2 T48224	probable transcrip
70	25.0	578	2 B64609	probable Gt-like t
71	25.0	578	2 S55102	hypothetical prote
72	25.0	582	2 A71906	homeotic protein B
73	25.0	592	2 A32107	homeotic protein B
74	25.0	598	2 B71095	protein kinase (EC
75	25.0	601	2 T00119	hypothetical prote
76	25.0	603	2 F96797	hypothetical prote
77	25.0	605	2 S48940	hypothetical threo
78	25.0	640	2 A41726	probable membrane
79	25.0	642	2 S27806	transcription fact
80	25.0	648	1 JQ1150	hypothetical prote
81	25.0	654	2 T21618	envelope protein E
82	25.0	658	2 T20042	hypothetical prote
83	25.0	658	2 T41309	hypothetical threo
84	25.0	674	2 S66937	probable membrane
85	25.0	676	2 S61977	transcription fact
86	25.0	677	2 T45682	hypothetical prote
87	25.0	682	2 T10319	envelope protein E
88	25.0	694	2 S59753	hypothetical prote
89	25.0	702	2 T41792	ODV-E66 orf46 - Bo
90	25.0	704	2 F72855	occlusion-derived
91	25.0	704	2 S21911	BRCore-NS-23 prote
92	25.0	722	2 H97217	uncharacterized co
93	25.0	730	2 S50543	GLN3 protein - yea
94	25.0	753	2 A27041	tyrosine kinase-re
95	25.0	759	2 B84538	hypothetical prote
96	25.0	779	1 S40382	box A-binding fact
97	25.0	803	2 T39530	hypothetical prote
98	25.0	848	2 G86708	aconitate hydratase
99	25.0	864	2 A49070	ecdysone-inducible
100	25.0	876	2 G90592	hypothetical prote
101	25.0	914	2 S46593	finger protein AZP
102	25.0	920	2 T08853	protein phosphatas

103	6	25.0	932	2	S09151	176	5	20.8	67	1	B48180	small acid-soluble
104	6	25.0	941	2	T49136	177	5	20.8	68	1	A24033	small acid-soluble
105	6	25.0	947	2	T08605	178	5	20.8	70	1	A61028	small acid-soluble
106	6	25.0	950	1	PWEYR1	179	5	20.8	72	1	C48180	SLA class II DR-be
107	6	25.0	959	2	D71619	180	5	20.8	72	2	I47166	HLA-DRB sigma anti
108	6	25.0	960	1	A39651	181	5	20.8	72	2	PT0164	HLA-DRB sigma anti
109	6	25.0	969	2	S54594	182	5	20.8	72	2	PH0154	HLA-DRB sigma anti
110	6	25.0	970	2	F64230	183	5	20.8	72	2	PT0169	DRB1 transplanta
111	6	25.0	1001	2	H64593	184	5	20.8	73	2	I79651	hypothetical prote
112	6	25.0	1061	2	T18085	185	5	20.8	73	2	AB1810	MHC protein - cott
113	6	25.0	1074	2	G96504	186	5	20.8	76	2	I68908	hypothetical prote
114	6	25.0	1111	1	A42640	187	5	20.8	76	2	S70428	hypothetical prote
115	6	25.0	1113	2	S28925	188	5	20.8	77	2	B30849	unknown protein en
116	6	25.0	1121	2	S54504	189	5	20.8	77	2	H85706	calcium-binding pr
117	6	25.0	1123	2	T28139	190	5	20.8	79	1	KLPFGI	MHC HLA-DR-beta-1
118	6	25.0	1138	2	A48944	191	5	20.8	80	2	I54469	MHC HLA-DR-beta-1
119	6	25.0	1140	2	S73786	192	5	20.8	80	2	I68777	HLA DRB1*1202 - hu
120	6	25.0	1154	2	S69206	193	5	20.8	81	2	I54550	apovitellenin I -
121	6	25.0	1178	2	S54073	194	5	20.8	82	1	VLDK1	apovitellenin I -
122	6	25.0	1228	2	S37621	195	5	20.8	82	2	I61810	gene MHC DQ-beta 1
123	6	25.0	1244	2	S25327	196	5	20.8	82	2	I51147	MHC class II beta
124	6	25.0	1256	2	S14556	197	5	20.8	82	2	I51147	apovitellenin I -
125	6	25.0	1314	1	TNBYR6	198	5	20.8	84	1	VLEU1	ubiquinol-cytochro
126	6	25.0	1397	2	T10466	199	5	20.8	85	2	T41058	class II histocomp
127	6	25.0	1402	2	T24664	200	5	20.8	87	2	S03117	myosin - human (fr
128	6	25.0	1403	2	S24548	201	5	20.8	87	2	I61696	MHC class II antig
129	6	25.0	1435	2	T32930	202	5	20.8	88	2	I59656	MHC class II histo
130	6	25.0	1436	2	D71618	203	5	20.8	89	2	S38676	myosin - human (fr
131	6	25.0	1447	2	S02160	204	5	20.8	89	2	I61699	MHC class II histo
132	6	25.0	1462	2	T06819	205	5	20.8	89	2	I68555	H-2 class II histo
133	6	25.0	1464	2	T13716	206	5	20.8	89	2	PL0126	myosin - human (fr
134	6	25.0	1473	2	S53599	207	5	20.8	90	2	I61691	C15L protein - vac
135	6	25.0	1475	2	A60026	208	5	20.8	91	2	H42502	HLA-DRB1 protei
136	6	25.0	1485	1	IS2PT2	209	5	20.8	94	2	T01409	probable membrane
137	6	25.0	1520	2	T23620	210	5	20.8	94	2	C97352	hypothetical prote
138	6	25.0	1526	2	JN0598	211	5	20.8	100	2	A70424	hypothetical prote
139	6	25.0	1526	2	A44406	212	5	20.8	101	2	T14780	thioredoxin [impor
140	6	25.0	1528	2	JS0703	213	5	20.8	103	2	A11228	thioredoxin [impor
141	6	25.0	1530	2	A40493	214	5	20.8	103	2	AC1582	thioredoxin [impor
142	6	25.0	1532	2	T18438	215	5	20.8	103	2	T28354	hypothetical prote
143	6	25.0	1572	2	T00027	216	5	20.8	103	2	S64759	thioredoxin [impor
144	6	25.0	1584	2	T18276	217	5	20.8	104	2	H95206	thioredoxin-disulf
145	6	25.0	1589	2	T13606	218	5	20.8	104	2	H98071	hypothetical prote
146	6	25.0	1612	2	S59969	219	5	20.8	107	2	C69354	hypothetical prote
147	6	25.0	1613	2	JE0272	220	5	20.8	107	2	C69354	hypothetical prote
148	6	25.0	1613	2	JE0273	221	5	20.8	109	2	T77444	hypothetical prote
149	6	25.0	1626	2	A39242	222	5	20.8	109	2	T49551	conserved hypotet
150	6	25.0	1655	2	T13998	223	5	20.8	109	2	B95043	tcpi protein - Vib
151	6	25.0	1664	2	T18216	224	5	20.8	113	2	S37091	conserved hypotet
152	6	25.0	1677	2	T43021	225	5	20.8	113	2	D79913	hypothetical prote
153	6	25.0	1737	2	A59235	226	5	20.8	115	2	H64030	MHC class II histo
154	6	25.0	1855	2	S41649	227	5	20.8	116	2	I38898	hypothetical prote
155	6	25.0	1891	2	T13594	228	5	20.8	117	2	C64378	hypothetical prote
156	6	25.0	1920	2	T13893	229	5	20.8	117	2	C90556	ORF MSV220 hypot
157	6	25.0	2023	2	T13154	230	5	20.8	120	2	T28381	MHC class II histo
158	6	25.0	2038	2	T18397	231	5	20.8	121	2	S64834	hypothetical prote
159	6	25.0	2109	2	T13552	232	5	20.8	122	2	S64834	transcription regu
160	6	25.0	2150	2	S71629	233	5	20.8	123	2	C39777	conserved hypotet
161	6	25.0	2167	2	S06558	234	5	20.8	123	2	E95372	hypothetical prote
162	6	25.0	2175	1	S03170	235	5	20.8	124	2	T24982	hypothetical prote
163	6	25.0	2269	2	T18472	236	5	20.8	125	2	T15993	conserved hypotet
164	6	25.0	2359	2	T03094	237	5	20.8	126	2	G95409	conserved hypotet
165	6	25.0	3130	2	T13828	238	5	20.8	128	2	F82515	iron-sulfur cluste
166	6	25.0	3973	2	B71612	239	5	20.8	129	2	H69397	hypothetical prote
167	5	20.8	20	2	I59073	240	5	20.8	131	2	S42040	hypothetical prote
168	5	20.8	57	2	I68900	241	5	20.8	134	2	C90527	chitinase (EC 3.2.
169	5	20.8	57	2	I35057	242	5	20.8	135	2	T14185	hypothetical prote
170	5	20.8	57	2	B43603	243	5	20.8	138	2	T28243	probable nucleic a
171	5	20.8	57	2	D71096	244	5	20.8	139	2	B28756	hypothetical prote
172	5	20.8	62	2	AH3059	245	5	20.8	140	2	T00616	class II histocomp
173	5	20.8	64	2	F97143	246	5	20.8	142	2	T00616	hypothetical prote
174	5	20.8	65	2	T17665	247	5	20.8	143	2	F82186	hypothetical prote
175	5	20.8	66	2	H84489	248	5	20.8	144	2	G72056	nucleoside diphosp

249	5	20.8	144	2	H86567	nucleoside-2-P kin	322	5	20.8	217	2	H71566	probable ribonucle
250	5	20.8	144	2	G70023	hypothetical prote	323	5	20.8	219	2	B49181	beta B2-crystallin
251	5	20.8	148	2	H90424	conserved hypotet	324	5	20.8	219	2	AF1525	probable transcrip
252	5	20.8	151	2	C95069	hypothetical prote	325	5	20.8	220	2	JC2337	T-cell receptor al
253	5	20.8	151	2	B97937	hypothetical prote	326	5	20.8	220	2	T27980	hypothetical prote
254	5	20.8	153	2	A36079	insulin-like growt	327	5	20.8	224	1	A64599	hydrogenase (BC 1.
255	5	20.8	153	2	C90405	hypothetical prote	328	5	20.8	224	2	D71915	hydrogenase, cytoc
256	5	20.8	154	2	A36591	superoxide dismuta	329	5	20.8	224	2	T19959	hypothetical prote
257	5	20.8	156	2	H84689	hypothetical prote	330	5	20.8	226	2	T28268	hypothetical prote
258	5	20.8	158	2	S47140	pathogenesis-relat	331	5	20.8	227	2	JG0176	EEP-2 precursor pr
259	5	20.8	158	2	E87723	protein R06A10.3 [	332	5	20.8	229	2	JQ0928	coat protein - com
260	5	20.8	158	2	T13738	hypothetical prote	333	5	20.8	230	2	S71747	DAG protein precu
261	5	20.8	160	2	C69900	hypothetical prote	334	5	20.8	231	2	S73469	probable lipoprote
262	5	20.8	160	2	B86614	CT832 hypothetical	335	5	20.8	231	2	AI3632	transcription regu
263	5	20.8	160	2	F72010	CT832 hypothetical	336	5	20.8	232	1	HLMSK2	H-2 class II histo
264	5	20.8	163	2	C85582	unknown protein en	337	5	20.8	232	2	H98807	exotoxin 12 (impor
265	5	20.8	163	2	H90731	hypothetical prote	338	5	20.8	233	2	E89807	glucosamine-6-phos
266	5	20.8	163	2	B81530	N utilization subs	339	5	20.8	233	2	H95184	MHC class II prote
267	5	20.8	164	2	T26534	hypothetical prote	340	5	20.8	236	2	I55654	3-oxoacyl-l-acyl-ca
268	5	20.8	166	2	F68898	single-strand bind	341	5	20.8	237	2	T11638	MHC class II histo
269	5	20.8	167	2	T39286	probable ubiquitin	342	5	20.8	237	2	B28043	H-2 class II histo
270	5	20.8	168	2	T47054	hypothetical prote	343	5	20.8	237	2	A21200	hypothetical prote
271	5	20.8	169	2	A81489	hypothetical prote	344	5	20.8	237	2	T04913	pur operon repress
272	5	20.8	169	2	S66862	probable membrane	345	5	20.8	238	1	F75185	beta-crystallin B1
273	5	20.8	172	2	S43397	stellate protein -	346	5	20.8	238	1	JYECR	dye resistance pro
274	5	20.8	172	2	S24398	hypothetical prote	347	5	20.8	238	2	AF0607	arginine transport
275	5	20.8	174	2	F85028	hypothetical prote	348	5	20.8	238	2	F64824	arginine transport
276	5	20.8	174	2	D83309	probable transcrip	349	5	20.8	238	2	E85597	arginine 3rd trans
277	5	20.8	176	2	F86881	conserved hypotet	350	5	20.8	238	2	A90747	arginine 3rd trans
278	5	20.8	177	2	T37212	hypothetical prote	351	5	20.8	238	2	AH0164	arginine transport
279	5	20.8	177	2	A86735	transcription regu	352	5	20.8	238	2	AF1076	global response re
280	5	20.8	179	2	T06962	hypothetical prote	353	5	20.8	238	2	G91298	dye resistance pro
281	5	20.8	180	2	H95260	transcription regu	354	5	20.8	238	2	A86140	dye resistance pro
282	5	20.8	180	2	E98126	conserved hypotet	355	5	20.8	238	2	H82084	aerobic respiratio
283	5	20.8	183	2	A41351	multidrug resistan	356	5	20.8	238	2	AG0056	glucosamine-6-phos
284	5	20.8	184	2	D64218	ribosomal protein	357	5	20.8	240	2	G98030	probable zinc fing
285	5	20.8	184	2	AD0232	hypothetical prote	358	5	20.8	240	2	T09602	I-E (beta) protei
286	5	20.8	184	2	T17446	hypothetical 21.1K	359	5	20.8	241	2	I48657	hypothetical prote
287	5	20.8	184	2	S35751	lex10 protein - le	360	5	20.8	241	2	S63458	hypothetical prote
288	5	20.8	185	2	S37479	T-cell receptor al	361	5	20.8	242	2	T40458	hypothetical prote
289	5	20.8	186	2	T51412	bZIP DNA-binding p	362	5	20.8	243	2	A99387	SAW-dependent meth
290	5	20.8	187	2	S69466	hypothetical prote	363	5	20.8	243	2	T24981	hypothetical prote
291	5	20.8	187	2	H89981	hypothetical prote	364	5	20.8	244	2	G91093	type III secretion
292	5	20.8	188	2	G69225	hypothetical prote	365	5	20.8	245	2	AI0634	conserved hypotet
293	5	20.8	190	2	T39622	probable phosphate	366	5	20.8	245	2	C90805	hypothetical prote
294	5	20.8	192	2	A45836	MHC class II histo	367	5	20.8	245	2	H85664	hypothetical prote
295	5	20.8	193	2	T00595	hypothetical prote	368	5	20.8	245	2	AE0248	conserved hypotet
296	5	20.8	193	2	C86334	hypothetical prote	369	5	20.8	245	2	G64845	ycdX protein - Esc
297	5	20.8	195	2	AF2496	hypothetical prote	370	5	20.8	246	2	E82908	hypothetical prote
298	5	20.8	198	2	F70371	hypothetical prote	371	5	20.8	249	2	T05424	probable lipote p
299	5	20.8	199	2	H89781	hypothetical prote	372	5	20.8	249	2	B71024	homeobox protein H
300	5	20.8	201	2	S54475	hypothetical prote	373	5	20.8	251	2	T52370	probable PHD-type
301	5	20.8	202	2	T29252	hypothetical prote	374	5	20.8	251	2	T49950	soj protein homolo
302	5	20.8	204	2	T51669	myb-related transc	375	5	20.8	251	2	F89529	probable C2H2-type
303	5	20.8	205	1	CYBOB	beta-crystallin B2	376	5	20.8	252	1	HLMSBF	hypothetical prote
304	5	20.8	205	2	JC2009	beta-crystallin B2	377	5	20.8	253	2	E69098	H-2 class II histo
305	5	20.8	205	2	JC4964	beta-B2-crystallin	378	5	20.8	253	2	D86839	phosphate transpor
306	5	20.8	205	2	S05015	beta-crystallin B2	379	5	20.8	253	2	E64652	phosphate ABC tran
307	5	20.8	206	2	B82095	probable lipoprote	380	5	20.8	256	2	E72427	conserved hypotet
308	5	20.8	207	2	A39757	beta-crystallin B2	381	5	20.8	256	2	A84437	oxidoreductase, sh
309	5	20.8	207	2	S32124	B2 protein - carro	382	5	20.8	257	2	E70330	probable PHD-type
310	5	20.8	207	2	D97190	hypothetical prote	383	5	20.8	257	2	B75038	soj protein homolo
311	5	20.8	208	2	A97011	probable Zn-finger	384	5	20.8	257	2	A84848	probable C2H2-type
312	5	20.8	208	2	C89804	hypothetical prote	385	5	20.8	257	2	T00406	hypothetical prote
313	5	20.8	209	2	S65300	hypothetical prote	386	5	20.8	258	2	A88618	protein ZKS20.2 [i
314	5	20.8	210	2	JH0603	beta-crystallin A4	387	5	20.8	258	2	I64070	cyclase hisP HI047
315	5	20.8	210	2	A64394	hypothetical prote	388	5	20.8	258	2	T05194	hypothetical prote
316	5	20.8	214	2	S49599	probable permease	389	5	20.8	259	1	PWBV3	H+-transporting tw
317	5	20.8	215	2	A49758	chloramphenicol O-	390	5	20.8	259	1	PWBVJ6	H+-transporting tw
318	5	20.8	215	2	T01951	probable CCAAT-box	391	5	20.8	259	2	G84685	probable DOF zinc
319	5	20.8	215	2	F84508	hypothetical prote	392	5	20.8	259	2	AB1718	ferrichrome ABC tr
320	5	20.8	216	2	E86154	hypothetical prote	393	5	20.8	259	2	AF1347	ferrichrome ABC tr
321	5	20.8	216	2	T20186	hypothetical prote	394	5	20.8	261	2	A60404	MHC class II histo

395	5	20.8	261	2	B60404	MHC class II histo	468	5	20.8	294	2	T08408	transcription fact
396	5	20.8	261	2	D90123	hypothetical prote	469	5	20.8	295	2	A11795	ABC transporter, A
397	5	20.8	262	2	H84152	hypothetical prote	470	5	20.8	296	2	T34910	hypothetical prote
398	5	20.8	262	2	B85939	hypothetical prote	471	5	20.8	296	2	S47594	cyclophilin B-bind
399	5	20.8	263	1	HLMSBS	H-2 class II histo	472	5	20.8	296	2	B40257	RNA5 protein - ye
400	5	20.8	263	1	HLMSBU	MHC class II histo	473	5	20.8	297	1	NBRT	paliporprotein H p
401	5	20.8	263	2	T11469	cytochrome-c oxida	474	5	20.8	297	2	S06267	surface antigen H
402	5	20.8	263	2	A61389	MHC class II histo	475	5	20.8	297	2	T51005	hypothetical prote
403	5	20.8	263	2	A25911	H-2 class II histo	476	5	20.8	299	2	S60529	envelope polyprote
404	5	20.8	263	2	F85986	probable FADA-type	477	5	20.8	299	2	S60528	envelope polyprote
405	5	20.8	263	2	C91141	probable transcrip	478	5	20.8	300	2	S60546	envelope polyprote
406	5	20.8	263	2	D65114	hypothetical prote	479	5	20.8	300	2	S60547	envelope polyprote
407	5	20.8	263	2	T38635	hypothetical prote	480	5	20.8	300	2	S60557	envelope polyprote
408	5	20.8	264	1	HLMSB1	H-2 class II histo	481	5	20.8	300	2	S60556	envelope polyprote
409	5	20.8	264	1	HLMSB	H-2 class II histo	482	5	20.8	300	2	S60555	envelope polyprote
410	5	20.8	264	1	F27579	T-cell receptor al	483	5	20.8	301	2	S60548	envelope polyprote
411	5	20.8	264	2	S11650	class II histocomp	484	5	20.8	303	2	AG1443	protein gp49 homol
412	5	20.8	264	2	A30529	H-2 class II histo	485	5	20.8	304	2	A40368	mrx protein - Esch
413	5	20.8	264	2	I56056	MHC E-beta-f - mou	486	5	20.8	304	2	C71637	rod shape-determin
414	5	20.8	264	2	T06601	hypothetical prote	487	5	20.8	306	2	S38183	probable purine nu
415	5	20.8	264	2	T05594	hypothetical prote	488	5	20.8	307	2	C95171	thiamin biosynthes
416	5	20.8	264	2	T24327	hypothetical prote	489	5	20.8	307	2	A45600	asparagine-rich bl
417	5	20.8	265	2	AF1890	WD-repeat protein	490	5	20.8	307	2	C98037	thiamin biosynthes
418	5	20.8	265	2	F75506	conserved hypotet	491	5	20.8	307	2	S37252	homeotic protein H
419	5	20.8	266	2	T31264	cis-1,2-dihydro-1,	492	5	20.8	310	2	S60425	probable membrane
420	5	20.8	266	2	I54295	lymphocyte antigen	493	5	20.8	310	2	C90277	hypothetical prote
421	5	20.8	266	2	I68733	MHC HLA-DR-beta ch	494	5	20.8	312	2	T32678	hypothetical prote
422	5	20.8	266	2	B39260	MHC class II histo	495	5	20.8	313	2	E81356	hypothetical prote
423	5	20.8	268	2	S57542	hypothetical prote	496	5	20.8	313	2	T29691	hypothetical prote
424	5	20.8	268	2	C70139	conserved hypotet	497	5	20.8	314	2	G64324	hypothetical prote
425	5	20.8	269	2	S57494	T-cell receptor al	498	5	20.8	315	2	H31090	H+-transporting tw
426	5	20.8	270	2	B70817	probable oxidoredu	499	5	20.8	315	2	D82559	riboflavin biosynt
427	5	20.8	272	2	S23684	erythrocyte membra	500	5	20.8	315	2	T13654	synthasin homolog -
428	5	20.8	273	2	PL0063	T-cell receptor al	501	5	20.8	315	2	C29624	spherulin 2a - sli
429	5	20.8	273	2	S21731	signal recognition	502	5	20.8	315	2	JC7572	somite Maf1 protei
430	5	20.8	273	2	S60751	homeotic protein s	503	5	20.8	315	2	T34528	hypothetical prote
431	5	20.8	274	2	AB1821	hypothetical prote	504	5	20.8	316	2	E84636	streptogramin lyas
432	5	20.8	275	1	RHWUAC	T-cell receptor al	505	5	20.8	316	2	A83588	transcription regu
433	5	20.8	275	2	A82257	oxidoreductase, sh	506	5	20.8	318	2	AB1792	probable beta-glyc
434	5	20.8	275	2	B75479	conserved hypotet	507	5	20.8	318	2	S51261	probable acetyl-Co
435	5	20.8	276	2	C82084	conserved hypotet	508	5	20.8	319	2	H81903	acetyl-CoA carboxy
436	5	20.8	277	2	AG1983	hypothetical prote	509	5	20.8	319	2	B81119	hypothetical prote
437	5	20.8	277	2	AB2461	hypothetical prote	510	5	20.8	319	2	C81390	hypothetical prote
438	5	20.8	277	2	T16020	hypothetical prote	511	5	20.8	319	2	S48355	STSL protein - yea
439	5	20.8	277	2	T24329	hypothetical prote	512	5	20.8	320	1	QQEV3M	myb-related protei
440	5	20.8	278	2	AD3253	chromosome partiti	513	5	20.8	322	2	T02987	hypothetical prote
441	5	20.8	279	2	D97026	nicotinate-nucleot	514	5	20.8	322	2	T23758	glutinin low molec
442	5	20.8	279	2	E97849	rod shape-determin	515	5	20.8	323	2	T06506	hypothetical prote
443	5	20.8	279	2	T16047	hypothetical prote	516	5	20.8	323	2	F86192	glycosyltransferas
444	5	20.8	280	2	H70089	hypothetical prote	517	5	20.8	323	2	AG3381	protein gp49 [Bact
445	5	20.8	280	2	A35872	steroid hormone re	518	5	20.8	324	2	AB1364	stem cell antigen
446	5	20.8	281	2	G82201	hypothetical prote	519	5	20.8	325	2	I65354	SfmH protein [impo
447	5	20.8	284	2	A84682	probable zinc-fing	520	5	20.8	325	2	C90703	protein involved i
448	5	20.8	284	2	B84146	transglutaminase t	521	5	20.8	325	2	F85553	sfmH protein precu
449	5	20.8	285	2	C86423	unknown protein, 1	522	5	20.8	325	2	D64785	hypothetical prote
450	5	20.8	286	2	H96706	probable transcrip	523	5	20.8	327	2	S57121	hypothetical prote
451	5	20.8	286	2	T12522	hypothetical prote	524	5	20.8	328	2	G84826	hypothetical prote
452	5	20.8	287	2	B96717	unknown protein, 3	525	5	20.8	328	2	T07726	hypothetical prote
453	5	20.8	288	2	AE0056	probable right ori	526	5	20.8	329	2	T18615	hypothetical prote
454	5	20.8	288	2	T21770	hypothetical prote	527	5	20.8	329	2	T13016	hypothetical prote
455	5	20.8	289	2	AB1075	right origin-bind	528	5	20.8	330	2	T02525	probable DOF zinc
456	5	20.8	289	2	JU0158	right oriC-binding	529	5	20.8	330	2	T25939	hypothetical prote
457	5	20.8	289	2	B91298	right origin-bind	530	5	20.8	332	2	T10886	iron utilization p
458	5	20.8	289	2	D86139	right origin-bind	531	5	20.8	332	2	T42370	probable glucan 1,
459	5	20.8	289	2	F97322	uncharacterized co	532	5	20.8	332	2	H84443	homeodomain transc
460	5	20.8	290	2	G72203	sugar ABC transpor	533	5	20.8	332	2	B71606	probable integrac
461	5	20.8	290	2	T05009	hypothetical prote	534	5	20.8	333	2	C41080	glyceradehyde-3-p
462	5	20.8	291	2	T51668	myb-related trans	535	5	20.8	333	2	T27883	hypothetical prote
463	5	20.8	292	2	S28832	microtubule-associ	536	5	20.8	334	1	A40166	gap junction prote
464	5	20.8	292	2	F82385	hypothetical prote	537	5	20.8	334	1	B34575	gap junction prote
465	5	20.8	293	2	T24165	hypothetical prote	538	5	20.8	334	2	C22735	hypothetical nox2
466	5	20.8	294	2	C64048	major ferric iron-	539	5	20.8	334	2	AH0300	conserved hypotet
467	5	20.8	294	2	H84591	hypothetical prote	540	5	20.8	334	2	T23444	hypothetical prote



541	5	20.8	336	2	T17370	NADH2 dehydrogenas	614	5	20.8	381	2	T43517	dnaJ protein homol
542	5	20.8	336	2	D88102	protein w10G11.9 [	615	5	20.8	381	2	A46358	steroid/thyroid ho
543	5	20.8	337	2	T18431	hypothetical prote	616	5	20.8	382	1	A35853	gap junction prote
544	5	20.8	338	2	T17366	NADH2 dehydrogenas	617	5	20.8	382	2	E64866	myosin-like protei
545	5	20.8	338	2	T17114	NADH2 dehydrogenas	618	5	20.8	382	2	I52565	stem cell antigen
546	5	20.8	338	2	T14130	NADH2 dehydrogenas	619	5	20.8	382	2	AH2728	glycosyl transfera
547	5	20.8	338	2	T17112	NADH2 dehydrogenas	620	5	20.8	382	2	S51651	cyclin delta-2 - A
548	5	20.8	338	2	T17371	NADH2 dehydrogenas	621	5	20.8	384	2	T10187	S-locus-specific g
549	5	20.8	338	2	T17374	NADH2 dehydrogenas	622	5	20.8	384	2	E96797	hypothetical prote
550	5	20.8	339	2	T17113	NADH2 dehydrogenas	623	5	20.8	385	2	H89046	protein C10G8.8 [i
551	5	20.8	339	2	T17375	NADH2 dehydrogenas	624	5	20.8	385	2	T24324	hypothetical prote
552	5	20.8	339	2	T17376	NADH2 dehydrogenas	625	5	20.8	386	2	T27287	dnaJ related prote
553	5	20.8	339	2	T46713	hypothetical prote	626	5	20.8	387	2	T27287	hypothetical prote
554	5	20.8	340	2	AF0867	probable regulator	627	5	20.8	389	2	B82479	D-alanyl-D-alanine
555	5	20.8	340	2	T07615	antigen fbpc2 - My	628	5	20.8	389	2	H90083	polyadenylate-bind
556	5	20.8	340	2	T02120	hypothetical prote	629	5	20.8	389	2	S53612	gene MSP-2 protei
557	5	20.8	340	2	A44019	membrane protein S	630	5	20.8	390	2	T49619	hypothetical prote
558	5	20.8	340	2	T23367	hypothetical prote	631	5	20.8	391	2	S14577	asparagine-rich pr
559	5	20.8	341	2	T04050	hypothetical prote	632	5	20.8	391	2	E64474	hypothetical prote
560	5	20.8	341	2	T24954	hypothetical prote	633	5	20.8	392	2	T13722	NADH2 dehydrogenas
561	5	20.8	342	2	T01735	homeobox protein N	634	5	20.8	392	2	B86549	polymorphic outer
562	5	20.8	344	2	T23028	hypothetical prote	635	5	20.8	392	2	B72075	polymorphic outer
563	5	20.8	345	2	S07114	MHC class I histoc	636	5	20.8	393	2	T13501	NADH2 dehydrogenas
564	5	20.8	345	2	D91201	type III secretion	637	5	20.8	393	2	T13565	NADH2 dehydrogenas
565	5	20.8	345	2	H86047	escu [imported] -	638	5	20.8	393	2	T12630	NADH2 dehydrogenas
566	5	20.8	345	2	AB1813	hypothetical prote	639	5	20.8	393	2	T12609	NADH2 dehydrogenas
567	5	20.8	348	2	S29990	histocompatibility	640	5	20.8	393	2	B84758	probable katanin [
568	5	20.8	348	2	D84922	probable sugar tra	641	5	20.8	393	2	A97510	probable hexosyltr
569	5	20.8	348	2	S19873	single-stranded DN	642	5	20.8	394	1	BWH1XD	bexD protein - Hae
570	5	20.8	349	1	E64442	probable arsenical	643	5	20.8	395	2	T13756	NADH2 dehydrogenas
571	5	20.8	352	2	AG0762	probable membrane	644	5	20.8	395	2	T22751	hypothetical prote
572	5	20.8	352	2	T33433	hypothetical prote	645	5	20.8	395	2	A95860	hypothetical prote
573	5	20.8	353	2	C85572	hypothetical prote	646	5	20.8	395	2	A43700	hypothetical prote
574	5	20.8	353	2	E90721	hypothetical prote	647	5	20.8	396	1	ADMZRB	BN51 protein - hum
575	5	20.8	353	2	T24010	hypothetical prote	648	5	20.8	396	1	BMH02	argininosuccinate
576	5	20.8	355	2	S04317	homeobox protein L	649	5	20.8	396	2	AF3168	bone morphogenetic
577	5	20.8	357	2	S33144	leucoanthocyanidin	650	5	20.8	397	2	F72072	conserved hypothet
578	5	20.8	357	2	JQ2174	hypothetical 39.2K	651	5	20.8	397	2	C86552	probable transamin
579	5	20.8	357	2	S27909	hypothetical prote	652	5	20.8	397	2	T36119	aspartate aminotra
580	5	20.8	358	1	PKWKG	H+-transporting tw	653	5	20.8	397	2	E88533	hypothetical prote
581	5	20.8	358	2	B81302	probable alcohol d	654	5	20.8	397	2	T17008	probable zinc fing
582	5	20.8	358	2	AB2041	hypothetical prote	655	5	20.8	398	1	R3BYM1	ribosomal protein
583	5	20.8	358	2	T10244	G-Box binding prot	656	5	20.8	400	2	D71520	probable transamin
584	5	20.8	358	2	D96579	hypothetical prote	657	5	20.8	401	2	T00897	prochlorophyllid
585	5	20.8	360	2	S06287	fragmin - eline mo	658	5	20.8	402	2	A84581	probable disease r
586	5	20.8	361	2	C84613	probable cyclin D	659	5	20.8	402	2	T13614	N-acetyltransferas
587	5	20.8	362	2	A60384	MHC class I histoc	660	5	20.8	403	2	S47659	CDC2/CDC13 suppres
588	5	20.8	362	2	C81453	flagellar biosynth	661	5	20.8	404	2	A46165	envelope surface g
589	5	20.8	362	2	C64807	ybgO protein - Esc	662	5	20.8	405	2	F89930	hypothetical prote
590	5	20.8	364	2	A81261	probable periplasm	663	5	20.8	406	2	D86895	membrane protein l
591	5	20.8	365	2	S62542	hypothetical coile	664	5	20.8	406	2	AG3021	hypothetical prote
592	5	20.8	365	2	F88449	protein F54D8.4 [i	665	5	20.8	406	2	C98263	probable exo-beta-
593	5	20.8	366	2	S53898	conserved hypothet	666	5	20.8	407	2	T39282	regulatory protein
594	5	20.8	366	2	AH0445	probable heat shoc	667	5	20.8	407	2	S49890	asparagine-rich bl
595	5	20.8	366	2	F27203	phosphoprotein pho	668	5	20.8	409	2	C45600	2-octaprenyl-6-met
596	5	20.8	369	1	PABY21	hypothetical prote	669	5	20.8	409	2	B87262	eukaryotic release
597	5	20.8	369	2	T24205	glycosyltransferas	670	5	20.8	409	2	S74704	hypothetical prote
598	5	20.8	370	2	G97277	probable acetyl-Co	671	5	20.8	409	2	T25935	hypothetical prote
599	5	20.8	371	2	T07938	hypothetical prote	672	5	20.8	413	1	S03631	tapC protein - Aer
600	5	20.8	372	2	A64176	single-stranded DN	673	5	20.8	413	2	S70874	protein let-756 [i
601	5	20.8	372	2	I38042	hypothetical prote	674	5	20.8	413	2	H88481	sensory transducti
602	5	20.8	373	2	S63262	hypothetical prote	675	5	20.8	413	2	A62205	hypothetical prote
603	5	20.8	373	2	S72368	single-stranded DN	676	5	20.8	414	2	A86229	hypothetical prote
604	5	20.8	375	2	T06096	hypothetical prote	677	5	20.8	414	2	F29826	probable ammonium
605	5	20.8	376	2	E85435	cysteine proteinas	678	5	20.8	416	2	A89996	site-specific DNA-
606	5	20.8	376	2	G71828	hypothetical prote	679	5	20.8	417	2	S34333	hypothetical prote
607	5	20.8	377	1	S01615	site-specific DNA-	680	5	20.8	418	2	T25368	asparagine-rich pr
608	5	20.8	377	2	F84473	hypothetical prote	681	5	20.8	419	2	S14508	hypothetical prote
609	5	20.8	378	2	A44443	basic helix-loop-h	682	5	20.8	422	2	T20588	hypothetical prote
610	5	20.8	378	2	T51647	myb-related transc	683	5	20.8	423	2	A99242	hypothetical prote
611	5	20.8	380	2	T20269	hypothetical prote	684	5	20.8	423	2	AC3044	hypothetical prote
612	5	20.8	380	2	T24678	NADH2 dehydrogenas	685	5	20.8	426	2	E83981	pyruvate dehydroge
613	5	20.8	381	2	T13701		686	5	20.8				

687	5	20.8	426	2	S58304	hypothetical prote	760	5	20.8	483	2	A11665	glutamyl-tRNA(Gln)
688	5	20.8	427	2	AF0839	4-aminobutyrate tr	761	5	20.8	485	2	S48650	catalase [EC 1.11.
689	5	20.8	428	2	PC4163	toxin-co-regulated	762	5	20.8	486	2	S66097	cell-cycle protein
690	5	20.8	429	1	JCS861	endo-1,4-beta-xyla	763	5	20.8	486	2	D64474	hypothetical prote
691	5	20.8	430	2	S24705	probable segment i	764	5	20.8	486	2	E85433	SCARECROW-like pro
692	5	20.8	431	2	T07812	S-locus-specific g	765	5	20.8	487	2	F84727	hypothetical prote
693	5	20.8	432	2	T47528	hypothetical prote	766	5	20.8	487	2	T49351	hypothetical prote
694	5	20.8	433	2	E86236	protein F14N23.7 [	767	5	20.8	488	2	A59291	myosin-14 - malari
695	5	20.8	433	2	S63143	cell division cont	768	5	20.8	490	2	A35546	muscarinic acetyl
696	5	20.8	434	2	T37350	probable 49.8K pro	769	5	20.8	490	2	A46391	CAMP receptor subt
697	5	20.8	434	2	A72159	ISR protein - vari	770	5	20.8	490	2	S52830	HMS1 protein - yea
698	5	20.8	434	2	S33082	G5R protein - vari	771	5	20.8	492	1	CS5V	catalase [EC 1.11.
699	5	20.8	434	2	T28505	hypothetical prote	772	5	20.8	492	2	T18969	catalase [EC 1.11.
700	5	20.8	434	2	C82885	membrane nuclease	773	5	20.8	492	2	S52079	catalase [EC 1.11.
701	5	20.8	434	2	AF0563	inosine-guanosine	774	5	20.8	492	2	T12300	catalase [EC 1.11.
702	5	20.8	436	2	I51237	translation elonga	775	5	20.8	492	2	S10770	catalase [EC 1.11.
703	5	20.8	436	2	S20060	translation elonga	776	5	20.8	492	2	S17493	catalase [EC 1.11.
704	5	20.8	436	2	A38145	invariant surface	777	5	20.8	492	2	S10395	catalase [EC 1.11.
705	5	20.8	437	2	S60957	transcription modu	778	5	20.8	492	2	T05779	catalase [EC 1.11.
706	5	20.8	437	2	S05357	hypothetical prote	779	5	20.8	492	2	S46297	catalase [EC 1.11.
707	5	20.8	438	2	E84522	hypothetical prote	780	5	20.8	492	2	S46298	catalase [EC 1.11.
708	5	20.8	439	2	T52291	probable DNA-bind	781	5	20.8	492	2	T10902	catalase [EC 1.11.
709	5	20.8	439	2	F85189	disease resistance	782	5	20.8	492	2	T28025	hypothetical prote
710	5	20.8	441	2	T32350	hypothetical prote	783	5	20.8	492	1	S39532	aldehyde dehydroge
711	5	20.8	442	2	G83672	6-phospho-beta-glu	784	5	20.8	493	2	T07911	catalase [EC 1.11.
712	5	20.8	442	2	H86276	F14L17.4 protein -	785	5	20.8	493	2	SS1450	probable membrane
713	5	20.8	443	2	E84449	hypothetical prote	786	5	20.8	493	2	S06025	GLO3 protein - yea
714	5	20.8	443	2	A54813	CAMP receptor CAR4	787	5	20.8	494	1	CSPM	catalase [EC 1.11.
715	5	20.8	446	2	C87130	sugar transport pe	788	5	20.8	495	2	S31493	env polyprotein -
716	5	20.8	447	2	A84718	hypothetical prote	789	5	20.8	498	2	F83523	probable colicin-1
717	5	20.8	448	2	S07711	larvicidal toxin 5	790	5	20.8	500	1	S00364	aldehyde dehydroge
718	5	20.8	448	2	A28211	larvicidal toxin 5	791	5	20.8	500	2	S97995	hypothetical prote
719	5	20.8	448	2	C28211	mosquitocidal toxi	792	5	20.8	501	2	T43047	retrovirus-related
720	5	20.8	448	2	T01570	hypothetical prote	793	5	20.8	503	1	VCVDA	transforming prote
721	5	20.8	448	2	S06961	hypothetical prote	794	5	20.8	505	2	B88206	protein F21D12.3 [
722	5	20.8	451	2	A23535	hypothetical prote	795	5	20.8	506	2	AF1214	hypothetical prote
723	5	20.8	452	2	JC2459	clustered asparagi	796	5	20.8	506	2	T02400	probable beta-gluc
724	5	20.8	452	2	S77436	gastrin/cholecysto	797	5	20.8	507	2	S05542	hypothetical prote
725	5	20.8	452	2	T33049	sigma factor sibG	798	5	20.8	508	2	S11513	usp protein - frui
726	5	20.8	454	2	A43501	hypothetical prote	799	5	20.8	508	2	T13737	steroid hormone re
727	5	20.8	457	2	I54340	DNA-binding protei	800	5	20.8	509	1	IS1281	steroid 17alpha-mo
728	5	20.8	458	2	T49114	hypothetical prote	801	5	20.8	509	2	T31706	hypothetical prote
729	5	20.8	459	2	I64224	aromatic amino aci	802	5	20.8	512	2	T02498	probable WRKY-type
730	5	20.8	460	1	YKBYC	citrate (ci)-synth	803	5	20.8	512	2	T04708	hypothetical prote
731	5	20.8	460	2	C27311	NADH2 dehydrogenas	804	5	20.8	513	2	B96524	hypothetical prote
732	5	20.8	462	2	S65570	dihydrofolate redu	805	5	20.8	514	2	S25009	monosaccharide tra
733	5	20.8	462	2	B48326	cytb intron la pro	806	5	20.8	514	2	D81952	type I site-specif
734	5	20.8	462	2	T19652	hypothetical prote	807	5	20.8	514	2	F81152	type I site-specif
735	5	20.8	466	2	T41375	probable phosphogl	808	5	20.8	514	2	T15338	hypothetical prote
736	5	20.8	467	2	T41053	triglyceride lipas	809	5	20.8	517	1	S26606	myb-related protei
737	5	20.8	467	2	T51574	hypothetical prote	810	5	20.8	518	2	D69813	ABC transporter (A
738	5	20.8	468	1	A41242	interleukin-6 rece	811	5	20.8	520	2	S02166	type I site-specif
739	5	20.8	469	2	H97064	probable sugar-pro	812	5	20.8	521	1	A44267	protein-tyrosine-p
740	5	20.8	469	2	E90105	putative RNA-depen	813	5	20.8	521	2	T27192	hypothetical prote
741	5	20.8	469	2	T46230	NAC2-like protein	814	5	20.8	522	2	H86248	protein T23J18.22
742	5	20.8	470	2	C95055	6-phospho-beta-gal	815	5	20.8	523	2	S25015	monosaccharide tra
743	5	20.8	470	2	H97924	hypothetical prote	816	5	20.8	524	2	G90109	T-complex protein
744	5	20.8	471	2	T49175	hypothetical prote	817	5	20.8	525	1	KGHUGH	histidine-rich gly
745	5	20.8	471	2	T32788	hypothetical prote	818	5	20.8	525	2	F97305	spore germination
746	5	20.8	472	2	T20454	hypothetical prote	819	5	20.8	528	2	C85056	probable DNA-bind
747	5	20.8	472	2	S34955	hypothetical prote	820	5	20.8	529	1	YRHU1	monophenol monooxy
748	5	20.8	472	2	S28026	gene 10 protein -	821	5	20.8	531	2	JT0531	muscarinic acetyl
749	5	20.8	472	2	A26357	nuclear pore compl	822	5	20.8	531	2	AH1491	hypothetical prote
750	5	20.8	473	2	T04799	homeotic protein C	823	5	20.8	532	2	JT0530	hypothetical prote
751	5	20.8	475	2	A87396	hypothetical prote	824	5	20.8	533	1	YRMSCS	muscarinic acetyl
752	5	20.8	475	2	T39486	sensor histidine k	825	5	20.8	533	2	S63270	monophenol monooxy
753	5	20.8	476	2	AG2868	hypothetical prote	826	5	20.8	533	2	D36710	probable membrane
754	5	20.8	479	2	T02623	succinoglycan bios	827	5	20.8	534	2	S09625	F24J5.16 imported
755	5	20.8	480	2	E81407	hypothetical prote	828	5	20.8	534	2	C85774	hypothetical prote
756	5	20.8	480	2	E88656	probable membrane	829	5	20.8	535	2	D64924	hypothetical prote
757	5	20.8	482	2	H71400	protein F56D6.2 [i	830	5	20.8	535	2	S53957	hypothetical prote
758	5	20.8	482	2	S5950	hypothetical prote	831	5	20.8	536	2	A45409	atrial natriuretic
759	5	20.8	483	2	AC1294	glutamyl-tRNA(Gln)	832	5	20.8	536	2	H71563	hypothetical prote

833	5	20.8	537	1	A28111	natriuretic peptid	906	5	20.8	610	2	T18441	asparagine synthas
834	5	20.8	537	2	D86520	CTP synthetase [im	907	5	20.8	610	2	S05807	SAN1 protein - yea
835	5	20.8	537	2	E81568	CTP synthase CP052	908	5	20.8	612	2	T13616	hypothetical prote
836	5	20.8	537	2	A72103	ctp synthetase - C	909	5	20.8	613	2	T47483	receptor like prot
837	5	20.8	537	2	A23770	asparagine-rich pr	910	5	20.8	613	2	JC7762	SOX-3 protein - gu
838	5	20.8	537	2	B97013	and cellulose-bind	911	5	20.8	614	2	T29902	hypothetical prote
839	5	20.8	538	2	T40298	membrane transport	912	5	20.8	614	2	S58306	WD-40 repeat regul
840	5	20.8	538	2	H86329	F6F9.25 protein -	913	5	20.8	614	2	T29937	hypothetical prote
841	5	20.8	539	2	T00149	hypothetical prote	914	5	20.8	616	2	C95861	probable ABC trans
842	5	20.8	540	1	VGN2B3	cell fusion glycop	915	5	20.8	617	2	A72123	hypothetical prote
843	5	20.8	540	2	B83121	probable AMP-bindl	916	5	20.8	618	2	T04237	hypothetical prote
844	5	20.8	541	2	S73383	probable lipoprote	917	5	20.8	620	2	D82274	toxin co-regulated
845	5	20.8	542	2	S45557	resB protein - Bac	918	5	20.8	621	1	S59632	endo-1,4-beta-xyla
846	5	20.8	542	2	A98021	hypothetical prote	919	5	20.8	621	2	T18737	hypothetical prote
847	5	20.8	543	2	B93369	homeotic protein B	920	5	20.8	622	2	A90570	lipoprotein [impor
848	5	20.8	544	2	S65231	tRNA-pseudouridine	921	5	20.8	623	1	S33167	gene pointed prote
849	5	20.8	544	2	H84790	hypothetical prote	922	5	20.8	623	1	G86860	serine/threonine p
850	5	20.8	546	2	B97645	integral membrane	923	5	20.8	627	2	G86860	probable homeodoma
851	5	20.8	547	1	ERADP4	60.5K fiber protei	924	5	20.8	628	2	S51422	probable membrane
852	5	20.8	547	2	S15028	chromatin-binding	925	5	20.8	631	2	S70908	transferin-bindin
853	5	20.8	547	2	S41618	probable DNA-direc	926	5	20.8	632	2	A25784	hypothetical 70K p
854	5	20.8	547	2	T03901	hypothetical prote	927	5	20.8	633	2	S13352	amino acid transpo
855	5	20.8	548	2	T06266	germacrene C synth	928	5	20.8	633	2	T14612	hypothetical prote
856	5	20.8	548	2	G06265	phosphatase ABC tran	929	5	20.8	633	2	T04835	probable serine/th
857	5	20.8	548	2	G82286	J-kappa recombinat	930	5	20.8	635	2	F71621	hypothetical prote
858	5	20.8	550	2	A41585	hypothetical ser-p	931	5	20.8	635	2	JC5896	killer cell inhibi
859	5	20.8	551	2	T39092	probable secreted	932	5	20.8	635	2	S67605	hypothetical prote
860	5	20.8	552	2	T29114	probable membrane	933	5	20.8	639	1	VCWVSA	env polyprotein pr
861	5	20.8	553	2	E91120	probable membrane	934	5	20.8	639	2	S20887	actA protein precu
862	5	20.8	553	2	E85965	hypothetical prote	935	5	20.8	639	2	AE1100	actin-assembly ind
863	5	20.8	553	2	A65093	hypothetical prote	936	5	20.8	640	2	T07923	acetyl-CoA carboxy
864	5	20.8	554	2	S24949	pollen-specific pr	937	5	20.8	642	2	D96777	hypothetical prote
865	5	20.8	559	1	JQ2010	transcription fact	938	5	20.8	645	1	VCWVSS	env polyprotein pr
866	5	20.8	559	2	AF0891	probable exported	939	5	20.8	646	2	T02398	hypothetical prote
867	5	20.8	561	2	S57784	4-coumarate-CoA li	940	5	20.8	647	2	T33141	hypothetical prote
868	5	20.8	562	1	ERADN2	60.5K fiber protei	941	5	20.8	647	2	S06450	steroid hormone re
869	5	20.8	563	2	S70196	kfiB protein - Bac	942	5	20.8	649	2	T32967	hypothetical prote
870	5	20.8	567	2	T01032	hypothetical prote	943	5	20.8	650	2	S16706	transcription acti
871	5	20.8	567	2	T15574	hypothetical prote	944	5	20.8	651	2	T03889	Na+/Ca2+, K+-exchan
872	5	20.8	567	2	A71619	membrane transport	945	5	20.8	655	2	S51884	probable protein k
873	5	20.8	567	2	T18462	hypothetical prote	946	5	20.8	656	2	T10568	probable serine/th
874	5	20.8	570	1	S50933	myb-related protei	947	5	20.8	657	2	S64073	hypothetical prote
875	5	20.8	571	2	G89123	protein K07C11.4 [	948	5	20.8	659	2	C96730	probable ABC trans
876	5	20.8	572	2	A87156	unknown permease [	949	5	20.8	659	2	A36664	S59/2 homeotic pro
877	5	20.8	572	2	B89782	hypothetical prote	950	5	20.8	661	2	S21221	hemocyanin chain c
878	5	20.8	575	2	AF2374	hypothetical prote	951	5	20.8	663	2	S55164	hypothetical prote
879	5	20.8	576	2	S69214	deformed epidermal	952	5	20.8	664	2	B85122	serine/threonine k
880	5	20.8	577	2	B44307	aspartyl-tRNA synt	953	5	20.8	664	2	T10573	probable serine/th
881	5	20.8	577	2	D75406	catechol oxidase (	954	5	20.8	666	2	S50452	hypothetical prote
882	5	20.8	583	2	S34785	catechol oxidase (	955	5	20.8	666	2	S36218	hepatocyte nuclear
883	5	20.8	583	2	S30930	probable myosin he	956	5	20.8	667	2	B84018	two-component sens
884	5	20.8	583	2	C84788	excinuclease ABC s	957	5	20.8	668	2	S39836	hypothetical prote
885	5	20.8	584	2	H82898	hypothetical prote	958	5	20.8	669	1	DNMUU5	NADH2 dehydrogenas
886	5	20.8	584	2	T39704	topoisomerase I-re	959	5	20.8	669	2	S64795	suppressor protein
887	5	20.8	584	2	S51882	hypothetical prote	960	5	20.8	669	2	S14535	asparagine-rich pr
888	5	20.8	587	2	D96578	hypothetical prote	961	5	20.8	672	2	S61463	p83/100 protein -
889	5	20.8	587	2	E82431	methyl-accepting c	962	5	20.8	672	2	S63043	MEF4 protein - yea
890	5	20.8	588	2	S34786	catechol oxidase (	963	5	20.8	674	2	S75662	sensory transducti
891	5	20.8	588	2	S30929	catechol oxidase (	964	5	20.8	675	2	D85065	receptor protein k
892	5	20.8	590	2	A26638	homeotic protein D	965	5	20.8	678	2	S62939	hypothetical prote
893	5	20.8	591	2	T25636	hypothetical prote	966	5	20.8	679	2	S48939	hypothetical prote
894	5	20.8	594	2	A42770	Suppressor of Hair	967	5	20.8	679	2	S37842	hypothetical prote
895	5	20.8	595	2	T17590	probable glutamine	968	5	20.8	684	2	D71683	phospholipase A2-1
896	5	20.8	597	1	S43743	probable dual spec	969	5	20.8	686	2	E71895	proteinase II (ptr
897	5	20.8	597	2	G84825	probable CCH-type	970	5	20.8	686	2	A71607	probable heavy-met
898	5	20.8	597	2	T51889	related to clathri	971	5	20.8	686	2	S62939	Mtn3/RAG1P-like p
899	5	20.8	597	2	T15324	hypothetical prote	972	5	20.8	688	2	H83070	conserved hypothet
900	5	20.8	602	2	F84432	probable C2H2-type	973	5	20.8	688	2	S61464	p83/100 protein -
901	5	20.8	603	2	B83022	transport protein	974	5	20.8	693	2	I40090	p93 protein - Lyme
902	5	20.8	604	2	T51936	probable 9-cis-epo	975	5	20.8	695	2	E75099	hypothetical prote
903	5	20.8	604	2	S05447	finger protein gla	976	5	20.8	698	2	JH0163	No-on-transient A
904	5	20.8	605	2	T07123	nine-cis-epoxycaro	977	5	20.8	699	1	QRHUUT	lutropin-choriogon
905	5	20.8	610	2	H71612	asparagine-tRNA li	978	5	20.8	699	2	T12163	NADH2 dehydrogenas

979	5	20.8	699	2	T12169	NADH2 dehydrogenas
980	5	20.8	699	2	T12170	NADH2 dehydrogenas
981	5	20.8	699	2	T12167	NADH2 dehydrogenas
982	5	20.8	699	2	T12172	NADH2 dehydrogenas
983	5	20.8	699	2	T12164	NADH2 dehydrogenas
984	5	20.8	699	2	T12173	NADH2 dehydrogenas
985	5	20.8	699	2	T12168	NADH2 dehydrogenas
986	5	20.8	699	2	S67773	hypothetical prote
987	5	20.8	700	2	I77463	lutropinizing hormo
988	5	20.8	700	2	A42395	lutropin receptor
989	5	20.8	700	2	A49744	probable serine/th
990	5	20.8	700	2	T10566	No-on-transient A
991	5	20.8	700	2	JH0162	Na+/H+ antiporter
992	5	20.8	701	2	F70155	hypothetical prote
993	5	20.8	702	2	T34313	probable protein k
994	5	20.8	704	2	T38117	NADH2 dehydrogenas
995	5	20.8	707	2	T12759	NADH2 dehydrogenas
996	5	20.8	707	2	T12658	NADH2 dehydrogenas
997	5	20.8	707	2	T12664	NADH2 dehydrogenas
998	5	20.8	707	2	T12665	NADH2 dehydrogenas
999	5	20.8	707	2	T12668	NADH2 dehydrogenas
1000	5	20.8	707	2	T12671	NADH2 dehydrogenas

ALIGNMENTS

RESULT 1  
A40402  
CD9 antigen [validated] - human  
N:Alternate names: motility-related protein-1  
C:Species: Homo sapiens (man)  
C:Date: 06-Dec-1991 #sequence\_revision 07-Jul-1995 #text\_change 09-Jul-2004  
C:Accession: A46123; A40402; JH0555; A39029; S10564  
R:Rubinstein, E.; Benoit, P.; Billard, M.; Plaisance, S.; Prenant, M.; Uzan, G.; Bouchei  
Genomics 16, 132-138, 1993  
A:Title: Organization of the human CD9 gene.  
A:Reference number: A46123; MUID:93252369; PMID:8486348  
A:Accession: A46123  
A:Molecule type: DNA  
A:Residues: 1-228 <RUB>  
A:Cross-references: UNIPROT:P21926; UNIPARC:UPI000003B45A; GB:S60489; NID:g300112; PIDN:  
A:Experimental source: leukocyte  
A:Note: sequence extracted from NCBI backbone (NCBIN:131318, NCBIN:131326, NCBIN:131328,  
R:Rianza, F.; Wolf, D.; Fox, C.F.; Kieffer, N.; Seyer, J.M.; Fried, V.A.; Coughlin, S.R.;  
J. Biol. Chem. 266, 10638-10645, 1991  
A:Title: CDNA cloning and expression of platelet p24/CD9. Evidence for a new family of m  
A:Reference number: A40402; MUID:91244846; PMID:2037603  
A:Accession: A40402  
A>Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-228 <LAN>  
A:Cross-references: UNIPARC:UPI000003B45A; GB:L34068; GB:M61880; NID:g508495; PIDN:AAA59  
A:Note: parts of this sequence, including the amino end of the mature protein, were conf  
R:Miyaake, M.; Koyama, M.; Seno, M.; Ikeyama, S.  
J. Exp. Med. 174, 1347-1354, 1991  
A:Title: Identification of the motility-related protein (MRP-1), recognized by monoclonal  
A:Reference number: JH0555; MUID:92078843; PMID:1720807  
A:Accession: JH0555  
A:Molecule type: mRNA  
A:Residues: 1-228 <MIY>  
A:Cross-references: UNIPARC:UPI000003B45A; GB:X60111; NID:g34768; PIDN:CAA42708.1; PID:9  
A:Experimental source: breast carcinoma  
A:Note: This protein has the epitope defined by cell motility-inhibiting monoclonal anti  
R:Bouchaix, C.; Benoit, P.; Frachet, P.; Billard, M.; Worthington, R.E.; Gagnon, J.; Uza  
J. Biol. Chem. 266, 117-122, 1991  
A:Title: Molecular cloning of the CD9 antigen. A new family of cell surface proteins.  
A:Reference number: A39029; MUID:91093112; PMID:1840589  
A:Accession: A39029  
A:Molecule type: mRNA  
A:Residues: 1-8,'S',10-66,'A',68-193,195-228 <BOU>  
A:Cross-references: UNIPARC:UPI000017414B; GB:M38690  
A:Note: parts of this sequence, including the amino end of the mature protein, were conf

R:Higashihara, M.; Takahata, K.; Yatomi, Y.; Nakahara, K.; Kurokawa, K.  
FEBS Lett. 264, 270-274, 1990  
A:Title: Purification and partial characterization of CD9 antigen of human platelets.  
A:Reference number: S10564; MUID:90292223; PMID:2358073  
A:Accession: S10564  
A:Molecule type: protein  
A:Residues: 2-8,'X',10-21 <HIG>  
A:Cross-references: UNIPARC:UPI000017414C  
C:Genetics:  
A:Gene: GDB:CD9; MIC3  
A:Cross-references: GDB:120582; OMIM:143030  
A:Map position: 12p13-12p13  
C:Superfamily: CD9 antigen  
C:Keywords: glycoprotein; transmembrane protein  
F:2-228/Product: CD9 antigen #status experimental <MAT>  
F:2-11/Domain: intracellular #status predicted <CY1>  
F:12-35/Domain: transmembrane #status predicted <TM1>  
F:36-55/Domain: extracellular #status predicted <EX1>  
F:56-82/Domain: transmembrane #status predicted <TM2>  
F:83-86/Domain: intracellular #status predicted <CY2>  
F:87-111/Domain: transmembrane #status predicted <TM3>  
F:112-194/Domain: extracellular #status predicted <EX2>  
F:195-221/Domain: transmembrane #status predicted <TM4>  
F:222-228/Domain: intracellular #status predicted <CY3>  
F:53/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 24; DB 1; Length 228;  
Best Local Similarity 100.0%; Pred. No. 2.3e-17;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSTKSIPEQETNNNSSFYT 24  
DB 35 LRFDSTKSIPEQETNNNSSFYT 58

RESULT 2  
A42929  
CD9 antigen - green monkey  
N:Alternate names: 27K diphtheria toxin receptor-associated protein DRAP27  
C:Species: Cercopithecus aethiops (green monkey, grivet)  
C:Date: 01-Oct-1992 #sequence\_revision 09-Aug-1996 #text\_change 09-Jul-2004  
C:Accession: A42929  
R:Miamura, T.; Iwamoto, R.; Umata, T.; Yomo, T.; Urabe, I.; Tsuneoka, M.; Mekada, E.  
J. Cell Biol. 118, 1389-1399, 1992  
A:Title: The 27-kD diphtheria toxin receptor-associated protein (DRAP27) from vero cells  
ceptors on toxin-sensitive cells.  
A:Reference number: A42929; MUID:92394967; PMID:1522113  
A:Accession: A42929  
A>Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-228 <MIT>  
A:Cross-references: UNIPROT:P30409; UNIPARC:UPI000016C3B8; GB:D10726; NID:g218565; PIDN:  
C:Superfamily: CD9 antigen  
C:Keywords: glycoprotein; transmembrane protein  
F:2-228/Product: CD9 antigen #status predicted <MAT>  
F:2-11/Domain: intracellular #status predicted <CY1>  
F:12-35/Domain: transmembrane #status predicted <TM1>  
F:36-55/Domain: extracellular #status predicted <EX1>  
F:56-82/Domain: transmembrane #status predicted <TM2>  
F:83-86/Domain: intracellular #status predicted <CY2>  
F:87-111/Domain: transmembrane #status predicted <TM3>  
F:112-194/Domain: extracellular #status predicted <EX2>  
F:195-221/Domain: transmembrane #status predicted <TM4>  
F:222-228/Domain: intracellular #status predicted <CY3>  
F:52.53/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 24; DB 1; Length 228;  
Best Local Similarity 100.0%; Pred. No. 2.3e-17;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSTKSIPEQETNNNSSFYT 24  
DB 35 LRFDSTKSIPEQETNNNSSFYT 58

```
RESULT 3
S39262
CD9 antigen - rat
N/Alternate names: platelet cell surface glycoprotein
C:Species: Rattus norvegicus (Norway rat)
C>Date: 06-Jan-1995 #sequence_revision 09-Aug-1996 #text_change 09-Jul-2004
C:Accession: I56562; S39262
R:Kaprielian, Z.; Cho, K.O.; Hadjiargyrou, M.; Patterson, P.H.
J. Neurosci. 15, 562-573, 1995
A:Title: CD9, a major platelet cell surface glycoprotein, is a ROCA antigen and is expressed in the rat platelet.
A:Reference number: I56562; MUID:95123481; PMID:7823164
A:Accession: I56562
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-226 <RES>
A:Cross-references: UNIPROT:P40241; UNIPARC:UPI00001708C6; EMBL:X76489; NID:9434314; PID:
C:Gene: CD9
C:Superfamily: CD9 antigen
C:Keywords: glycoprotein; transmembrane protein
F:2-11/Domain: intracellular #status predicted <CV1>
F:12-35/Domain: transmembrane #status predicted <TM1>
F:36-53/Domain: extracellular #status predicted <EX1>
F:54-80/Domain: transmembrane #status predicted <TM2>
F:81-84/Domain: intracellular #status predicted <CV2>
F:85-109/Domain: transmembrane #status predicted <TM3>
F:110-192/Domain: extracellular #status predicted <EX2>
F:193-219/Domain: transmembrane #status predicted <TM4>
F:220-226/Domain: intracellular #status predicted <CV3>
F:50/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 56.7%; Score 16; DB 1; Length 226;
Best Local Similarity 100.0%; Pred. No. 3.1e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSQTKSIFQEQTN 16
|||||
DB 35 LRFDSQTKSIFQEQTN 50

RESULT 4
JX0221
CD9 antigen - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 09-Oct-1992 #sequence_revision 09-Aug-1996 #text_change 09-Jul-2004
C:Accession: JX0221
R:Martin-Alonso, J.M.; Hernando, N.; Ghosh, S.; Coca-Prados, M.
J. Biochem. 112, 63-67, 1992
A:Title: Molecular cloning of the bovine CD9 antigen from ocular ciliary epithelial cell
A:Reference number: JX0221; MUID:93054422; PMID:1339429
A:Accession: JX0221
A:Molecule type: mRNA
A:Residues: 1-226 <MAR>
A:Cross-references: UNIPROT:P30932; UNIPARC:UPI0000167C21; GB:M81720; NID:9162820; PID:
A:Experimental source: ocular ciliary epithelial cell
C:Superfamily: CD9 antigen
C:Keywords: glycoprotein; transmembrane protein
F:2-226/Product: CD9 antigen #status predicted <MAT>
F:2-11/Domain: intracellular #status predicted <CV1>
F:12-35/Domain: transmembrane #status predicted <TM1>
F:36-53/Domain: extracellular #status predicted <EX1>
F:54-76/Domain: transmembrane #status predicted <TM2>
F:77-80/Domain: intracellular #status predicted <CV2>
F:81-109/Domain: transmembrane #status predicted <TM3>
F:110-192/Domain: extracellular #status predicted <EX2>
F:193-219/Domain: transmembrane #status predicted <TM4>
F:220-226/Domain: intracellular #status predicted <CV3>
F:50/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 58.3%; Score 14; DB 1; Length 226;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSQTKSIFQEQTN 16
|||||
DB 35 LRFDSQTKSIFQEQTN 50
```

```
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSQTKSIFQE 14
|||||
DB 35 LRFDSQTKSIFQE 48

RESULT 5
I49589
antigen - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I49589
R:Rubinstein, E.; Billard, M.; Plaisance, S.; Prenant, M.; Boucheix, C.
Thromb. Res. 71, 377-383, 1993
A:Title: Molecular cloning of the mouse equivalent of CD9 antigen.
A:Reference number: I49589; MUID:94054345; PMID:8236164
A:Accession: I49589
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-226 <RES>
A:Cross-references: UNIPROT:P40240; UNIPARC:UPI0000003E37; GB:L08115; NID:9388911; PID:
C:Superfamily: CD9 antigen

Query Match 58.3%; Score 14; DB 2; Length 226;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSQTKSIFQE 14
|||||
DB 35 LRFDSQTKSIFQE 48

RESULT 6
H84774
probable homeodomain transcription factor [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: H84774
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, L.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: H84420; MUID:20083487; PMID:10617197
A:Accession: H84774
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-680 <STO>
A:Cross-references: UNIPROT:Q9SJ56; UNIPARC:UPI000009E071; GB:AE002093; NID:94510375; P
C:Genetics:
A:Gene: At2g35940
A:Map position: 2

Query Match 33.3%; Score 8; DB 2; Length 680;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TNNNNSSP 22
|||||
DB 59 TNNNNSSP 66

RESULT 7
A96913
ABC-type sulfate transporter, ATPase component CAC0107 [imported] - Clostridium acetobu
C:Species: Clostridium acetobutylicum
C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 31-Dec-2004
C:Accession: A96913
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl.
```

A;Reference number: A96900; MUID:21359325; PMID:21359325  
A;Accession: A96913  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-279 <KUR>  
A;Cross-references: UNIPROT:Q97MT4; UNIPARC:UPI00000C9D67; GB:AE001437; PIDN:AAK78092.1;  
A;Experimental source: Clostridium acetobutylicum ATCC824  
C;Genetics:  
A;Gene: CAC0107

Query Match 29.2%; Score 7; DB 2; Length 279;  
Best Local Similarity 100.0%; Pred. No. 5.2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DSQTKSI 10  
|||  
Db 165 DSQTKSI 171

RESULT 8  
T18420  
hypothetical protein C0130c - malaria parasite (Plasmodium falciparum)  
C;Species: Plasmodium falciparum  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T18420  
R;Lawson, D.; Bowman, S.; Barrell, B.  
Submitted to the EMBL Data Library, July 1997  
A;Reference number: Z18934  
A;Accession: T18420  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-419 <LAW>  
A;Cross-references: UNIPROT:O77316; UNIPARC:UPI0000076B8E; EMBL:Z97348; NID:e1323671; PIDN:AAK78092.1;  
C;Genetics:  
A;Note: C0130c

Query Match 29.2%; Score 7; DB 2; Length 419;  
Best Local Similarity 100.0%; Pred. No. 7.5;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 NNNNSF 22  
|||  
Db 394 NNNNSF 400

RESULT 9  
S59405  
probable membrane protein YLR436c - Yeast (Saccharomyces cerevisiae)  
N;Alternate names: hypothetical protein L9753.7  
C;Species: Saccharomyces cerevisiae  
C;Date: 30-Nov-1995 #sequence\_revision 23-Feb-1996 #text\_change 09-Jul-2004  
C;Accession: S59405  
R;Du, Z.

submitted to the EMBL Data Library, February 1995  
A;Description: The sequence of S. cerevisiae cosmid 9753.  
A;Reference number: S59401  
A;Accession: S59405  
A;Molecule type: DNA  
A;Residues: 1-1274 <DUZ>  
A;Cross-references: UNIPROT:Q06673; UNIPARC:UPI0000052EAF; EMBL:U21094; NID:g665967; PIDN:AAK78092.1;  
A;Experimental source: strain S288C (AB972)  
C;Genetics:

A;Gene: SGD:ECM30  
A;Cross-references: SGD:S0004428; MIPS:YLR436c  
A;Map position: 12R  
C;Superfamily: Saccharomyces cerevisiae probable membrane protein YLR436c  
C;Keywords: transmembrane protein  
F;117-133/Domain: transmembrane #status predicted <TM1>  
F;242-258/Domain: transmembrane #status predicted <TM2>  
F;529-545/Domain: transmembrane #status predicted <TM3>  
F;710-726/Domain: transmembrane #status predicted <TM4>

Query Match 29.2%; Score 7; DB 2; Length 1274;

Best Local Similarity 100.0%; Pred. No. 20;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 ETNNNS 20  
|||  
Db 1134 ETNNNS 1140

RESULT 10  
A48180  
small acid-soluble spore protein 1 - Sporosarcina ureae  
C;Species: Sporosarcina ureae  
C;Date: 10-Mar-1994 #sequence\_revision 19-May-1994 #text\_change 09-Jul-2004  
C;Accession: A48180  
R;Magill, N.G.; Loshon, C.A.; Setlow, P.  
FEMS Microbiol. Lett. 72, 293-298, 1990  
A;Title: Small, acid-soluble, spore proteins and their genes from two species of Sporosarcina  
A;Reference number: A48180  
A;Accession: A48180  
A;Molecule type: DNA  
A;Residues: 1-69 <MAG>  
A;Cross-references: UNIPROT:P52968; UNIPARC:UPI000004AB1B; GB:X55158; NID:g47971; PIDN:AAK78092.1;  
C;Comment: Saturation of DNA with this alpha/beta-type small acid-soluble spore protein  
during the first minutes of germination, after an initial cleavage by the spore protein  
C;Superfamily: alpha/beta-type small acid-soluble spore protein  
C;Keywords: DNA binding; germination; sporulation; storage protein  
F;2-69/Product: small acid-soluble spore protein 1 #status predicted <MAT>  
F;27-28/Cleavage site: Glu-1le (spore-specific proteinase) #status predicted

Query Match 25.0%; Score 6; DB 1; Length 69;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TNNNS 20  
|||  
Db 2 TNNNS 7

RESULT 11  
B85911  
hypothetical protein Z3937 [imported] - Escherichia coli (strain O157:H7, substrain EDL57)  
C;Species: Escherichia coli  
C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
C;Accession: B85911  
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,  
Nature 409, 529-533, 2001  
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A;Reference number: A85480; MUID:21074935; PMID:11206551  
A;Accession: B85911  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-92 <STO>  
A;Cross-references: UNIPROT:Q8X978; UNIPARC:UPI00001658D6; GB:AE005174; NID:g12517070; F;27-28/Cleavage site: Glu-1le (spore-specific proteinase) #status predicted

Query Match 25.0%; Score 6; DB 2; Length 92;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DSQTKS 9  
|||  
Db 60 DSQTKS 65

RESULT 12  
S52508  
probable membrane protein YDL011c - yeast (Saccharomyces cerevisiae)  
N;Alternate names: hypothetical protein D2885  
C;Species: Saccharomyces cerevisiae  
C;Date: 08-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 09-Jul-2004

C;Accession: S52508; S67543  
R;Andre, B.; Viissers, S.; Urrestarazu, L.  
submitted to the EMBL Data Library, February 1995  
A;Description: The sequence of a 42 kb segment located on the left arm of chromosome IV  
A;Reference number: S52492  
A;Accession: S52508  
A;Molecule type: DNA  
A;Residues: 1-107 <AND>  
A;Cross-references: UNIPROT:Q12023; UNIPARC:UPI000006C1A5; EMBL:Z48432; NID:g683669; PID:11258796  
R;Urrestarazu, L.A.; Andre, B.; Viissers, S.  
submitted to the Protein Sequence Database, July 1996  
A;Reference number: S67535  
A;Accession: S67543  
A;Molecule type: DNA  
A;Residues: 1-107 <URR>  
A;Cross-references: UNIPARC:UPI000006C1A5; EMBL:Z74059; NID:g1430970; PID:g1430971; MIPS:11258796  
A;Experimental source: strain S288C  
C;Genetics:  
A;Cross-references: SGD:S0002169  
A;Map position: 4L  
C;Superfamily: Saccharomyces cerevisiae probable membrane protein YDL011c  
C;Keywords: transmembrane protein  
F;50-66/Domain: transmembrane #status predicted <TM1>  
F;86-102/Domain: transmembrane #status predicted <TM2>  
Query Match 25.0%; Score 6; DB 2; Length 107;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 15 TNNNS 20  
Db 80 TNNNS 85  
RESULT 13  
B91067  
hypothetical lipoprotein [imported] - Escherichia coli (strain O157:H7, substrain RMD 0  
C;Species: Escherichia coli  
C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004  
C;Accession: B91067  
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
gaawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene  
A;Reference number: A99629; MUID:21156231; PMID:11258796  
A;Accession: B91067  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-131 <HAY>  
A;Cross-references: UNIPROT:Q8X978; UNIPARC:UPI00000D085E; GB:BA000007; PIDN:BA836929.1;  
A;Experimental source: strain O157:H7, substrain RMD 0509952  
C;Genetics:  
A;Gene: EC83506  
Query Match 25.0%; Score 6; DB 2; Length 131;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 DSQTKS 9  
Db 99 DSQTKS 104  
RESULT 14  
T17640  
hypothetical protein a149L - Chlorella virus PBCV-1  
C;Species: Chlorella virus PBCV-1  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T17640  
R;Graves, M.V.; Van Etten, J.L.  
submitted to the EMBL Data Library, May 1999  
A;Reference number: Z18806

A;Accession: T17640  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-136 <GRA>  
A;Cross-references: UNIPROT:Q84469; UNIPARC:UPI00000F0AAC; EMBL:U42580; NID:g4028896; P  
A;Experimental source: specific host Chlorella strain NC64A  
C;Genetics:  
A;Note: a149L  
C;Superfamily: Chlorella virus PBCV-1 hypothetical protein A149L  
Query Match 25.0%; Score 6; DB 2; Length 136;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 RFDSQT 7  
Db 89 RFDSQT 94  
RESULT 15  
D95131  
hypothetical protein SP1135 [imported] - Streptococcus pneumoniae (strain TIGR4)  
C;Species: Streptococcus pneumoniae  
C;Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 09-Jul-2004  
C;Accession: D95131  
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Hel  
on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,  
nson, T.; Hickey, E.K.; Holt, I.E.  
Science 293, 498-506, 2001  
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison  
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.  
A;Reference number: A95000; MUID:21357209; PMID:11463916  
A;Accession: D95131  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-150 <KUR>  
A;Cross-references: UNIPROT:Q97QR5; UNIPARC:UPI000005170C; GB:AE005672; PIDN:AAK75245.1  
A;Experimental source: strain TIGR4  
C;Genetics:  
A;Gene: SP1135  
Query Match 25.0%; Score 6; DB 2; Length 150;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 SQTksi 10  
Db 37 SQTksi 42  
Search completed: January 20, 2006, 17:44:35  
Job time : 18.5385 secs

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OM protein - protein search, using sw model

Run on: January 20, 2006, 17:34:35 ; Search time 30.2308 Seconds  
(without alignments)  
560.114 Million cell updates/sec

Title: US-10-619-323-1\_COPY\_35\_58

Perfect score: 24  
Sequence: 1 LRPDSQTSIFQETNNNNSSPYT 24

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Uniprot\_05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	182	2	Q56CY1_HUMAN
2	24	100.0	227	1	CD9_CERAE
3	24	100.0	227	1	CD9_HUMAN
4	24	100.0	228	2	Q5J7W6_HUMAN
5	16	66.7	225	1	CD9_RAT
6	14	58.3	225	1	CD9_BOVIN
7	14	58.3	225	1	CD9_MOUSE
8	14	58.3	225	1	CD9_PIG
9	14	58.3	226	2	Q8MJ48_PIG
10	13	54.2	225	1	CD9_FELCA
11	8	33.3	228	2	Q8AV92_FETWA
12	8	33.3	228	2	Q6GQES_XENLA
13	8	33.3	607	2	Q56F04_9CAUD
14	8	33.3	607	2	Q6U9U5_9CAUD
15	8	33.3	607	2	Q76XLO_9CAUD
16	8	33.3	680	2	Q94KL4_ARATH
17	8	33.3	680	2	Q9SU56_ARATH
18	7	29.2	77	2	Q70905_9HIV1
19	7	29.2	88	2	Q69744_9HIV1
20	7	29.2	88	2	Q70907_9HIV1
21	7	29.2	89	2	Q70906_9HIV1
22	7	29.2	89	2	Q70908_9HIV1
23	7	29.2	91	2	Q70904_9HIV1
24	7	29.2	91	2	Q70910_9HIV1
25	7	29.2	92	2	Q70909_9HIV1
26	7	29.2	110	2	Q9BADI_FUCVE
27	7	29.2	131	2	Q7PX92_ANOGA
28	7	29.2	133	2	Q4YMU0_PLABE
29	7	29.2	137	2	Q8R7G8_THETN
30	7	29.2	166	2	Q5CDE4_CRYHO
31	7	29.2	224	2	Q9IBC9_CHICK

32	7	29.2	234	2	Q6TBF6_9ROSI	Q6tbf6 trigonia ni
33	7	29.2	271	2	Q4NR07_BACCE	Q4nr07 bacillus ce
34	7	29.2	271	2	Q72V61_BACCI	Q72v61 bacillus ce
35	7	29.2	271	2	Q6HBN7_BACHK	Q6hbn7 bacillus th
36	7	29.2	271	2	Q631V1_BACCC	Q631v1 bacillus ce
37	7	29.2	271	2	Q81XHS_BACAN	Q81xhs bacillus an
38	7	29.2	272	2	Q6VS45_9APIC	Q6vs45 plasmodium
39	7	29.2	279	2	Q97MT4_CLOAB	Q97mt4 clostridium
40	7	29.2	309	2	Q9P4W5_KLULA	Q9p4w5 kluyveromyc
41	7	29.2	320	2	Q66078_9LACT	Q66078 lactococcus
42	7	29.2	331	2	Q78EL4_NEUCR	Q78el4 neurospora
43	7	29.2	333	2	Q8T986_DROME	Q8t986 drosophila
44	7	29.2	336	2	Q5XWK5_SOLTU	Q5xwk5 solanum tub
45	7	29.2	363	2	Q93ZD2_ARATH	Q93zd2 arabidopsis
46	7	29.2	363	2	Q9CSA2_ARATH	Q9csa2 arabidopsis
47	7	29.2	402	2	Q54JN3_DICDI	Q54jn3 dictyosteli
48	7	29.2	419	2	Q77316_PLAF7	Q77316 plasmodium
49	7	29.2	469	2	Q5RHM6_BRARE	Q5rhm6 brachydanio
50	7	29.2	479	2	Q54CR0_DICDI	Q54cr0 dictyosteli
51	7	29.2	487	2	Q5GRL4_WOLTR	Q5grl4 wolbachia s
52	7	29.2	524	2	Q54N32_DICDI	Q54n32 dictyosteli
53	7	29.2	539	2	Q4RW38_TETNG	Q4rw38 tetraodon n
54	7	29.2	544	2	Q70147_9HIV1	Q70147 human immun
55	7	29.2	556	2	Q59LE2_CANAL	Q59le2 candida alb
56	7	29.2	606	2	Q7Y5D4_BPR69	Q7y5d4 bacterioph
57	7	29.2	608	2	Q4YJS0_PLABE	Q4yjs0 plasmodium
58	7	29.2	647	2	Q869Q4_DICDI	Q869q4 dictyosteli
59	7	29.2	674	2	Q55513_DICDI	Q55513 dictyosteli
60	7	29.2	688	2	Q55FD6_DICDI	Q55fd6 dictyosteli
61	7	29.2	779	2	Q5Y775_CRYPV	Q5y775 cryptospori
62	7	29.2	779	2	Q5CL11_CRYHO	Q5cl11 cryptospori
63	7	29.2	824	2	Q54JC5_DICDI	Q54jc5 dictyosteli
64	7	29.2	846	2	Q54WR0_DICDI	Q54wr0 dictyosteli
65	7	29.2	851	2	Q70145_9HIV1	Q70145 human immun
66	7	29.2	858	2	Q6BC37_9HIV1	Q6bc37 human immun
67	7	29.2	864	2	Q9YP39_9HIV1	Q9yp39 human immun
68	7	29.2	879	2	Q54P37_DICDI	Q54p37 dictyosteli
69	7	29.2	981	2	Q54SW0_DICDI	Q54sw0 dictyosteli
70	7	29.2	1016	2	Q54DW8_DICDI	Q54dw8 dictyosteli
71	7	29.2	1043	2	Q8SSW7_DICDI	Q8ssw7 dictyosteli
72	7	29.2	1056	2	Q6YHU9_SCHNA	Q6yhu9 schistosoma
73	7	29.2	1264	2	Q7S9R1_NEUCR	Q7s9r1 neurospora
74	7	29.2	1274	1	ECM30_YEAST	Q06673 saccharomyc
75	7	29.2	1304	2	Q9VBE5_DROME	Q9vbe5 drosophila
76	7	29.2	1333	2	Q54XA8_DICDI	Q54xa8 dictyosteli
77	7	29.2	1480	2	Q54VW9_DICDI	Q54vw9 dictyosteli
78	7	29.2	1550	2	Q54GSI_DICDI	Q54gsi dictyosteli
79	7	29.2	1861	2	Q55F12_DICDI	Q55f12 dictyosteli
80	7	29.2	1964	2	Q81IX6_PLAF7	Q81ix6 plasmodium
81	7	29.2	1992	2	Q55BR0_DICDI	Q55br0 dictyosteli
82	7	29.2	2825	2	Q81D16_PLAF7	Q81d16 plasmodium
83	7	29.2	3078	2	Q81KH4_PLAF7	Q81kh4 plasmodium
84	7	29.2	5222	2	Q54L33_DICDI	Q54l33 dictyosteli
85	6	25.0	44	2	Q53IG5_PLAF7	Q53ig5 plasmodium
86	6	25.0	46	2	Q53IG7_PLAF7	Q53ig7 plasmodium
87	6	25.0	48	2	Q54VH6_DICDI	Q54vh6 dictyosteli
88	6	25.0	49	2	Q53IG9_PLAF7	Q53ig9 plasmodium
89	6	25.0	52	2	Q4XPCS_PLACH	Q4xpcs plasmodium
90	6	25.0	52	2	Q53IH0_PLAF7	Q53ih0 plasmodium
91	6	25.0	53	2	Q53IG6_PLAF7	Q53ig6 plasmodium
92	6	25.0	55	2	Q53IG6_PLAF7	Q53ig6 plasmodium
93	6	25.0	67	2	Q4L388_STAHI	Q4l388 staphylococ
94	6	25.0	67	2	Q7YVP7_9TRYP	Q7yvp7 trypanosoma
95	6	25.0	69	1	SASI_SFOUR	P52968 sporosarcin
96	6	25.0	78	2	Q61M90_CAEBR	Q61m90 caenorhabdi
97	6	25.0	78	2	Q8TIK3_METAC	Q8tik3 methanosarc
98	6	25.0	82	2	Q55F08_DICDI	Q55f08 dictyosteli
99	6	25.0	90	2	Q81FL5_PLAF7	Q81fl5 plasmodium
100	6	25.0	91	2	Q61T84_ONCPA	Q61t84 oncopeltus
101	6	25.0	91	2	Q8HCF8_EURSO	Q8hcf8 eurosta sol
102	6	25.0	92	2	Q8X978_ECO57	Q8x978 escherichia
103	6	25.0	96	2	Q5YK64_MYCGE	Q5yk64 mycoplasma
104	6	25.0	97	2	Q8TF84_YEAST	Q8tf84 saccharomyc

105	6	25.0	98	2	Q4YP43_PLABE	Q4YP43_plasmodium	178	6	25.0	176	2	Q7XXZ9_MIMGU	Q7xxz9 mimulus gut
106	6	25.0	102	2	Q5AFP2_DICDI	Q54ff2 dictyosteli	179	6	25.0	176	2	Q7XY01_MIMGU	Q7xy01 mimulus gut
107	6	25.0	104	2	Q5AD14_CANAL	Q5ad14 candida alb	180	6	25.0	177	2	Q764J4_PLASMODIUM	Q764j4 plasmodium
108	6	25.0	107	2	Q12023_YEAST	Q12023 saccharomyc	181	6	25.0	177	2	Q4YTW4_PLABE	Q4ytw4 plasmodium
109	6	25.0	109	2	Q24542_DROME	Q24542 drosophila	182	6	25.0	177	2	Q7X611_MIMNA	Q7x611 mimulus nas
110	6	25.0	110	2	Q57VW7_TRYP	Q57vw7 trypanosoma	183	6	25.0	177	2	Q7X7K4_MIMNA	Q7x7k4 mimulus nas
111	6	25.0	113	2	Q54R21_DICDI	Q54r21 dictyosteli	184	6	25.0	177	2	Q7XXV6_MIMNA	Q7xxv6 mimulus nas
112	6	25.0	115	2	Q5DDF3_SCHJA	Q5ddf3 schistosoma	185	6	25.0	177	2	Q7XXM4_MIMGU	Q7xxm4 mimulus gut
113	6	25.0	118	2	Q9U9Z1_LINUN	Q9u9z1 lingua ung	186	6	25.0	177	2	Q7X6X6_MIMPL	Q7x6x6 mimulus pia
114	6	25.0	120	2	Q8EN11_OCEIH	Q8en11 oceanobacil	187	6	25.0	178	2	Q7XXU9_MIMNA	Q7xxu9 mimulus nas
115	6	25.0	122	2	Q54NI2_DICDI	Q54ni2 dictyosteli	188	6	25.0	178	2	Q7XXV1_MIMNA	Q7xxv1 mimulus nas
116	6	25.0	124	2	Q36886_SCHJA	Q36886 schistosoma	189	6	25.0	178	2	Q7XXW0_MIMGU	Q7xxw0 mimulus gut
117	6	25.0	126	2	Q7YX21_CABEL	Q7yx21 caenorhabdi	190	6	25.0	178	2	Q7XXZ6_MIMGU	Q7xxz6 mimulus gut
118	6	25.0	126	2	Q6Y9V5_9SOLA	Q6y9v5 schizanthus	191	6	25.0	179	2	Q9XZ40_PLAFA	Q9xz40 plasmodium
119	6	25.0	127	2	Q5R9V4_9SOLA	Q5r9v4 schizanthus	192	6	25.0	179	2	Q7XXU6_MIMNA	Q7xxu6 mimulus nas
120	6	25.0	128	2	Q54RF1_DICDI	Q54rf1 dictyosteli	193	6	25.0	179	2	Q7XXV7_MIMGU	Q7xxv7 mimulus gut
121	6	25.0	129	2	Q69QZ5_ORYSA	Q69qz5 oryza sativ	194	6	25.0	180	2	Q25945_PLAFA	Q25945 plasmodium
122	6	25.0	131	2	Q65XW5_ORYSA	Q65xw5 oryza sativ	195	6	25.0	180	2	Q9TXC4_PLAFA	Q9txc4 plasmodium
123	6	25.0	131	2	Q7ABG0_ECOS7	Q7abg0 escherichia	196	6	25.0	180	2	Q7XXU8_MIMNA	Q7xxu8 mimulus nas
124	6	25.0	133	1	RBFA_CHLMU	Q9pkul chlamydia m	197	6	25.0	180	2	Q7XXV9_MIMGU	Q7xxv9 mimulus gut
125	6	25.0	134	2	Q88F39_9TREM	Q88f39 schistosoma	198	6	25.0	180	2	Q7XXX9_MIMGU	Q7xxx9 mimulus gut
126	6	25.0	136	2	Q84469_CHVP1	Q84469 paramecium	199	6	25.0	180	2	Q7XXZ0_MIMGU	Q7xxz0 mimulus gut
127	6	25.0	137	2	Q6U5F8_PLAFA	Q6u5f8 plasmodium	200	6	25.0	181	2	Q7X6G8_MIMGU	Q7x6g8 mimulus gut
128	6	25.0	137	2	Q55DG1_DICDI	Q55dg1 dictyosteli	201	6	25.0	181	2	Q7XXV4_MIMNA	Q7xxv4 mimulus nas
129	6	25.0	137	2	Q4YX33_PLABE	Q4yx33 plasmodium	202	6	25.0	181	2	Q7XXW9_MIMGU	Q7xxw9 mimulus gut
130	6	25.0	138	2	Q5C585_SCHJA	Q5c585 schistosoma	203	6	25.0	182	2	Q81RT8_DROME	Q81rt8 drosophila
131	6	25.0	138	2	Q95T66_DROME	Q95t66 drosophila	204	6	25.0	182	2	Q41TY8_PLAFA	Q41ty8 plasmodium
132	6	25.0	138	2	Q98K76_RHILO	Q98k76 rhizobium l	205	6	25.0	182	2	Q7X6N7_MIMNA	Q7x6n7 mimulus nas
133	6	25.0	139	2	Q6WHX9_BPKV4	Q6whx9 bacterioph	206	6	25.0	182	2	Q7X706_MIMGU	Q7x706 mimulus gut
134	6	25.0	141	2	Q94HJ6_ORYSA	Q94hj6 oryza sativ	207	6	25.0	182	2	Q7XXU4_MIMLA	Q7xxu4 mimulus lac
135	6	25.0	142	2	Q5C2K3_SCHJA	Q5c2k3 schistosoma	208	6	25.0	182	2	Q7XXU5_MIMNA	Q7xxu5 mimulus nas
136	6	25.0	143	2	Q59X66_CANAL	Q59x66 candida alb	209	6	25.0	182	2	Q7XXX0_MIMGU	Q7xxx0 mimulus gut
137	6	25.0	144	2	Q59XB4_CANAL	Q59xb4 candida alb	210	6	25.0	183	2	Q6U9A7_PLAFA	Q6ua97 plasmodium
138	6	25.0	145	2	Q25711_PLAFA	Q25711 plasmodium	211	6	25.0	183	2	Q86QX1_PLAFA	Q86qx1 plasmodium
139	6	25.0	146	2	Q7T7U6_RHOBA	Q7t7u6 rhodopirell	212	6	25.0	183	2	Q9U0B5_PLAFA	Q9u0b5 plasmodium
140	6	25.0	147	2	Q15805_PLAFA	Q15805 plasmodium	213	6	25.0	183	2	Q9U0B6_PLAFA	Q9u0b6 plasmodium
141	6	25.0	147	2	Q6U5F7_PLAFA	Q6u5f7 plasmodium	214	6	25.0	183	2	Q7X7H2_MIMGU	Q7x7h2 mimulus gut
142	6	25.0	150	2	Q97QR5_STRPN	Q97qr5 streptococ	215	6	25.0	184	2	Q5DEB3_SCHJA	Q5ded3 schistosoma
143	6	25.0	151	2	Q6U9A9_PLAFA	Q6ua99 plasmodium	216	6	25.0	184	2	Q86QX2_PLAFA	Q86qx2 plasmodium
144	6	25.0	152	2	Q25697_PLAFA	Q25697 plasmodium	217	6	25.0	184	2	Q9TY34_PLAFA	Q9ty34 plasmodium
145	6	25.0	155	2	Q6U5F5_PLAFA	Q6u5f5 plasmodium	218	6	25.0	184	2	Q9U0B8_PLAFA	Q9u0b8 plasmodium
146	6	25.0	155	2	Q6U9A8_PLAFA	Q6ua98 plasmodium	219	6	25.0	184	2	Q9U0B9_PLAFA	Q9u0b9 plasmodium
147	6	25.0	157	2	Q25713_PLAFA	Q25713 plasmodium	220	6	25.0	184	2	Q7XXW1_MIMGU	Q7xxw1 mimulus gut
148	6	25.0	159	2	Q6U5F3_PLAFA	Q6u5f3 plasmodium	221	6	25.0	185	2	Q6U9A9_PLAFA	Q6ua99 plasmodium
149	6	25.0	161	2	Q59I16_CANAL	Q59i16 candida alb	222	6	25.0	185	2	Q4G402_MACMU	Q4g402 macaca mula
150	6	25.0	161	2	Q6U9A0_PLAFA	Q6uaa0 plasmodium	223	6	25.0	185	2	Q35069_MOUSE	Q35069 mus musculus
151	6	25.0	162	2	Q25702_PLAFA	Q25702 plasmodium	224	6	25.0	185	2	Q80RK5_PRRSV	Q80rk5 porcine rep
152	6	25.0	162	2	Q25714_PLAFA	Q25714 plasmodium	225	6	25.0	186	2	Q764J5_PLAFA	Q764j5 plasmodium
153	6	25.0	162	2	Q6QV33_9RETR	Q6qv33 equine infe	226	6	25.0	186	2	Q86QX3_PLAFA	Q86qx3 plasmodium
154	6	25.0	163	2	Q9LY93_ARATH	Q9ly93 arabidopsis	227	6	25.0	186	2	Q55EQ1_DICDI	Q55eq1 dictyosteli
155	6	25.0	163	2	Q7XXW5_MIMGU	Q7xxw5 mimulus gut	228	6	25.0	186	2	Q7XXU2_MIMNU	Q7xxu2 mimulus nud
156	6	25.0	166	2	Q25698_PLAFA	Q25698 plasmodium	229	6	25.0	187	2	Q6U5G0_PLAFA	Q6u5g0 plasmodium
157	6	25.0	166	2	Q86QX0_PLAFA	Q86qx0 plasmodium	230	6	25.0	187	2	Q9XZ39_PLAFA	Q9xz39 plasmodium
158	6	25.0	167	2	Q27911_POIMI	Q27911 polyandroca	231	6	25.0	188	2	Q6XJ05_DROYA	Q6xj05 drosophila
159	6	25.0	168	2	Q6U5E9_PLAFA	Q6u5e9 plasmodium	232	6	25.0	188	2	Q7XXW7_MIMGU	Q7xxw7 mimulus gut
160	6	25.0	169	2	Q5C7B4_SCHJA	Q5c7b4 schistosoma	233	6	25.0	188	2	Q7XXV3_MIMGU	Q7xxv3 mimulus gut
161	6	25.0	169	2	Q5HRZ4_STAEP	Q5hrz4 staphylococ	234	6	25.0	189	2	Q7X781_MIMNA	Q7x781 mimulus nas
162	6	25.0	169	2	Q8CQP5_STAEP	Q8cp5 staphylococ	235	6	25.0	189	2	Q7X782_MIMGU	Q7x782 mimulus gut
163	6	25.0	170	2	Q4L341_STAEP	Q4l341 staphylococ	236	6	25.0	189	2	Q7X7R0_MIMNA	Q7x7r0 mimulus nas
164	6	25.0	171	2	Q4XDB7_PLACH	Q4xdb7 plasmodium	237	6	25.0	189	2	Q7XXW3_MIMGU	Q7xxw3 mimulus gut
165	6	25.0	171	2	Q7XXU3_MIMLA	Q7xxu3 mimulus lac	238	6	25.0	189	2	Q7XXX1_MIMGU	Q7xxx1 mimulus gut
166	6	25.0	171	2	Q6UDP0_9HIV1	Q6udp0 human immun	239	6	25.0	189	2	Q7XXX3_MIMGU	Q7xxx3 mimulus gut
167	6	25.0	172	2	Q7XXZ7_MIMGU	Q7xxz7 mimulus gut	240	6	25.0	189	2	Q7XXY2_MIMGU	Q7xxy2 mimulus gut
168	6	25.0	173	2	Q9BJP5_PLAFA	Q9bjp5 plasmodium	241	6	25.0	189	2	Q7XXY4_MIMGU	Q7xxy4 mimulus gut
169	6	25.0	173	2	Q81GK9_DROME	Q81gk9 drosophila	242	6	25.0	189	2	Q7XXY7_MIMGU	Q7xxy7 mimulus gut
170	6	25.0	173	2	Q7XXX6_MIMGU	Q7xxx6 mimulus gut	243	6	25.0	189	2	Q7XXZ2_MIMGU	Q7xxz2 mimulus gut
171	6	25.0	174	2	Q9U0C4_PLAFA	Q9u0c4 plasmodium	244	6	25.0	190	2	Q7X827_MIMGU	Q7x827 mimulus gut
172	6	25.0	175	2	Q7XXV2_MIMNA	Q7xxv2 mimulus nas	245	6	25.0	190	2	Q7X8S8_MIMGU	Q7x8s8 mimulus gut
173	6	25.0	175	2	Q7XXV5_MIMNA	Q7xxv5 mimulus nas	246	6	25.0	190	2	Q7XXW8_MIMGU	Q7xxw8 mimulus gut
174	6	25.0	176	2	Q6U5F0_PLAFA	Q6u5f0 plasmodium	247	6	25.0	190	2	Q7XXX4_MIMGU	Q7xxx4 mimulus gut
175	6	25.0	176	2	Q7X6J7_MIMNA	Q7x6j7 mimulus nas	248	6	25.0	190	2	Q7XXX7_MIMGU	Q7xxx7 mimulus gut
176	6	25.0	176	2	Q7XXV0_MIMNA	Q7xxv0 mimulus nas	249	6	25.0	190	2	Q7XXX8_MIMGU	Q7xxx8 mimulus gut
177	6	25.0	176	2	Q7XXV3_MIMNA	Q7xxv3 mimulus nas	250	6	25.0	190	2	Q7XXY5_MIMGU	Q7xxy5 mimulus gut

251	6	25.0	190	2	Q7XXZ5_MIMGU	Q7xxz5 mimulus gut	324	6	25.0	223	2	Q8IT84_PLAFA	Q8it84 plasmodium
252	6	25.0	190	2	Q7XY00_MIMGU	Q7xy00 mimulus gut	325	6	25.0	223	2	Q5XZ56_PLAFA	Q5xz56 plasmodium
253	6	25.0	191	2	Q6QLY1_PLAFA	Q6qly1 plasmodium	326	6	25.0	225	2	Q5CXM1_CRYPV	Q5cxm1 cryptospori
254	6	25.0	191	2	Q9UOC1_PLAFA	Q9uoc1 plasmodium	327	6	25.0	226	2	Q9UOB2_PLAFA	Q9uob2 plasmodium
255	6	25.0	191	2	Q7X664_MIMGU	Q7x664 mimulus gut	328	6	25.0	227	2	Q4X4K4_PLACH	Q4x4k4 plasmodium
256	6	25.0	191	2	Q7X7A2_MIMGU	Q7x7a2 mimulus gut	329	6	25.0	228	2	Q24166_DROME	Q24166 drosophila
257	6	25.0	191	2	Q7XXW6_MIMGU	Q7xxw6 mimulus gut	330	6	25.0	229	2	Q9VD73_DROME	Q9vd73 drosophila
258	6	25.0	191	2	Q7XXX2_MIMGU	Q7xxx2 mimulus gut	331	6	25.0	229	1	LB11_ARATH	Q9sk08 arabidopsis
259	6	25.0	191	2	Q7XXX5_MIMGU	Q7xxx5 mimulus gut	332	6	25.0	230	2	Q95N16_TRICA	Q95n16 tribolium c
260	6	25.0	191	2	Q7XXY1_MIMGU	Q7xxy1 mimulus gut	333	6	25.0	230	2	Q4YAS3_PLABE	Q4yas3 plasmodium
261	6	25.0	191	2	Q7XXY6_MIMGU	Q7xxy6 mimulus gut	334	6	25.0	231	2	Q8LLY1_ORYSA	Q8lly1 oryza sativ
262	6	25.0	192	2	Q4Y612_PLACH	Q4y612 plasmodium	335	6	25.0	233	2	Q9UOC2_PLAFA	Q9uoc2 plasmodium
263	6	25.0	192	2	Q7X7C6_MIMNA	Q7x7c6 mimulus nas	336	6	25.0	233	2	Q6E769_SAPPE	Q6e769 saprolegnia
264	6	25.0	192	2	Q7XXU7_MIMNA	Q7xxu7 mimulus nas	337	6	25.0	234	2	Q25769_PLAFA	Q25769 plasmodium
265	6	25.0	193	2	Q5ALZ1_CANAL	Q5alz1 candida alb	338	6	25.0	234	2	Q8XI71_CLOPE	Q8xi71 clostridium
266	6	25.0	193	2	Q6USG1_PLAFA	Q6usg1 plasmodium	339	6	25.0	235	2	Q81GN6_DROME	Q81gn6 drosophila
267	6	25.0	193	2	Q4HFN2_CAMCO	Q4hfn2 campylobact	340	6	25.0	237	2	Q6G0E7_BARQU	Q6g0e7 bartonella
268	6	25.0	194	2	Q764J6_PLAFA	Q764j6 plasmodium	341	6	25.0	238	2	Q5AAD1_CANAL	Q5aad1 candida alb
269	6	25.0	194	2	Q9FIP6_ARATH	Q9fip6 arabidopsis	342	6	25.0	238	2	Q54T68_DICDI	Q54t68 dictyosteli
270	6	25.0	194	2	Q82W50_NITEU	Q82w50 nitrosomona	343	6	25.0	238	2	Q8T174_DICDI	Q8t174 dictyosteli
271	6	25.0	194	2	Q8YGC9_BRUME	Q8ygc9 brucella me	344	6	25.0	240	2	Q6B923_GRATL	Q6b923 gracilaria
272	6	25.0	195	2	Q25694_PLAFA	Q25694 plasmodium	345	6	25.0	240	2	Q94F99_MINNA	Q94f99 mimulus nas
273	6	25.0	195	2	Q25715_PLAFA	Q25715 plasmodium	346	6	25.0	241	2	Q4TM29_PLABE	Q4ym29 plasmodium
274	6	25.0	195	2	Q25948_PLAFA	Q25948 plasmodium	347	6	25.0	241	2	Q9SV16_ARATH	Q9sv16 arabidopsis
275	6	25.0	196	2	Q25947_PLAFA	Q25947 plasmodium	348	6	25.0	242	2	Q54P36_DICDI	Q54p36 dictyosteli
276	6	25.0	196	2	Q25951_PLAFA	Q25951 plasmodium	349	6	25.0	242	2	Q8GMF3_ARATH	Q8gmf3 arabidopsis
277	6	25.0	196	2	Q764J7_PLAFA	Q764j7 plasmodium	350	6	25.0	243	2	Q4X4S5_PLACH	Q4x4s5 plasmodium
278	6	25.0	196	2	Q9GQY7_PLAFA	Q9gqy7 plasmodium	351	6	25.0	245	2	Q54I25_DICDI	Q54i25 dictyosteli
279	6	25.0	196	2	Q9UOB7_PLAFA	Q9uob7 plasmodium	352	6	25.0	245	2	Q7ZXI4_XENLA	Q7zxy4 xenopus lae
280	6	25.0	196	2	Q54XLS_DICDI	Q54xls dictyosteli	353	6	25.0	246	1	YOR4_ANATH	Q4408 anaerocellu
281	6	25.0	196	2	Q57E21_BRUAB	Q57e21 brucella ab	354	6	25.0	247	2	Q95Z54_PLAFA	Q95z54 plasmodium
282	6	25.0	196	2	Q5GT34_WOLTR	Q5gt34 wolbachia s	355	6	25.0	249	2	Q4PGL0_USTMA	Q4pgl0 ustilago ma
283	6	25.0	196	2	Q8G1J3_BRUSU	Q8g1j3 brucella su	356	6	25.0	249	2	Q54YG3_DICDI	Q54yg3 dictyosteli
284	6	25.0	197	2	Q6U5F6_PLAFA	Q6u5f6 plasmodium	357	6	25.0	249	2	Q9VPW8_DROME	Q9vpw8 drosophila
285	6	25.0	200	2	Q513H2_PRESV	Q513h2 porcine rep	358	6	25.0	249	2	Q90S11_9HIV1	Q90s11 human immun
286	6	25.0	201	2	Q9YNP3_9HIV1	Q9ynp3 human immun	359	6	25.0	251	2	Q51351_9RETR	Q51351 equine infe
287	6	25.0	202	2	Q25952_PLAFA	Q25952 plasmodium	360	6	25.0	251	2	Q51359_9RETR	Q51359 equine infe
288	6	25.0	202	2	Q7SKT8_9HIV1	Q7skt8 human immun	361	6	25.0	252	2	Q9FY93_ARATH	Q9fy93 arabidopsis
289	6	25.0	203	2	Q15806_PLAFA	Q15806 plasmodium	362	6	25.0	252	2	Q4SGB0_TETNG	Q4sgb0 tetraodon n
290	6	25.0	203	2	Q9UOC0_PLAFA	Q9uoc0 plasmodium	363	6	25.0	253	2	Q51362_9RETR	Q51362 equine infe
291	6	25.0	203	2	Q736D0_BACCL	Q736d0 bacillus ce	364	6	25.0	254	2	Q531P8_GIBFU	Q531p8 gibberella
292	6	25.0	204	2	Q9UOB4_PLAFA	Q9uob4 plasmodium	365	6	25.0	254	2	Q51372_9RETR	Q51372 equine infe
293	6	25.0	204	2	Q54MC8_DICDI	Q54mc8 dictyosteli	366	6	25.0	255	2	Q6MTG2_MYCMA	Q6mtg2 mycoplasma
294	6	25.0	205	2	Q25944_PLAFA	Q25944 plasmodium	367	6	25.0	256	2	Q6R795_9HERP	Q6r795 ostreid her
295	6	25.0	205	2	Q25946_PLAFA	Q25946 plasmodium	368	6	25.0	257	2	Q6FJH4_CANGA	Q6fjha candida gla
296	6	25.0	205	2	Q9TXC5_PLAFA	Q9txc5 plasmodium	369	6	25.0	257	2	Q54H93_DICDI	Q54h93 dictyosteli
297	6	25.0	205	2	Q54NI7_DICDI	Q54ni7 dictyosteli	370	6	25.0	257	2	Q54HH8_DICDI	Q54hn8 dictyosteli
298	6	25.0	206	2	Q9UOC3_PLAFA	Q9uoc3 plasmodium	371	6	25.0	257	2	Q8SWV1_DROME	Q8swv1 drosophila
299	6	25.0	206	2	Q86L16_DICDI	Q86l16 dictyosteli	372	6	25.0	257	2	Q9A7B3_CAUCR	Q9a7b3 caulobacter
300	6	25.0	206	2	Q95Z57_PLAFA	Q95z57 plasmodium	373	6	25.0	257	2	Q6W987_9PERC	Q6w987 spheeroides
301	6	25.0	207	2	Q25701_PLAFA	Q25701 plasmodium	374	6	25.0	258	2	Q68LB3_9DIPT	Q68lb3 drosophila
302	6	25.0	208	2	Q25949_PLAFA	Q25949 plasmodium	375	6	25.0	258	2	Q512Z4_9RETR	Q512z4 equine infe
303	6	25.0	208	2	Q9UOA0_PLAFA	Q9uoa0 plasmodium	376	6	25.0	258	2	Q512Z5_9RETR	Q512z5 equine infe
304	6	25.0	209	2	Q86JH2_DICDI	Q86jh2 dictyosteli	377	6	25.0	258	2	Q512Z6_9RETR	Q512z6 equine infe
305	6	25.0	210	2	Q707X1_CANGA	Q707x1 candida gla	378	6	25.0	258	2	Q512Z7_9RETR	Q512z7 equine infe
306	6	25.0	212	2	Q95Z55_PLAFA	Q95z55 plasmodium	379	6	25.0	258	2	Q51304_9RETR	Q51304 equine infe
307	6	25.0	213	1	YFEL_ECOLI	P76543 escherichia	380	6	25.0	258	2	Q51310_9RETR	Q51310 equine infe
308	6	25.0	213	2	Q5ABQ6_CANAL	Q5abq6 candida alb	381	6	25.0	258	2	Q51315_9RETR	Q51315 equine infe
309	6	25.0	213	2	Q4XB89_PLACH	Q4xb89 plasmodium	382	6	25.0	258	2	Q51317_9RETR	Q51317 equine infe
310	6	25.0	214	2	Q5TNZ3_ANOGA	Q5tnz3 anopheles g	383	6	25.0	258	2	Q51320_9RETR	Q51320 equine infe
311	6	25.0	214	2	Q9V9Y2_DROME	Q9v9y2 drosophila	384	6	25.0	258	2	Q51338_9RETR	Q51338 equine infe
312	6	25.0	216	2	Q9U099_PLAFA	Q9u099 plasmodium	385	6	25.0	258	2	Q51342_9RETR	Q51342 equine infe
313	6	25.0	216	2	Q4IS91_AZOVI	Q4is91 azotobacter	386	6	25.0	258	2	Q51363_9RETR	Q51363 equine infe
314	6	25.0	217	2	Q81FN2_PLAP7	Q81fn2 plasmodium	387	6	25.0	258	2	Q51364_9RETR	Q51364 equine infe
315	6	25.0	217	2	Q8ACZ2_9HIV1	Q8acz2 human immun	388	6	25.0	258	2	Q51368_9RETR	Q51368 equine infe
316	6	25.0	218	2	Q9XY03_DUGJA	Q9xy03 dugesia jap	389	6	25.0	258	2	Q51370_9RETR	Q51370 equine infe
317	6	25.0	218	2	Q50HP5_TAV	Q50hp5 tomato aspe	390	6	25.0	258	2	Q51371_9RETR	Q51371 equine infe
318	6	25.0	219	2	Q88WK7_LACPL	Q88wk7 lactobacill	391	6	25.0	258	2	Q51374_9RETR	Q51374 equine infe
319	6	25.0	220	2	Q9UOB3_PLAFA	Q9uob3 plasmodium	392	6	25.0	258	2	Q51375_9RETR	Q51375 equine infe
320	6	25.0	221	2	Q8VZS8_ARATH	Q8vzs8 arabidopsis	393	6	25.0	258	2	Q51376_9RETR	Q51376 equine infe
321	6	25.0	221	2	Q6SU90_MANSM	Q6su90 manheimia	394	6	25.0	258	2	Q51377_9RETR	Q51377 equine infe
322	6	25.0	222	2	Q9UOB1_PLAFA	Q9uob1 plasmodium	395	6	25.0	258	2	Q51378_9RETR	Q51378 equine infe
323	6	25.0	223	2	Q25788_PLAFA	Q25788 plasmodium	396	6	25.0	259	2	Q51321_9RETR	Q51321 equine infe

397	6	25.0	260	2	Q81T83_PLAFA	Q81c83 plasmodium	470	6	25.0	287	2	Q52GI9_MAGGR	Q52gi9 magnaporthe
398	6	25.0	262	1	MSA2_PLAFC	Q99317 plasmodium	471	6	25.0	287	2	Q7KPY4_PLAFA	Q7kpy4 plasmodium
399	6	25.0	264	2	Q5ALP1_CANAL	Q5alp1 candida alb	472	6	25.0	287	2	Q25954_PLAFA	Q25954 bacillus su
400	6	25.0	264	2	Q96920_PLAFA	Q96920 plasmodium	473	6	25.0	287	2	Q52953_BACSU	Q52953 bacillus su
401	6	25.0	266	2	Q68LB8_9DIPT	Q68LB8 drosophila	474	6	25.0	288	2	Q8LF29_ARATH	Q8lf29 arabidopsis
402	6	25.0	267	2	Q7RDF2_PLAYO	Q7rdf2 plasmodium	475	6	25.0	288	2	Q8FJ33_ARATH	Q8fj33 arabidopsis
403	6	25.0	267	2	Q8ARB7_LINNU	Q8arb7 linaria vul	476	6	25.0	289	2	Q86L26_9DIPT	Q86l26 drosophila
404	6	25.0	267	2	Q94FA7_MINGU	Q94fal mimulus gut	477	6	25.0	290	2	Q54GM4_CRYHO	Q54gm4 dictyosteli
405	6	25.0	268	2	Q557D6_DICDI	Q557d6 dictyosteli	478	6	25.0	290	2	Q5CKZ8_CRYHO	Q5ckz8 cryptospori
406	6	25.0	268	2	Q68LB6_9DIPT	Q68lb6 drosophila	479	6	25.0	291	2	Q25789_PLAFA	Q25789 plasmodium
407	6	25.0	268	2	Q86101_DICDI	Q86101 dictyosteli	480	6	25.0	292	2	Q54CX2_DICDI	Q54cx2 dictyosteli
408	6	25.0	268	2	Q4X934_PLACH	Q4x934 plasmodium	481	6	25.0	292	2	Q8YTY9_ANASP	Q8yty9 anabaena sp
409	6	25.0	268	2	Q95PK4_TRICA	Q95pk4 tribolium c	482	6	25.0	293	2	Q25785_PLAFA	Q25785 plasmodium
410	6	25.0	272	1	MSA2_PLAF7	P50498 plasmodium	483	6	25.0	295	2	Q8MRE5_DROME	Q8mre5 drosophila
411	6	25.0	272	2	Q9TY97_PLAF7	Q9ty97 plasmodium	484	6	25.0	297	2	Q7K405_TRICA	Q7k405 tribolium c
412	6	25.0	274	1	MSA2_PLAF6	P50497 plasmodium	485	6	25.0	298	2	Q9FNN6_ARATH	Q9fnn6 arabidopsis
413	6	25.0	274	2	Q555M2_DICDI	Q555m2 dictyosteli	486	6	25.0	299	2	Q8IT95_CAEBR	Q8it95 caenorhabdi
414	6	25.0	274	2	Q68LB4_9DIPT	Q68lb4 drosophila	487	6	25.0	299	2	Q54PY9_DICDI	Q54py9 dictyosteli
415	6	25.0	274	2	P81395_ANTMA	P81395 antirrhinum	488	6	25.0	299	2	Q4Z406_PLABE	Q4z406 plasmodium
416	6	25.0	276	1	MSA2_PLAF8	Q99320 plasmodium	489	6	25.0	300	1	MSA2_PLAF1	Q93644 plasmodium
417	6	25.0	276	2	Q4SG06_TETNG	Q4sg06 tetraodon n	490	6	25.0	300	1	MSA2_PLAF2	Q54645 plasmodium
418	6	25.0	277	2	Q54E16_DICDI	Q54e16 dictyosteli	491	6	25.0	302	1	MSA2_PLAF9	Q54kf9 dictyosteli
419	6	25.0	277	2	Q68L92_9DIPT	Q68l92 drosophila	492	6	25.0	302	1	MSA2_PLAF9	Q54kf9 dictyosteli
420	6	25.0	278	2	Q25862_PLAFA	Q25862 plasmodium	493	6	25.0	302	2	Q4NZI7_9BELT	Q4nzi7 anaeromyxob
421	6	25.0	279	1	Y170_BUCBP	Q89a82 buchnera ap	494	6	25.0	303	2	Q9PWL2_PETMA	Q9pw12 petromyzon
422	6	25.0	279	2	Q68L83_9DIPT	Q68l83 drosophila	495	6	25.0	305	2	Q54C26_DICDI	Q54c26 dictyosteli
423	6	25.0	279	2	Q68L68_9DIPT	Q68l68 drosophila	496	6	25.0	305	2	Q54CE1_DICDI	Q54ce1 dictyosteli
424	6	25.0	279	2	Q68L99_9DIPT	Q68l99 drosophila	497	6	25.0	305	2	Q4Y106_PLACH	Q4y106 plasmodium
425	6	25.0	280	2	Q5A893_CANAL	Q5a893 candida alb	498	6	25.0	307	2	Q4J809_SULAC	Q4j809 sulfolobus
426	6	25.0	280	2	Q68L89_9DIPT	Q68l89 drosophila	499	6	25.0	308	2	Q54GW6_DICDI	Q54gw6 dictyosteli
427	6	25.0	280	2	Q68L21_9DIPT	Q68l21 drosophila	500	6	25.0	308	2	Q4YXZ2_PLABE	Q4yxz2 plasmodium
428	6	25.0	280	2	Q68L81_9DIPT	Q68l81 drosophila	501	6	25.0	310	2	Q54V44_DICDI	Q54v44 dictyosteli
429	6	25.0	280	2	Q68LAI_9DIPT	Q68lai drosophila	502	6	25.0	311	2	Q6B718_DROVI	Q6b718 drosophila
430	6	25.0	280	2	Q93239_CABEL	Q93239 caenorhabdi	503	6	25.0	311	2	Q4YEA7_PLABE	Q4yea7 plasmodium
431	6	25.0	280	2	Q8UVY9_BRARE	Q8uvy9 brachydanio	504	6	25.0	312	2	Q9BK04_TRICA	Q9bk04 tribolium c
432	6	25.0	280	2	Q6P612_BRARE	Q6p612 brachydanio	505	6	25.0	312	2	Q9SUA8_TRICA	Q9sua8 tribolium c
433	6	25.0	281	1	MSA2_PLAFH	Q99319 plasmodium	506	6	25.0	312	2	Q9NHB7_TRICA	Q9nhb7 tribolium c
434	6	25.0	281	2	Q68KZ6_9DIPT	Q68kz6 drosophila	507	6	25.0	313	2	Q7RKQ6_PLAYO	Q7rkq6 plasmodium
435	6	25.0	281	2	Q68L43_9DIPT	Q68l43 drosophila	508	6	25.0	314	2	Q86A98_DICDI	Q86a98 dictyosteli
436	6	25.0	281	2	Q68L79_9DIPT	Q68l79 drosophila	509	6	25.0	315	2	Q6BSN7_DBBHA	Q6bsn7 debaryomyce
437	6	25.0	281	2	Q68L81_9DIPT	Q68l81 drosophila	510	6	25.0	315	2	Q54U06_DICDI	Q54u06 dictyosteli
438	6	25.0	281	2	Q54M55_DICDI	Q54m55 dictyosteli	511	6	25.0	316	2	Q55BA7_DICDI	Q55bj7 dictyosteli
439	6	25.0	281	2	Q54ND8_DICDI	Q54nd8 dictyosteli	512	6	25.0	316	2	Q48607_9LACT	Q48607 lactococcus
440	6	25.0	282	2	Q68L07_9DIPT	Q68l07 drosophila	513	6	25.0	317	2	Q7REW9_PLAYO	Q7rew9 plasmodium
441	6	25.0	282	2	Q68L12_9DIPT	Q68l12 drosophila	514	6	25.0	317	2	Q4XEY8_PLACH	Q4xey8 plasmodium
442	6	25.0	282	2	Q68L14_9DIPT	Q68l14 drosophila	515	6	25.0	318	2	Q55B73_DICDI	Q55b73 dictyosteli
443	6	25.0	282	2	Q68L84_9DIPT	Q68l84 drosophila	516	6	25.0	321	2	Q54VG5_DICDI	Q54vg5 dictyosteli
444	6	25.0	282	2	Q68L90_9DIPT	Q68l90 drosophila	517	6	25.0	323	2	Q96835_DROME	Q96835 drosophila
445	6	25.0	282	2	Q68L91_9DIPT	Q68l91 drosophila	518	6	25.0	323	2	Q7RTG6_PLAYO	Q7rtg6 plasmodium
446	6	25.0	282	2	Q68L94_9DIPT	Q68l94 drosophila	519	6	25.0	324	1	HAM1_STRT1	Q5ml14 streptococc
447	6	25.0	282	2	Q68L96_9DIPT	Q68l96 drosophila	520	6	25.0	324	1	HAM1_STRT2	Q5m626 streptococc
448	6	25.0	282	2	Q68LA4_9DIPT	Q68la4 drosophila	521	6	25.0	324	2	Q54BG2_DICDI	Q54bg2 dictyosteli
449	6	25.0	282	2	Q7RF40_PLAYO	Q7rf40 plasmodium	522	6	25.0	324	2	Q54NM1_DICDI	Q54nm1 dictyosteli
450	6	25.0	283	2	Q9LK28_ARATH	Q9lk28 arabidopsis	523	6	25.0	324	2	Q9M4G1_SOLITU	Q9m4g1 solanum tub
451	6	25.0	283	2	Q68L88_9DIPT	Q68l88 drosophila	524	6	25.0	325	2	Q5C116_SCHJA	Q5c116 schistosoma
452	6	25.0	283	2	Q68L02_9DIPT	Q68l02 drosophila	525	6	25.0	328	2	Q5CYS1_CRYPV	Q5cys1 cryptospori
453	6	25.0	283	2	Q68L15_9DIPT	Q68l15 drosophila	526	6	25.0	328	2	Q5CKD9_CRYHO	Q5ckd9 cryptospori
454	6	25.0	283	2	Q68L44_9DIPT	Q68l44 drosophila	527	6	25.0	330	2	Q7RQG0_PLAYO	Q7rqg0 plasmodium
455	6	25.0	283	2	Q68L72_9DIPT	Q68l72 drosophila	528	6	25.0	330	2	Q585G1_9TRYP	Q585g1 trypanosoma
456	6	25.0	283	2	Q68L86_9DIPT	Q68l86 drosophila	529	6	25.0	330	2	Q7RFJ2_PLAYO	Q7rfj2 plasmodium
457	6	25.0	284	2	Q68LA2_9DIPT	Q68la2 drosophila	530	6	25.0	330	2	Q7ZW50_BRARE	Q7zw50 brachydanio
458	6	25.0	284	2	Q68L11_9DIPT	Q68l11 drosophila	531	6	25.0	331	2	Q54M88_DICDI	Q54m88 dictyosteli
459	6	25.0	284	2	Q68L60_9DIPT	Q68l60 drosophila	532	6	25.0	332	2	Q54DCM9_SCHJA	Q54dcm9 schistosoma
460	6	25.0	284	2	Q68L93_9DIPT	Q68l93 drosophila	533	6	25.0	332	2	Q6T4R0_9BILA	Q6t4r0 ptychodera
461	6	25.0	284	2	Q9V4R9_9DIPT	Q9v4r9 drosophila	534	6	25.0	334	2	Q55GI1_DICDI	Q55gi1 dictyosteli
462	6	25.0	284	2	Q9V4R9_DROME	Q9v4r9 drosophila	535	6	25.0	334	2	Q5KV26_GEOKA	Q5kv26 geobacillus
463	6	25.0	285	2	Q68L80_9DIPT	Q68l80 drosophila	536	6	25.0	336	2	Q59LJ8_CANAL	Q59lj8 candida alb
464	6	25.0	285	2	Q68L97_9DIPT	Q68l97 drosophila	537	6	25.0	336	2	Q6BFU4_PARTE	Q6bfu4 paramecium
465	6	25.0	286	1	MSA2_PLAF1	P50496 plasmodium	538	6	25.0	336	2	Q54D24_DICDI	Q54d24 dictyosteli
466	6	25.0	286	2	Q54TC8_DICDI	Q54tc8 dictyosteli	539	6	25.0	338	2	Q9GPT6_DICDI	Q9gpt6 dictyosteli
467	6	25.0	286	2	Q68L38_9DIPT	Q68l38 drosophila	540	6	25.0	338	2	Q7RNB8_PLAYO	Q7rnb8 plasmodium
468	6	25.0	286	2	Q68L42_9DIPT	Q68l42 drosophila	541	6	25.0	340	2	Q5AD61_CANAL	Q5ad61 candida alb
469	6	25.0	287	1	MSA2_PLAFG	P19260 plasmodium	542	6	25.0	340	2	Q5ADJ0_CANAL	Q5adj0 candida alb

543	6	25.0	341	2	Q8ILN6_PLAF7	Q8iln6 plasmodium	616	6	25.0	388	2	Q8LFN5_ARATH	Q8lfns arabidopsis
544	6	25.0	342	2	Q61K72_CAEBA	Q61k72 caenorhabdi	617	6	25.0	390	2	Q59YU0_CANAL	Q59yu0 candida alb
545	6	25.0	343	2	Q53EF5_9NEOB	Q53ef5 eleutheroda	618	6	25.0	390	2	Q54H17_DICDI	Q54h17 dictyosteli
546	6	25.0	344	2	Q8QS68_9BETA	Q8qs68 pongine her	619	6	25.0	390	2	Q7MYC8_PHOLL	Q7myc8 photorhabdu
547	6	25.0	347	1	MSA2_PLAF2	Q03646 plasmodium	620	6	25.0	391	2	Q6CTE1_KUULA	Q6cte1 kluyveromyc
548	6	25.0	348	2	Q9GBZ9_BURPA	Q9gbz9 burramys pa	621	6	25.0	391	2	Q7SK08_DICDI	Q7sk08 dictyosteli
549	6	25.0	352	2	Q8XOP7_NEUCR	Q8xop7 neurospora	622	6	25.0	395	2	Q6FT46_CANGA	Q6ft46 candida gla
550	6	25.0	352	2	Q54DL2_DICDI	Q54dl2 dictyosteli	623	6	25.0	396	2	Q9FH24_ARATH	Q9fh24 arabidopsis
551	6	25.0	353	2	Q70W03_CIOIN	Q70w03 ciona intes	624	6	25.0	397	2	Q54UG1_DICDI	Q54ug1 dictyosteli
552	6	25.0	354	1	URE2_YEAST	P23202 saccharomyc	625	6	25.0	398	1	KNAT1_ARATH	P46639 arabidopsis
553	6	25.0	354	2	Q8NI66_YEAST	Q8ni66 saccharomyc	626	6	25.0	398	2	Q9W4Q1_DROME	Q9w4q1 drosophila
554	6	25.0	354	2	Q8NI17_YEAST	Q8ni17 saccharomyc	627	6	25.0	398	2	Q8EF23_SHEON	Q8ef23 shewanella
555	6	25.0	355	2	Q8NIQ9_YEAST	Q8niq9 saccharomyc	628	6	25.0	399	2	Q8HFS0_SACSE	Q8hfs0 saccharomyc
556	6	25.0	356	2	Q948W9_BRACM	Q948w9 brassica ca	629	6	25.0	399	2	Q4YN01_PLABE	Q4yn01 plasmodium
557	6	25.0	356	2	Q948X0_BRACM	Q948x0 brassica ca	630	6	25.0	400	2	Q7Y1H5_NEUCR	Q7y1h5 neurospora
558	6	25.0	357	2	Q4P797_USTMA	Q4p797 ustilago ma	631	6	25.0	400	2	Q95RV8_DROME	Q95rv8 drosophila
559	6	25.0	357	2	Q54E12_DICDI	Q54e12 dictyosteli	632	6	25.0	400	2	Q551X7_DICDI	Q551x7 dictyosteli
560	6	25.0	358	2	Q54KM1_DICDI	Q54km1 dictyosteli	633	6	25.0	400	2	Q8S3L9_ARATH	Q8s3l9 arabidopsis
561	6	25.0	359	1	URE2_SACPA	Q96x44 saccharomyc	634	6	25.0	400	2	Q8S3M0_ARATH	Q8s3m0 arabidopsis
562	6	25.0	359	1	URE2_SACPA	Q711z8 saccharomyc	635	6	25.0	401	2	Q54XJ5_DICDI	Q54xj5 dictyosteli
563	6	25.0	359	2	Q9AYQ7_9RHOD	Q9ayq7 porphyra de	636	6	25.0	402	2	Q9W4N3_DROME	Q9w4n3 drosophila
564	6	25.0	360	2	Q59S54_CANAL	Q59s54 candida alb	637	6	25.0	402	2	Q9MB69_PORTE	Q9mb69 porphyra te
565	6	25.0	361	2	Q96424_9TRYP	Q96424 herpetonoma	638	6	25.0	402	2	Q9MB67_PORYE	Q9mb67 porphyra ye
566	6	25.0	362	2	Q9NGG4_DROSI	Q9ngg4 drosophila	639	6	25.0	402	2	Q9MB68_BANAT	Q9mb68 bangia atro
567	6	25.0	362	2	Q9NG83_DROSI	Q9ng83 drosophila	640	6	25.0	403	2	Q54PX6_DICDI	Q54px6 dictyosteli
568	6	25.0	362	2	Q9NG84_DROSI	Q9ng84 drosophila	641	6	25.0	404	2	Q4G199_HUMAN	Q4g199 homo sapien
569	6	25.0	362	2	Q9NG85_DROSI	Q9ng85 drosophila	642	6	25.0	406	2	Q5JHX4_PYRKO	Q5jhx4 pyrococcus
570	6	25.0	365	2	Q86156_DICDI	Q86156 dictyosteli	643	6	25.0	406	2	Q81T55_DROME	Q81t55 drosophila
571	6	25.0	365	2	Q9PFN6_ARATH	Q9pfn6 arabidopsis	644	6	25.0	406	2	Q4XNP7_PLACH	Q4xnp7 plasmodium
572	6	25.0	365	2	Q8EV30_MYCPE	Q8ev30 mycoplasma	645	6	25.0	407	2	Q7KMW0_DICDI	Q7kwm0 dictyosteli
573	6	25.0	367	2	Q8GUG6_ARATH	Q8gug6 arabidopsis	646	6	25.0	408	2	Q5SG94_DICDI	Q5sg94 dictyosteli
574	6	25.0	368	1	YB11_YEAST	P38180 saccharomyc	647	6	25.0	408	2	Q4X5R6_PLACH	Q4x5r6 plasmodium
575	6	25.0	368	2	Q9UZV5_PVRAB	Q9uzv5 pyrococcus	648	6	25.0	409	2	Q86K12_DICDI	Q86k12 dictyosteli
576	6	25.0	368	2	Q54CX7_DICDI	Q54cx7 dictyosteli	649	6	25.0	410	1	MRAY_PARUW	Q6mb83 parachlamyd
577	6	25.0	368	2	Q54QL4_DICDI	Q54ql4 dictyosteli	650	6	25.0	410	2	Q6B8H8_9HEMI	Q6ebh8 darnis part
578	6	25.0	368	2	Q9VRB1_DROME	Q9vrb1 drosophila	651	6	25.0	410	2	Q5WU57_LEGPL	Q5wu57 legionella
579	6	25.0	368	2	Q5JZR1_SOYBN	Q5jzr1 glycine max	652	6	25.0	410	2	Q5X2D6_LEGPA	Q5x2d6 legionella
580	6	25.0	369	1	D0P25_ARATH	Q92py0 arabidopsis	653	6	25.0	411	2	Q86HD7_DICDI	Q86hd7 dictyosteli
581	6	25.0	369	2	Q86175_DICDI	Q86175 dictyosteli	654	6	25.0	411	2	Q9SSA4_ARATH	Q9ssaa4 arabidopsis
582	6	25.0	370	2	Q43458_SOYBN	Q43458 glycine max	655	6	25.0	412	2	Q54X20_DICDI	Q54x20 dictyosteli
583	6	25.0	372	2	O82805_PEA	Q82805 pisum sativ	656	6	25.0	412	2	Q5ZSX6_LEGPH	Q5zsx6 legionella
584	6	25.0	372	1	COL9_ARATH	Q9ses5 arabidopsis	657	6	25.0	413	2	Q9GRY9_CABEL	Q9gry9 caenorhabdi
585	6	25.0	372	2	Q81JVB_PLAF7	Q81jvb plasmodium	658	6	25.0	414	2	Q4H2S3_CIOIN	Q4h2s3 ciona intes
586	6	25.0	372	2	Q91X18_ARATH	Q91x18 arabidopsis	659	6	25.0	416	1	SO_DROME	Q27350 drosophila
587	6	25.0	372	2	Q651U3_BACLD	Q651u3 bacillus li	660	6	25.0	416	2	Q6ZG17_BURMA	Q6zgj7 burkholderi
588	6	25.0	373	2	Q9U217_CABEL	Q9u217 caenorhabdi	661	6	25.0	418	2	Q6EJM2_9HIV1	Q6ejm2 human immun
589	6	25.0	374	2	Q54LM3_DICDI	Q54lm3 dictyosteli	662	6	25.0	419	2	Q6DBW2_BRARE	Q6dbw2 brachydanio
590	6	25.0	374	2	Q54TA8_DICDI	Q54ta8 dictyosteli	663	6	25.0	420	2	Q54YH2_DICDI	Q54yh2 dictyosteli
591	6	25.0	374	2	Q54WE6_DICDI	Q54we6 dictyosteli	664	6	25.0	421	2	Q5AME8_CANAL	Q5ame8 candida alb
592	6	25.0	374	2	Q72YN0_XENLA	Q72yn0 xenopus lae	665	6	25.0	421	2	Q54J70_DICDI	Q54j70 dictyosteli
593	6	25.0	375	2	Q59VK5_CANAL	Q59vk5 candida alb	666	6	25.0	421	2	Q8MTX3_9ANNE	Q8mtx3 theromyzon
594	6	25.0	375	2	Q8S154_9TREM	Q8s154 orientobilh	667	6	25.0	421	2	Q9LGX8_ORYSA	Q9lgx8 oryza sativ
595	6	25.0	375	2	Q8S157_9TREM	Q8s157 schistosoma	668	6	25.0	422	2	Q9Y1V4_HALRO	Q9y1v4 halocynthia
596	6	25.0	375	2	Q8S166_9TREM	Q8s166 gigantobilh	669	6	25.0	422	2	Q54LT6_DICDI	Q54lt6 dictyosteli
597	6	25.0	376	2	Q8S167_9TREM	Q8s167 dendritobil	670	6	25.0	423	2	Q96TM5_DICDI	Q96tm5 dictyosteli
598	6	25.0	378	2	Q514K4_DROAE	Q514k4 drosophila	671	6	25.0	423	2	Q8T1C6_DICDI	Q8t1c6 dictyosteli
599	6	25.0	378	2	Q54DL0_DICDI	Q54dl0 dictyosteli	672	6	25.0	423	2	Q4XYN4_PLACH	Q4xyn4 plasmodium
600	6	25.0	378	2	Q86188_DICDI	Q86188 dictyosteli	673	6	25.0	423	2	Q95TK1_DROME	Q95tk1 drosophila
601	6	25.0	379	2	Q59W09_CANAL	Q59w09 candida alb	674	6	25.0	423	2	Q6EJMS_9HIV1	Q6ejms human immun
602	6	25.0	379	2	Q55C29_DICDI	Q55c29 dictyosteli	675	6	25.0	423	2	Q6EJMJ_9HIV1	Q6ejmj human immun
603	6	25.0	380	2	Q7S7N8_NEUCR	Q7s7n8 neurospora	676	6	25.0	424	2	Q6EJMJ_9HIV1	Q6ejmj human immun
604	6	25.0	381	2	Q514K0_DROAE	Q514k0 drosophila	677	6	25.0	424	2	Q4XZJ4_9HIV1	Q4xzj4 human immun
605	6	25.0	381	2	Q55FK1_DICDI	Q55fk1 dictyosteli	678	6	25.0	425	2	Q4XZJ9_PLACH	Q4xzj9 plasmodium
606	6	25.0	382	2	Q968T5_SCHJA	Q968t5 schistosoma	679	6	25.0	426	2	Q5APN2_CANAL	Q5apn2 candida alb
607	6	25.0	382	2	Q9FRV6_9RHOD	Q9frv6 porphyra on	680	6	25.0	426	2	Q4Y1R5_PLABE	Q4y1rs plasmodium
608	6	25.0	382	2	Q9FRV7_PORCA	Q9frv7 porphyra ca	681	6	25.0	427	1	BGH_DROME	Q04787 drosophila
609	6	25.0	382	2	Q9FRV5_PORTE	Q9frv5 porphyra te	682	6	25.0	428	2	Q9Y1V5_HALRO	Q9y1v5 halocynthia
610	6	25.0	384	1	ERD1_KUULA	P41771 kluyveromyc	683	6	25.0	429	2	Q86J11_DICDI	Q86j11 dictyosteli
611	6	25.0	385	2	Q54DV6_DICDI	Q54dv6 dictyosteli	684	6	25.0	429	2	Q618V6_CAEBA	Q618v6 caenorhabdi
612	6	25.0	386	2	Q9VRA9_DROME	Q9vra9 drosophila	685	6	25.0	429	2	Q4V6V3_DROME	Q4v6v3 drosophila
613	6	25.0	388	2	Q54T14_DICDI	Q54t14 dictyosteli	686	6	25.0	431	2	Q12124_YEAST	Q12124 saccharomyc
614	6	25.0	388	2	Q81ZV5_PLAF7	Q81zv5 plasmodium	687	6	25.0	431	2	Q55SU7_DICDI	Q55su7 dictyosteli
615	6	25.0	388	2	Q54E41_DICDI	Q54e41 dictyosteli	688	6	25.0	434	2	Q63P56_BURPS	Q63p56 burkholderi

689	6	25.0	436	2	Q6PBC6	ACTAD	Q6fec6	acinetobact	762	6	25.0	482	2	Q40491	TOBAC	Q40491	nicotiana t
690	6	25.0	437	2	Q9VMQ7	DROME	Q9vmq7	drosoephila	763	6	25.0	483	2	Q40490	TOBAC	Q40490	nicotiana t
691	6	25.0	438	2	Q54SX2	DICDI	Q54sx2	dictyosteli	764	6	25.0	484	2	Q40514	TOBAC	Q40514	nicotiana t
692	6	25.0	439	2	Q5V6W5	HALMA	Q5v6w5	haloarcula	765	6	25.0	485	2	Q54JG7	DICDI	Q54jg7	dictyosteli
693	6	25.0	439	2	Q5UTU4	ANOQA	Q5utu4	anopheles g	766	6	25.0	486	2	Q875P0	SACKL	Q875p0	saccharomyc
694	6	25.0	439	2	Q4Z6M7	PLABE	Q4z6m7	plasmodium	767	6	25.0	488	2	Q54KL8	DICDI	Q54kl8	dictyosteli
695	6	25.0	439	2	Q6PG25	XENLA	Q6pg25	xenopus lae	768	6	25.0	490	2	Q4XXF6	PLACH	Q4xxf6	plasmodium
696	6	25.0	440	2	Q5B1X9	EMENI	Q5b1x9	aspergillus	769	6	25.0	490	2	Q9XG15	PLACH	Q9xg15	lycopersico
697	6	25.0	440	2	Q96110	PLAF7	Q96110	plasmodium	770	6	25.0	491	2	Q8IAZ2	PLAF7	Q8iaaz2	plasmodium
698	6	25.0	440	2	Q9VJ02	DROME	Q9vj02	drosoephila	771	6	25.0	491	2	Q85YH5	9ROSI	Q85yh5	euphorbia a
699	6	25.0	440	2	Q96686	DROME	Q96686	drosoephila	772	6	25.0	492	2	Q85YH4	9ROSI	Q85yh4	euphorbia l
700	6	25.0	442	2	Q54EK9	DICDI	Q54ek9	dictyosteli	773	6	25.0	493	1	ABDB	DROME	P09087	drosoephila
701	6	25.0	442	2	Q54U82	DICDI	Q54u82	dictyosteli	774	6	25.0	495	2	Q54EN1	DICDI	Q54en1	dictyosteli
702	6	25.0	443	2	Q555Q0	DICDI	Q555q0	dictyosteli	775	6	25.0	497	2	Q7RGQ7	PLAYO	Q7rgq7	plasmodium
703	6	25.0	443	2	Q7KVX1	DROME	Q7kvx1	drosoephila	776	6	25.0	500	2	Q54K78	DICDI	Q54k78	dictyosteli
704	6	25.0	444	2	Q4UHJ6	THEAN	Q4uhj6	theileria a	777	6	25.0	500	2	Q6R8D8	SODGL	Q6r8d8	sodalis glo
705	6	25.0	445	2	Q54U04	DICDI	Q54u04	dictyosteli	778	6	25.0	501	2	Q54DN6	DICDI	Q54dn6	dictyosteli
706	6	25.0	445	2	Q92B15	LISIN	Q92b15	listeria in	779	6	25.0	502	2	Q54CJ6	DICDI	Q54cj6	dictyosteli
707	6	25.0	446	2	Q7QVW4	GIALA	Q7qvn4	giardia lam	780	6	25.0	502	2	Q4YWB5	PLABE	Q4ywb5	plasmodium
708	6	25.0	446	2	Q54QY7	DICDI	Q54qy7	dictyosteli	781	6	25.0	502	2	Q15698	DICDI	Q15698	dictyosteli
709	6	25.0	447	1	SLF1	YEAST	Q12034	saccharomyc	782	6	25.0	503	2	Q96563	PLAFA	Q96563	plasmodium
710	6	25.0	447	2	Q6B1Z1	YEAST	Q6b1z1	saccharomyc	783	6	25.0	503	2	Q7RD97	PLAYO	Q7rd97	plasmodium
711	6	25.0	448	1	AAC2	DICDI	Q14196	dictyosteli	784	6	25.0	503	2	Q5SCB0	OSTTA	Q5scb0	ostreococcu
712	6	25.0	449	2	Q8PX08	METWA	Q8px08	methanosarc	785	6	25.0	505	2	Q70MC5	CUPSA	Q70mc5	cupienius
713	6	25.0	449	2	Q5AP66	DICDI	Q5af66	dictyosteli	786	6	25.0	507	2	Q8BRY5	MOUSE	Q8bry5	mus musculus
714	6	25.0	449	2	Q86KK1	DICDI	Q86kk1	dictyosteli	787	6	25.0	508	1	CPI17A	CAVPO	Q64410	cavia porce
715	6	25.0	449	2	Q4UNG4	THEAN	Q4ung4	theileria a	788	6	25.0	508	1	CROC	DROME	P32027	drosoephila
716	6	25.0	451	2	Q61L68	CABER	Q61l68	caenorhabdi	789	6	25.0	508	2	Q5SE40	DICDI	Q5se40	dictyosteli
717	6	25.0	451	2	Q4YXR7	PLABE	Q4yxr7	plasmodium	790	6	25.0	508	2	Q4YQ62	PLABE	Q4yq62	plasmodium
718	6	25.0	451	2	Q82690	LEPBU	Q82690	leptocinclis	791	6	25.0	508	2	Q53YH1	DROME	Q53yh1	drosoephila
719	6	25.0	455	2	Q86A18	DICDI	Q86a18	dictyosteli	792	6	25.0	509	2	Q86AF3	DICDI	Q86af3	dictyosteli
720	6	25.0	455	2	Q86HL1	DICDI	Q86hl1	dictyosteli	793	6	25.0	509	2	Q7VJL1	HELHP	Q7vj11	helicobacte
721	6	25.0	456	2	Q8TIV8	METAC	Q8t1v8	methanosarc	794	6	25.0	512	2	Q8DY11	STRAS	Q8dy11	streptococ
722	6	25.0	456	2	Q9V8V7	DROME	Q9v8v7	drosoephila	795	6	25.0	512	2	Q8E3N0	STRAS	Q8e3n0	streptococ
723	6	25.0	457	2	Q7SGR7	NEUCR	Q7sg7	neurospora	796	6	25.0	513	2	Q9NHP8	DROME	Q9nhp8	drosoephila
724	6	25.0	457	2	Q54E72	DICDI	Q54e72	dictyosteli	797	6	25.0	514	2	Q559E8	DICDI	Q559e8	dictyosteli
725	6	25.0	458	2	Q4N2N8	TRIPA	Q4n2n8	theileria p	798	6	25.0	514	2	Q86A26	DICDI	Q86a26	dictyosteli
726	6	25.0	458	2	Q5WYB1	LEGPL	Q5wb1	legionella	799	6	25.0	514	2	Q81LZ7	PLAF7	Q81lz7	plasmodium
727	6	25.0	459	1	STB1	YEAST	P42845	saccharomyc	800	6	25.0	514	2	Q9GZ33	TRYCR	Q9gz33	trypanosoma
728	6	25.0	461	2	Q4YDB8	PLABE	Q4ydb8	plasmodium	801	6	25.0	516	2	Q7FWQ4	ANOQA	Q7fwq4	anopheles g
729	6	25.0	462	2	Q4QUH5	9HIV1	Q4quh5	human immun	802	6	25.0	517	2	Q54S29	DICDI	Q54s29	dictyosteli
730	6	25.0	463	2	Q6BR67	DEBHA	Q6br67	debaromyce	803	6	25.0	518	2	Q9NJZ1	DROSIL	Q9njz1	drosoephila
731	6	25.0	463	2	Q61ZEB	CABER	Q61ze8	caenorhabdi	804	6	25.0	518	2	Q9NJZ5	DROME	Q9njz5	drosoephila
732	6	25.0	463	2	Q54U71	DICDI	Q54u71	dictyosteli	805	6	25.0	519	2	Q54LH2	DICDI	Q54lh2	dictyosteli
733	6	25.0	463	2	Q7RM05	PLAYO	Q7rm05	plasmodium	806	6	25.0	520	2	Q9VJ00	DROME	Q9vj00	drosoephila
734	6	25.0	464	2	Q54NT7	DICDI	Q54nt7	dictyosteli	807	6	25.0	521	2	Q54R09	DICDI	Q54r09	dictyosteli
735	6	25.0	465	2	Q5UR38	MIMIV	Q5ur38	mimivirus	808	6	25.0	521	2	Q54QQ9	DICDI	Q54qq9	dictyosteli
736	6	25.0	467	2	Q54RY6	DICDI	Q54ry6	dictyosteli	809	6	25.0	523	2	Q86P58	DROME	Q86p58	drosoephila
737	6	25.0	467	2	Q80010	CHICK	Q80010	gallus gall	810	6	25.0	525	1	ESR1	MICUN	P57753	microgogni
738	6	25.0	468	2	Q7RP17	PLAYO	Q7rp17	plasmodium	811	6	25.0	525	2	Q5TQB4	ANOQA	Q5tqb4	anopheles g
739	6	25.0	470	2	Q5AZL1	CANAL	Q5azl1	candida alb	812	6	25.0	527	2	Q54V97	DICDI	Q54v97	dictyosteli
740	6	25.0	472	1	SOX14	DROME	Q81ka4	plasmodium	813	6	25.0	531	2	Q57VM1	9TRYP	Q57vm1	trypanosoma
741	6	25.0	472	1	SOX14	DROME	P40656	drosoephila	814	6	25.0	531	2	Q7R9R0	PLAYO	Q7-r9r0	plasmodium
742	6	25.0	472	2	Q16804	DROME	Q16804	drosoephila	815	6	25.0	532	2	Q5AJI6	CANAL	Q5aji6	candida alb
743	6	25.0	472	2	Q7PNH3	ANOQA	Q7pnh3	anopheles g	816	6	25.0	533	1	YD3D	SCHPO	Q10277	schizosacch
744	6	25.0	473	2	Q818X1	ENTHI	Q818x1	entamoeba n	817	6	25.0	533	2	Q9CGU2	LACLA	Q9cgu2	lactococcus
745	6	25.0	473	2	Q869M2	DICDI	Q869m2	dictyosteli	818	6	25.0	534	2	Q5A479	CANAL	Q5a479	candida alb
746	6	25.0	473	2	Q73V86	MYCPA	Q73v86	mycobacteri	819	6	25.0	534	2	Q54L39	DICDI	Q54l39	candida alb
747	6	25.0	474	2	Q54LK7	DICDI	Q54lk7	dictyosteli	820	6	25.0	534	2	Q54Y77	DICDI	Q54y77	dictyosteli
748	6	25.0	475	2	Q54XW6	DICDI	Q54xw6	dictyosteli	821	6	25.0	535	2	Q9VZM2	DROME	Q9vzm2	drosoephila
749	6	25.0	475	2	Q9VEA3	DROME	Q9vea3	drosoephila	822	6	25.0	537	2	Q54MJ3	DICDI	Q54mj3	dictyosteli
750	6	25.0	478	2	Q9UEM8	HUMAN	Q9uem8	homo sapien	823	6	25.0	538	1	YAJ8	SCHPO	Q09908	schizosacch
751	6	25.0	478	2	Q9UIU5	HUMAN	Q9uiu5	homo sapien	824	6	25.0	538	2	Q75JS0	DICDI	Q75js0	dictyosteli
752	6	25.0	478	2	Q553R0	DICDI	Q553r0	dictyosteli	825	6	25.0	539	2	Q54VF0	DICDI	Q54vf0	dictyosteli
753	6	25.0	478	2	Q6ITT3	PIG	Q6itt3	sus scrofa	826	6	25.0	541	2	Q5AJM4	CANAL	Q5ajm4	candida alb
754	6	25.0	478	2	Q4R4A8	MACFA	Q4r4a8	macaca fasc	827	6	25.0	542	2	Q59LD1	CANAL	Q59ld1	candida alb
755	6	25.0	478	2	Q9D2X2	MOUSE	Q9d2x2	mus musculus	828	6	25.0	543	2	Q5TNB0	ANOQA	Q5tnb0	anopheles g
756	6	25.0	478	2	Q9D306	MOUSE	Q9d306	m mus muscu	829	6	25.0	546	2	Q7RNT2	PLAYO	Q7rnt2	plasmodium
757	6	25.0	479	1	YP66	YEAST	Q12194	saccharomyc	830	6	25.0	546	2	Q5E7Z2	VIBF1	Q5e7z2	vibrio fisc
758	6	25.0	479	2	Q8L459	ORYSA	Q8l459	oryza sativ	831	6	25.0	547	2	Q9B8Z3	SCHJA	Q9b8z3	schistosoma
759	6	25.0	480	2	Q9VWD5	DROME	Q9vwd5	drosoephila	832	6	25.0	549	2	Q6FV05	CANGA	Q6fv05	candida gla
760	6	25.0	480	2	Q9N572	CABEL	Q9n572	caenorhabdi	833	6	25.0	550	2	Q54DAL	DICDI	Q54dal	dictyosteli
761	6	25.0	480	2	Q8SXX1	DROME	Q8sxx1	drosoephila	834	6	25.0	550	2	Q24709	DROVI	Q24709	drosoephila



835	6	25.0	552	2	045117_WHITE	045117 chironomus	908	6	25.0	601	2	Q5DEC2_SCHJA	Q5dec2 schistosoma
836	6	25.0	552	2	Q4Y7Q4_PLACH	Q4y7q4 plasmidium	909	6	25.0	601	2	Q55C15_DICDI	Q55c15 dictyosteli
837	6	25.0	554	2	Q4Y761_PLACH	Q4y761 plasmidium	910	6	25.0	601	2	Q8S853_ORYSA	Q8s853 oryza sativ
838	6	25.0	555	2	Q76770_DICDI	Q76770 dictyosteli	911	6	25.0	603	2	Q6BZ23_DEBHA	Q6bz23 debaryomyce
839	6	25.0	555	2	Q61UB8_CABBR	Q61ub8 caenorhabdi	912	6	25.0	603	2	Q9C6K3_ARATH	Q9c6k3 arabidopsis
840	6	25.0	556	2	Q817Q3_BACCR	Q817q3 bacillus ce	913	6	25.0	605	1	WSC4_YEAST	P38739 saccharomyc
841	6	25.0	557	2	Q451T7_DICDI	Q451t7 dictyosteli	914	6	25.0	605	2	Q7S971_NEUCR	Q7s971 neurospora
842	6	25.0	557	2	Q4MS76_BACCE	Q4ms76 bacillus ce	915	6	25.0	606	2	Q4Y219_PLABE	Q4y219 plasmidium
843	6	25.0	557	2	Q6HD55_BACHK	Q6hd55 bacillus th	916	6	25.0	608	2	Q7RTD1_PLAYO	Q7rtd1 plasmidium
844	6	25.0	557	2	Q72ZV5_BACC1	Q72zv5 bacillus ce	917	6	25.0	609	2	Q54BH1_DICDI	Q54bh1 dictyosteli
845	6	25.0	557	2	Q633X3_BACCZ	Q633x3 bacillus ce	918	6	25.0	613	2	Q5SBD4_DICDI	Q5sbd4 dictyosteli
846	6	25.0	557	2	Q81LC0_BACAN	Q81lc0 bacillus an	919	6	25.0	613	2	Q9XZS8_DROME	Q9xzs8 drosophila
847	6	25.0	560	2	Q81516_PLAF7	Q81516 plasmidium	920	6	25.0	613	2	Q9S5V5_DROME	Q9s5v5 drosophila
848	6	25.0	560	2	Q81J78_PLAF7	Q81j78 plasmidium	921	6	25.0	616	2	Q875Y0_SACCA	Q875y0 saccharomyc
849	6	25.0	561	2	Q81J78_PLAF7	Q81j78 plasmidium	922	6	25.0	617	2	Q97240_PLAF7	Q97240 plasmidium
850	6	25.0	562	2	Q7RLP5_PLAYO	Q7rlp5 plasmidium	923	6	25.0	617	2	Q4X364_PLACH	Q4x364 plasmidium
851	6	25.0	562	2	Q23220_CABEL	Q23220 caenorhabdi	924	6	25.0	619	2	Q81JL5_PLAF7	Q81jl5 plasmidium
852	6	25.0	563	2	Q54J98_DICDI	Q54j98 dictyosteli	925	6	25.0	620	2	Q62004_BRAFL	Q62004 branchiosto
853	6	25.0	564	2	Q54YB7_DICDI	Q54yb7 dictyosteli	926	6	25.0	620	2	Q62007_BRALA	Q62007 branchiosto
854	6	25.0	565	2	Q54TY0_DICDI	Q54ty0 dictyosteli	927	6	25.0	620	2	Q8LLE0_SOLTU	Q8lle0 solanum tub
855	6	25.0	565	2	Q815X8_PLAF7	Q815x8 plasmidium	928	6	25.0	620	2	Q5M7Y0_BRARE	Q5m7y0 brachydanio
856	6	25.0	566	2	Q9U0J5_PLAF7	Q9u0j5 plasmidium	929	6	25.0	622	2	Q5SEJ7_DICDI	Q5sej7 dictyosteli
857	6	25.0	567	2	Q59LK6_CANAL	Q59lk6 candida alb	930	6	25.0	622	2	Q5SBE5_DICDI	Q5sbe5 dictyosteli
858	6	25.0	567	2	Q54RV4_DICDI	Q54rv4 dictyosteli	931	6	25.0	627	2	Q54L13_DICDI	Q54l13 dictyosteli
859	6	25.0	567	2	Q54X11_DICDI	Q54x11 dictyosteli	932	6	25.0	627	2	Q8ILG2_PLAF7	Q8ilg2 plasmidium
860	6	25.0	568	2	Q54PT1_DICDI	Q54pt1 dictyosteli	933	6	25.0	628	1	8IN3_ARATH	Q24606 arabidopsis
861	6	25.0	569	1	MANC_PIRSP	P55298 pitomyces s	934	6	25.0	628	2	Q81LB8_PLAF7	Q81lb8 plasmidium
862	6	25.0	569	2	Q5XXR5_ANOGA	Q5xxr5 anopheles g	935	6	25.0	628	2	Q5SDN7_DROME	Q5sdn7 drosophila
863	6	25.0	570	1	P2B2_DROME	Q27889 drosophila	936	6	25.0	630	2	Q5SD16_DICDI	Q5sd16 dictyosteli
864	6	25.0	571	1	MANE_PIRSP	P55297 pitomyces s	937	6	25.0	630	2	Q56C43_9CAUD	Q56c43 enterobacte
865	6	25.0	572	2	Q54H16_DICDI	Q54h16 dictyosteli	938	6	25.0	631	2	Q54WN7_DICDI	Q54wn7 dictyosteli
866	6	25.0	572	2	Q559A6_DICDI	Q559a6 dictyosteli	939	6	25.0	632	2	Q5CIY5_CRYHO	Q5ciy5 cryptospori
867	6	25.0	575	2	Q8LGJ2_ARATH	Q8lgj2 arabidopsis	940	6	25.0	633	2	Q9VD13_DROME	Q9vd13 drosophila
868	6	25.0	575	2	Q9LZM8_ARATH	Q9lzm8 arabidopsis	941	6	25.0	633	2	Q86AP6_DICDI	Q86ap6 dictyosteli
869	6	25.0	575	2	Q8HL47_ARATH	Q8hl47 arabidopsis	942	6	25.0	633	2	Q54ZV8_DICDI	Q54zv8 dictyosteli
870	6	25.0	575	2	Q8NT95_ERARE	Q8ny95 brachydanio	943	6	25.0	634	2	Q9S5R62_DROME	Q9s5r62 drosophila
871	6	25.0	578	1	PSP2_YEAST	P50109 saccharomyc	944	6	25.0	637	2	Q86B13_DICDI	Q86b13 dictyosteli
872	6	25.0	578	2	Q25419_HELPFY	Q25419 helicobacte	945	6	25.0	637	2	Q81I24_PLAF7	Q81i24 plasmidium
873	6	25.0	578	2	Q8QHLO_PAROL	Q8qhl0 paralichthy	946	6	25.0	637	2	Q81LI4_PLAF7	Q81li4 plasmidium
874	6	25.0	579	2	Q580V0_9TRYP	Q580v0 trypanosoma	947	6	25.0	638	2	Q5CQ13_CRYPV	Q5cq13 cryptospori
875	6	25.0	579	2	Q54DK8_DICDI	Q54dk8 dictyosteli	948	6	25.0	638	2	Q8T2T4_DICDI	Q8t2t4 dictyosteli
876	6	25.0	579	2	Q54PG2_DICDI	Q54pg2 dictyosteli	949	6	25.0	640	2	Q5CPA2_CRYHO	Q5cpa2 cryptospori
877	6	25.0	580	2	Q54VL8_DICDI	Q54vl8 dictyosteli	950	6	25.0	641	2	Q54Y11_DICDI	Q54y11 dictyosteli
878	6	25.0	580	2	Q86JP4_DICDI	Q86jp4 dictyosteli	951	6	25.0	641	2	Q54I00_DICDI	Q54iq0 dictyosteli
879	6	25.0	580	2	Q5SAB2_DICDI	Q5sab2 dictyosteli	952	6	25.0	642	2	Q9NH51_DROME	Q9nh51 drosophila
880	6	25.0	581	2	Q54UG5_DICDI	Q54ug5 dictyosteli	953	6	25.0	642	2	Q8RW12_ARATH	Q8rw12 arabidopsis
881	6	25.0	582	2	Q8SY46_DROME	Q8sy46 drosophila	954	6	25.0	643	2	Q9VZY3_DROME	Q9vzy3 drosophila
882	6	25.0	582	2	Q9ZLC5_HELPFJ	Q9zlc5 helicobacte	955	6	25.0	643	2	Q54Y78_DICDI	Q54y78 dictyosteli
883	6	25.0	583	2	Q6CM16_KJULA	Q6cm16 kluyveromyc	956	6	25.0	645	1	BARH2_DROME	Q24256 drosophila
884	6	25.0	584	2	Q81D54_PLAF7	Q81d54 plasmidium	957	6	25.0	647	2	Q5SAW1_DICDI	Q5saw1 dictyosteli
885	6	25.0	584	2	Q4XV15_PLACH	Q4xv15 plasmidium	958	6	25.0	647	2	Q8SZT1_DROME	Q8szt1 drosophila
886	6	25.0	586	2	Q54Z94_DICDI	Q54z94 dictyosteli	959	6	25.0	647	2	Q8IM96_DROME	Q8im96 drosophila
887	6	25.0	586	2	Q8MND9_DICDI	Q8mnd9 dictyosteli	960	6	25.0	648	1	KAPC_DICDI	P34099 plasmidium
888	6	25.0	587	2	Q55G76_DICDI	Q55g76 dictyosteli	961	6	25.0	648	2	Q6T7E7_PLAFA	Q6t7e7 drosophila
889	6	25.0	588	2	Q54VF4_DICDI	Q54vf4 dictyosteli	962	6	25.0	648	2	Q81IK0_DROVI	Q81ik0 drosophila
890	6	25.0	588	2	Q51IG7_ENTHI	Q51ig7 entamoeba h	963	6	25.0	648	2	Q5CUP3_CRYPV	Q5cup3 cryptospori
891	6	25.0	588	2	Q4YUJ3_PLABE	Q4yuj3 plasmidium	964	6	25.0	648	2	Q54QA9_DICDI	Q54qa9 dictyosteli
892	6	25.0	590	2	Q54D91_DICDI	Q54d91 dictyosteli	965	6	25.0	648	2	Q9TXB8_9MICE	Q9txb8 dictyosteli
893	6	25.0	591	2	Q4XUP3_PLACH	Q4xup3 plasmidium	966	6	25.0	649	2	Q9VW88_DROME	Q9vw88 drosophila
894	6	25.0	591	2	Q4YLL6_PLABE	Q4yll6 plasmidium	967	6	25.0	649	2	Q95SS7_DROME	Q95ss7 drosophila
895	6	25.0	592	1	HMDH1_ARATH	P14891 arabidopsis	968	6	25.0	650	2	Q9GZ01_PLAFA	Q9gz01 plasmidium
896	6	25.0	593	2	Q5XXR4_ANOGA	Q5xxr4 anopheles g	969	6	25.0	650	2	Q54DL3_DICDI	Q54dl3 dictyosteli
897	6	25.0	594	2	Q86JK0_DICDI	Q86jk0 dictyosteli	970	6	25.0	652	2	Q4WXU4_ASPPU	Q4wxu4 aspergillus
898	6	25.0	595	2	Q7SPY1_NEUCR	Q7spy1 neurospora	971	6	25.0	652	2	Q8X018_NEUCR	Q8x018 neurospora
899	6	25.0	595	2	Q54K19_DICDI	Q54k19 dictyosteli	972	6	25.0	652	2	Q54RJ3_DICDI	Q54rj3 dictyosteli
900	6	25.0	597	2	Q6WIA6_BPKVA	Q6wia6 bacterioph	973	6	25.0	652	2	Q81427_PLAF7	Q81427 plasmidium
901	6	25.0	597	2	Q81103_PRRAR	Q81103 prunus arme	974	6	25.0	652	2	Q5CFV3_CRYHO	Q5cfv3 cryptospori
902	6	25.0	598	2	Q58774_PYRHO	Q58774 pyrococcus	975	6	25.0	654	2	Q62199_CABEL	Q62199 caenorhabdi
903	6	25.0	598	2	Q8SSN1_DICDI	Q8ssn1 dictyosteli	976	6	25.0	655	2	Q55IA2_DICDI	Q55ia2 dictyosteli
904	6	25.0	599	2	Q5RA16_CANAL	Q5ra16 candida alb	977	6	25.0	655	2	Q815P8_PLAF7	Q815p8 plasmidium
905	6	25.0	600	2	Q4PHL9_USTMA	Q4phl9 ustilago ma	978	6	25.0	656	2	Q81YW2_ORYSA	Q81yw2 oryza sativ
906	6	25.0	600	2	Q54K20_DICDI	Q54k20 dictyosteli	979	6	25.0	657	2	Q558W6_DICDI	Q558w6 dictyosteli
907	6	25.0	601	1	KEN_DROME	Q77459 drosophila	980	6	25.0	658	2	Q59779_SCHPO	Q59779 schizosacch

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981 6 25.0 658 2 Q5ALR8 CANAL
982 6 25.0 658 2 Q18703_CAEEL
983 6 25.0 659 2 Q9VY77 DROSOPHILA
984 6 25.0 660 2 Q94485 DICTYOESTELI
985 6 25.0 662 2 Q55FD2 DICTDI
986 6 25.0 662 2 Q4VPM5 PLABE
987 6 25.0 662 2 Q5WBH7_BACSK
988 6 25.0 662 2 Q5XIZ8_BRARE
989 6 25.0 665 2 Q86HZ3_DICDI
990 6 25.0 666 2 Q8IM66_PLAP7
991 6 25.0 667 2 Q54QEB_DICDI
992 6 25.0 667 2 Q4UFQ5_THEAN
993 6 25.0 668 2 Q553D7_DICDI
994 6 25.0 668 2 Q86HC6_DICDI
995 6 25.0 668 2 Q5SGI4_DICDI
996 6 25.0 669 2 Q6C5E9_YARLI
997 6 25.0 671 2 Q51GF3_ENTHI
998 6 25.0 672 2 Q9UOK1_PLAFA
999 6 25.0 672 2 Q7K734_PLAP7
1000 6 25.0 673 2 Q55A01_DICDI
```

## ALIGNMENTS

```
RESULT 1
Q56CY1 HUMAN
ID Q56CY1 HUMAN PRELIMINARY; PRT; 182 AA.
AC Q56CY1;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Bladder cancer related CD9 variant.
GN Name=BTCC-1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Bladder;
RC "The full-length cloning of a differentially expressed EST sequence in
RT a bladder cancer subtractive cDNA library.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY966455; AAX78197.1; -; mRNA.
SQ SEQUENCE 182 AA; 20750 MW; C26F856F584AADEE CRC64;
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Query Match 100.0%; Score 24; DB 2; Length 182;
Best Local Similarity 100.0%; Pred. No. 7.5e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 LRFDSTQKSIPEQETNNNSFFYT 24
|||
Db 35 LRFDSTQKSIPEQETNNNSFFYT 58
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```
RESULT 2
ID CD9 CERAE
AC CD9 CERAE STANDARD; PRT; 227 AA.
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE CD9 antigen (27 kDa diphtheria toxin receptor-associated protein)
DE (DRAP27).
GN Name=CD9;
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecidae; Cercopitheciinae; Cercopithecus.
OX NCBI_TaxID=9534;
```

```
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=92394967; PubMed=1522113; DOI=10.1083/jcb.118.6.1389;
RA Mitamura T., Iwamoto R., Umata T., Yomo T., Urabe I., Tsuneoka M.,
RA Mekada E.;
RT "The 27-kD diphtheria toxin receptor-associated protein (DRAP27) from
RT vero cells is the monkey homologue of human CD9 antigen: expression of
RT DRAP27 elevates the number of diphtheria toxin receptors on toxin-
RT sensitive cells.";
RL J. Cell Biol. 118:1389-1399(1992).
CC -!- FUNCTION: Involved in platelet activation and aggregation.
CC Regulates paranodal junction formation. Required for gamete
CC fusion. Involved in cell adhesion, cell motility and tumor
CC metastasis (By similarity).
CC -!- FUNCTION: Expression of DRAP27 elevates the number of diphtheria
CC toxin receptors on toxin-sensitive cells.
CC -!- SUBUNIT: Forms both disulfide-linked homodimers and higher
CC heterooligomers as well as heterooligomers with other members of the
CC tetraspanin family. Associates with CR2/CD21 and with PTGFRN/CD9P1
CC (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- PTM: Phosphorylated on tyrosine following B-cell activation (By
CC similarity).
CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; D10726; BAA01569.1; -; mRNA.
DR PIR; A42929; A42929.
DR GO; GO:0005887; C:integral to plasma membrane; ISS.
DR GO; GO:0005515; P:protein binding; ISS.
DR GO; GO:0007155; P:cell adhesion; ISS.
DR GO; GO:0006928; P:cell motility; ISS.
DR GO; GO:0007342; P:fusion of sperm to egg plasma membrane; ISS.
DR GO; GO:0030913; P:paranodal junction formation; ISS.
DR GO; GO:0030168; P:platelet activation; ISS.
DR InterPro; IPR000301; Transmem 4.
DR Pfam; PF00335; Tetraspannin; 1.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM4_1; 1.
KW Antigen; Cell adhesion; Fertilization; Glycoprotein; Lipoprotein;
KW Palmitate; Phosphorylation; Transmembrane.
FT INIT MET 0
FT TOPO DOM 1 11 Cytoplasmic (Potential).
FT TRANSMEM 12 32 Potential.
FT TOPO DOM 33 54 Extracellular (Potential).
FT TRANSMEM 55 75 Potential.
FT TOPO DOM 76 86 Cytoplasmic (Potential).
FT TRANSMEM 87 110 Potential.
FT TOPO DOM 111 194 Extracellular (Potential).
FT TRANSMEM 195 220 Potential.
FT TOPO DOM 221 227 Cytoplasmic (Potential).
FT LIPID 8 8 S-palmitoyl cysteine (By similarity).
FT LIPID 77 77 S-palmitoyl cysteine (By similarity).
FT LIPID 78 78 S-palmitoyl cysteine (By similarity).
FT LIPID 86 86 S-palmitoyl cysteine (By similarity).
FT LIPID 217 217 S-palmitoyl cysteine (By similarity).
FT LIPID 218 218 S-palmitoyl cysteine (By similarity).
FT CARBOHYD 51 51 N-linked (GLCNAc...) (potential).
FT CARBOHYD 52 52 N-linked (GLCNAc...) (potential).
SQ SEQUENCE 227 AA; 25300 MW; 8E3474E7A590374A CRC64;
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Query Match 100.0%; Score 24; DB 1; Length 227;  
Best Local Similarity 100.0%; Pred. No. 9.1e-17;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LRFDSTQKSIPEQETNNNSFFYT 24  
|||||  
Db 34 LRFDSTQKSIPEQETNNNSFFYT 57



## RESULT 3

CD9\_HUMAN  
 ID CD9\_HUMAN STANDARD; PRT; 227 AA.  
 AC P21926; Q9SES4;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE CD9 antigen (p24) (Leukocyte antigen MIC3) (Motility-related protein)  
 DE (MRP-1) (Tetraspanin-29) (Tspan-29).  
 GN Name=CD9; Synonyms=MIC3, TSPAN29;  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 1-4.  
 RX MEDLINE=91093112; PubMed=1840589;  
 RA Boucheix C., Benoit P., Frachet P., Billard M., Worthington R.E.,  
 RA Gagnon J., Uzan G.;  
 RT "Molecular cloning of the CD9 antigen. A new family of cell surface  
 RT proteins.";  
 RL J. Biol. Chem. 266:117-122(1991).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE [MRNA], AND PARTIAL PROTEIN SEQUENCE.  
 RX MEDLINE=91244846; PubMed=2037603;  
 RA Lanza F., Wolf D., Fox C.P., Kieffer N., Seyer J.M., Fried V.A.,  
 RA Coughlin S.R., Phillips D.R., Jennings L.K.;  
 RT "cDNA cloning and expression of platelet p24/CD9. Evidence for a new  
 RT family of multiple membrane-spanning proteins.";  
 RL J. Biol. Chem. 266:10638-10645(1991).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=92078843; PubMed=1720807; DOI=10.1084/jem.174.6.1347;  
 RA Miyake M., Koyama M., Seno M., Ikegawa S.;  
 RT "Identification of the motility-related protein (MRP-1), recognized by  
 RT monoclonal antibody M31-15, which inhibits cell motility.";  
 RL J. Exp. Med. 174:1347-1354(1991).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 RC TISSUE=Leukocyte;  
 RX MEDLINE=93252369; PubMed=8486348;  
 RA Rubinstein E., Benoit P., Billard M., Plaisance S., Prenant M.,  
 RA Uzan G., Boucheix C.;  
 RT "Organization of the human CD9 gene.";  
 RL Genomics 16:132-138(1993).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 RA Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O.,  
 RA Rajkumar N., Yi Q., Nickerson D.A.;  
 RT "SeattleSNPs, NHLBI HL6682 program for genomic applications, UW-  
 RT FHCR, Seattle, WA (URL: <http://pga.gs.washington.edu>).";  
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RC TISSUE=Ovary;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Stapleton M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Munz N.D., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Falley J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [7]  
 RP PROTEIN SEQUENCE OF 1-20.  
 RC TISSUE=Platelet;  
 RX MEDLINE=90292223; PubMed=2358073; DOI=10.1016/0014-5793(90)80265-K;  
 RA Higashihara M., Takahata K., Yatomi Y., Nakahara K., Kurokawa K.;  
 RT "Purification and partial characterization of CD9 antigen of human  
 RT platelets.";  
 RL FEBS Lett. 264:270-274(1990).  
 RN [8]  
 RP ROLE IN CELL MOTILITY AND METASTASIS.  
 RX PubMed=8478605; DOI=10.1084/jem.177.5.1231;  
 RA Ikegawa S., Koyama M., Yamaoka M., Sasaki R., Miyake M.;  
 RT "Suppression of cell motility and metastasis by transfection with  
 RT human motility-related protein (MRP-1/CD9) DNA.";  
 RL J. Exp. Med. 177:1231-1237(1993).  
 RN [9]  
 RP ROLE IN CELL ADHESION.  
 RX PubMed=7511626;  
 RA Masellis-Smith A., Shaw A.R.;  
 RT "CD9-regulated adhesion. Anti-CD9 monoclonal antibody induce pre-B  
 RT cell adhesion to bone marrow fibroblasts through de novo recognition  
 RT of fibronectin.";  
 RL J. Immunol. 152:2768-2777(1994).  
 RN [10]  
 RP ROLE IN GAMETE FUSION.  
 RX PubMed=14575715; DOI=10.1016/j.bbrc.2003.09.196;  
 RA Higginbottom A., Takahashi Y., Bolling L., Connor S.A., White J.M.,  
 RA Partridge L.J., Monk P.N.;  
 RT "Structural requirements for the inhibitory action of the CD9 large  
 RT extracellular domain in sperm/oocyte binding and fusion.";  
 RL Biochem. Biophys. Res. Commun. 311:208-214(2003).  
 RN [11]  
 RP SUBUNIT.  
 RX PubMed=14556650; DOI=10.1042/BJ20031037;  
 RA Kovalenko O.V., Yang X., Kolesnikova T.V., Hemler M.E.;  
 RT "Evidence for specific tetraspanin homodimers: inhibition of  
 RT palmitoylation makes cysteine residues available for cross-linking.";  
 RL Biochem. J. 377:407-417(2004).  
 RN [12]  
 RP PHOSPHORYLATION.  
 RX MEDLINE=93327758; PubMed=7687539;  
 RA Chalupny N.J., Kanner S.B., Schieven G.L., Wee S., Gilliland L.K.,  
 RA Aruffo A., Ledbetter J.A.;  
 RT "Tyrosine phosphorylation of CD19 in pre-B and mature B cells.";  
 RL EMBO J. 12:2691-2696(1993).  
 RN [13]  
 RP PALMITOYLATION, AND MUTAGENESIS OF CYS-8; CYS-77; CYS-78; CYS-86;  
 RX CYS-217 AND CYS-218.  
 RX PubMed=11959120; DOI=10.1016/S0014-5793(02)02522-X;  
 RA Charrin S., Manie S., Oualid M., Billard M., Boucheix C.,  
 RA Rubinstein E.;  
 RT "Differential stability of tetraspanin/tetraspanin interactions: role  
 RT of palmitoylation.";  
 RL FEBS Lett. 516:139-144(2002).  
 RN [14]  
 RP INTERACTION WITH PTGFRN.  
 RX MEDLINE=21216740; PubMed=11278880; DOI=10.1074/jbc.M011297200;  
 RA Charrin S., Le Naour F., Oualid M., Billard M., Faure G., Hanash S.M.,  
 RA Boucheix C., Rubinstein E.;  
 RT "The major CD9 and CD81 molecular partner. Identification and  
 RT characterization of the complexes.";  
 RL J. Biol. Chem. 276:14329-14337(2001).  
 CC -!- FUNCTION: Involved in platelet activation and aggregation.  
 CC Regulates paracodal junction formation. Required for gamete  
 CC fusion. Involved in cell adhesion, cell motility and tumor  
 CC metastasis.  
 CC -!- SUBUNIT: Forms both disulfide-linked homodimers and higher

```
CC homooligomers as well as heterooligomers with other members of the
CC tetraspanin family. Associates with CR2/CD21 and with
CC PTGFRN/CD9P1.
CC
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed by a variety of hematopoietic and
CC epithelial cells.
CC -!- PTM: Protein exists in three forms with molecular masses between
CC 22 and 27 kDa, and is known to carry covalently linked fatty
CC acids.
CC
CC -!- PTM: Phosphorylated on tyrosine following B-cell activation.
CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; S60489; AAC60586.1; -; Genomic DNA.
CC EMBL; S60482; AAC60586.1; JOINED; Genomic DNA.
CC EMBL; S60463; AAC60586.1; JOINED; Genomic DNA.
CC EMBL; S60464; AAC60586.1; JOINED; Genomic DNA.
CC EMBL; S60700; AAC60586.1; JOINED; Genomic DNA.
CC EMBL; S60639; AAC60586.1; JOINED; Genomic DNA.
CC EMBL; S60465; AAC60586.1; JOINED; Genomic DNA.
CC EMBL; S60472; AAC60586.1; JOINED; Genomic DNA.
CC EMBL; M38690; AAC60320.1; -; mRNA.
CC EMBL; J34068; AAC59982.1; -; mRNA.
CC EMBL; X60111; CAA42708.1; -; mRNA.
CC EMBL; L08118; -; NOT ANNOTATED CDS; Genomic DNA.
CC EMBL; L08119; AAAS1954.1; ALT_SEQ; Genomic DNA.
CC EMBL; L08120; AAAS1955.1; ALT_SEQ; Genomic DNA.
CC EMBL; L08121; AAAS1956.1; -; Genomic DNA.
CC EMBL; L08122; AAAS1957.1; -; Genomic DNA.
CC EMBL; L08123; AAAS1958.1; -; Genomic DNA.
CC EMBL; L08124; AAAS1959.1; -; Genomic DNA.
CC EMBL; L08125; -; NOT ANNOTATED CDS; Genomic DNA.
CC EMBL; AV422198; AAQ87878.1; -; Genomic DNA.
CC EMBL; BC013988; AAH11988.1; -; mRNA.
CC F01; A46123; A40402.
CC EMBL; ENSG0000010278; Homo sapiens.
CC HGNC; HGNC:1709; CD9.
CC H-InvDB; HIX0010357; -.
CC Reactome; P21926; -.
CC MIM; 143030; -.
CC GO; GO:0005887; C:integral to plasma membrane; NAS.
CC GO; GO:0005886; C:plasma membrane; NAS.
CC GO; GO:0005515; F:protein binding; IPT.
CC GO; GO:0007155; P:cell adhesion; IDA.
CC GO; GO:0006928; P:cell motility; IDA.
CC GO; GO:0007342; P:fusion of sperm to egg plasma membrane; IDA.
CC GO; GO:0030913; P:paranodal junction formation; ISS.
CC GO; GO:0030168; P:platelet activation; NAS.
CC InterPro; IPR000301; Transmem 4.
CC Pfam; PF00335; Tetraspanin; I.
CC PRINTS; PR00259; TFOUR.
CC PROSITE; PS00421; TM4 1; 1.
CC Antigen; Cell adhesion; Direct protein sequencing; Fertilization;
CC
CC Query Match 100.0%; Score 24; DB 1; Length 227;
CC Best Local Similarity 100.0%; Pred. No. 9.1e-17;
CC Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 1 LRFDSQTKSIFQEQTNNNSFFY 24
CC |||||
CC Db 34 LRFDSQTKSIFQEQTNNNSFFY 57
CC
CC RESULT 4
CC Q5J7W6 HUMAN
CC ID Q5J7W6 HUMAN PRELIMINARY; PRT; 228 AA.
CC AC Q5J7W6;
CC DT 10-MAY-2005 (TrEMBLrel. 30, Created)
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DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Growth-inhibiting gene 2 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kim J.W.;
RT "Identification of a human growth inhibition gene 2 (GIG2).";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY423720; AAC00483.1; -; mRNA.
SQ SEQUENCE 228 AA; 25416 MW; F68333E0C20611D8 CRC64;
Query Match 100.0%; Score 24; DB 2; Length 228;
Best Local Similarity 100.0%; Pred. No. 9.2e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 1 LRFDSQTKSIFQEQTNNNSFFY 24
CC |||||
CC Db 35 LRFDSQTKSIFQEQTNNNSFFY 58
CC
CC RESULT 5
CC CD9_RAT
CC ID CD9_RAT STANDARD; PRT; 225 AA.
CC AC P40241;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE CD9 antigen.
GN Name=CD9;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=Sprague-Dawley; TISSUE=Sciatic nerve;
RX MEDLINE=95123481; PubMed=7823164;
RA Kaprielian Z., Cho K.O., Hadjiargyrou M., Patterson P.H.;
RT "CD9, a major platelet cell surface glycoprotein, is a ROCA antigen
RT and is expressed in the nervous system.";
RL J. Neurosci. 15:562-573(1995).
CC -!- FUNCTION: Involved in platelet activation and aggregation.
CC Regulates paranodal junction formation. Required for gamete
CC fusion. Involved in cell adhesion, cell motility and tumor
CC metastasis (By similarity).
CC -!- SUBUNIT: Forms both disulfide-linked homodimers and higher
CC homooligomers as well as heterooligomers with other members of the
CC tetraspanin family. Associates with CR2/CD21 and with PTGFRN/CD9P1
CC (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in the peripheral nervous system.
CC -!- PTM: Phosphorylated on tyrosine following B-cell activation (By
CC similarity).
CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; X76489; CAA54027.1; -; mRNA.
CC PIR; I56562; S39262.
CC EMBL; ENSRNOG00000019556; Rattus norvegicus.
CC RGD; 2318; Cd9.
CC GO; GO:0009986; C:cell surface; IDA.
CC GO; GO:0005887; C:integral to plasma membrane; ISS.
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DR	GO; GO:0005515; F:protein binding; IPI.	
DR	GO; GO:0007155; P:cell adhesion; ISS.	
DR	GO; GO:0006928; P:cell motility; ISS.	
DR	GO; GO:0007342; P:fusion of sperm to egg plasma membrane; ISS.	
DR	GO; GO:0030168; P:paranodal junction formation; ISS.	
DR	GO; GO:0030168; P:platelet activation; ISS.	
DR	InterPro: IPR000301; Transmem. 4.	
DR	Pfam: PF00335; Tetraspannin; 1.	
DR	PRINTS: PR00259; TMFOUR.	
DR	PROSITE: PS00421; TM4; 1.	
KW	Antigen; Cell adhesion; Fertilization; Glycoprotein; Lipoprotein;	
KW	Palmitate; Phosphorylation; Transmembrane.	
FT	INIT MET 0 0	By similarity.
FT	TOPO_DOM 1 11	Cytoplasmic (Potential).
FT	TRANSMEM 12 32	Potential.
FT	TOPO_DOM 33 52	Extracellular (Potential).
FT	TRANSMEM 53 73	Potential.
FT	TOPO_DOM 74 84	Cytoplasmic (Potential).
FT	TRANSMEM 85 108	Potential.
FT	TOPO_DOM 109 192	Extracellular (Potential).
FT	TRANSMEM 193 218	Potential.
FT	TOPO_DOM 219 225	Cytoplasmic (Potential).
FT	LIPID 8 8	S-palmitoyl cysteine (By similarity).
FT	LIPID 75 75	S-palmitoyl cysteine (By similarity).
FT	LIPID 76 76	S-palmitoyl cysteine (By similarity).
FT	LIPID 84 84	S-palmitoyl cysteine (By similarity).
FT	LIPID 215 215	S-palmitoyl cysteine (By similarity).
FT	LIPID 216 216	S-palmitoyl cysteine (By similarity).
FT	CARBOHYD 49 49	N-linked (GlcNAc. ) (Potential).
SEQ	SEQUENCE 225 AA; 25084 MW; 7889619FP99A59C9D CRC64;	

  

Query Match	66.7%;	Score 16;	DB 1;	Length 225;
Best Local Similarity	100.0%;	Pred. No. 1.5e-08;		
Matches 16;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

  

Qy	1	LRFDSQTSKSIPEQETN 16	
Db	34	LRFDSQTSKSIPEQETN 49	

  

RESULT 6	
CD9_BOVIN	
ID_CD9_BOVIN	STANDARD; PRT; 225 AA.
AC	P30932;
DT	01-JUL-1993 (Rel. 26, Created)
DT	01-JUL-1993 (Rel. 26, Last sequence update)
DT	13-SEP-2005 (Rel. 48, Last annotation update)
DE	Names antigen.
GN	CD9; CD9 antigen.
OS	Bos taurus (Bovine).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC	Peccora; Bovidae; Bovinae; Bos.
OC	NCBI_TaxId=9913;
	[1]
RP	NUCLEOTIDE SEQUENCE [MRNA].
RC	TISSUE=Ocular ciliary epithelium;
RX	MEDLINE=93054422; PubMed=1339429;
RA	Martin-Alonso J.M., Hernando N., Ghosh S., Coca-Prados M.;
RT	"Molecular cloning of the bovine CD9 antigen from ocular ciliary epithelial cells";
RL	J. Biochem. 112:63-67(1992).
CC	- FUNCTION: Involved in platelet activation and aggregation.
CC	- Regulates paranodal junction formation. Required for gamete fusion. Involved in cell adhesion, cell motility and tumor metastasis (By similarity).
CC	- SUBUNIT: Forms both disulfide-linked homodimers and higher homooligomers as well as heterooligomers with other members of the tetraspanin family. Associates with CR2/CD21 and with PTGFRN/CD9PI (By similarity).
CC	- SUBCELLULAR LOCATION: Integral membrane protein.
CC	- PM: Phosphorylated on tyrosine following B-cell activation (By similarity).

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RC STRAIN-C57BL/6J; TISSUE=Kidney;  
 RX MEDLINE=23254683; PubMed=12466851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nakaishi I., Furuno M., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojibori T.,  
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schriml L.M., Kanapin A., Matsuda H., Baralov S., Beisel K.W.,  
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G.,  
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shinada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,  
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs";  
 RL Nature 420:563-573 (2002).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RX MEDLINE=2338257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McKean P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S.E., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Yung A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [4]  
 RP ROLE IN PARANODAL FORMATION, AND TISSUE SPECIFICITY.  
 RX PubMed=10700183; DOI=10.1038/73502;  
 RA Kaji K., Oda S., Shikano T., Ohnuki T., Uematsu Y., Sakagami J.,  
 RA Tada N., Miyazaki S., Kudo A.;  
 RT "The gamete fusion process is defective in eggs of Cd9-deficient  
 RT mice";  
 RL Nat. Genet. 24:279-282 (2000).  
 RN [5]  
 RP ROLE IN PARANODAL FORMATION, AND TISSUE SPECIFICITY.  
 RX PubMed=14715942; DOI=10.1523/JNEUROSCI.1484-03.2004;  
 RA Ishibashi T., Ding L., Ikenaka K., Inoue Y., Miyado K., Mekada E.,  
 RA Baba H.;  
 RT "Tetrapanin protein Cd9 is a novel paranodal component regulating  
 RT paranodal junctional formation";  
 RL J. Neurosci. 24:96-102 (2004).  
 RN [6]  
 RP FUNCTION AS RECEPTOR FOR PSG17.  
 RX PubMed=11805154; DOI=10.1084/jem.20011741;  
 RA Waterhouse R., Ha C., Dveksler G.S.;  
 RT "Murine CD9 is the receptor for pregnancy-specific glycoprotein 17";  
 RL J. Exp. Med. 195:277-282 (2002).  
 CC -!- FUNCTION: Involved in platelet activation and aggregation.  
 CC Regulates paranodal junction formation. Required for gamete  
 CC fusion. Involved in cell adhesion, cell motility and tumor  
 CC metastasis. Acts as a receptor for PSG17.  
 CC -!- SUBUNIT: Forms both disulfide-linked homodimers and higher  
 CC homooligomers as well as heterooligomers with other members of the  
 CC tetrapanin family. Associates with CR2/CD21 and with PTGFRN/CD9P1  
 CC (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- TISSUE SPECIFICITY: Expressed predominantly in the peripheral  
 CC nervous system.  
 CC -!- PTM: Phosphorylated on tyrosine following B-cell activation (By  
 CC similarity).  
 CC -!- SIMILARITY: Belongs to the tetrapanin (TM4SF) family.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL; L08115; AAA37405.1; -; mRNA.  
 CC EMBL; AK002251; BAB21965.1; -; mRNA.  
 CC EMBL; AK012793; BAB28473.1; -; mRNA.  
 CC EMBL; BC070474; AAH70474.1; -; mRNA.  
 CC F01; I49589; I49589.  
 CC Ensembl; ENSMUSG00000030342; Mus musculus.  
 CC MGI; MGI:88348; Cd9.  
 CC GO; GO:0005887; C: integral to plasma membrane; ISS.  
 CC GO; GO:0005886; C: plasma membrane; TAS.  
 CC GO; GO:0005515; P: protein binding; IPI.  
 CC GO; GO:0007155; P: cell adhesion; ISS.  
 CC GO; GO:0006928; P: cell motility; ISS.  
 CC GO; GO:0007342; P: fusion of sperm to egg plasma membrane; IDA.  
 CC GO; GO:0030913; P: paranodal junction formation; IDA.  
 CC GO; GO:0030168; P: platelet activation; ISS.  
 CC InterPro; IPR000301; Transmem 4.  
 CC Pfam; PF00335; Tetrapanin; I.  
 CC PRINTS; PR00259; TMFOUR.  
 CC PROSITE; PS00421; TM4.1; 1.  
 CC Antigen; Cell adhesion; Fertilization; Glycoprotein; Lipoprotein;  
 CC Palmitate; Phosphorylation; Transmembrane.  
 CC INIT MET 0  
 CC TOPO\_DOM 1 11  
 CC TRANSMEM 12 32  
 CC TOPO\_DOM 33 52  
 CC TRANSMEM 53 73  
 CC TOPO\_DOM 74 84  
 CC TRANSMEM 85 108  
 CC TOPO\_DOM 109 192  
 CC TRANSMEM 193 218  
 CC TOPO\_DOM 219 225  
 CC LIPID 8 8  
 CC LIPID 75 75  
 CC LIPID 76 76  
 CC LIPID 84 84  
 CC LIPID 215 215  
 CC LIPID 216 216  
 CC CARBOHYD 49 49  
 CC SEQUENCE 225 AA; 25127 MW; 2BBE40B8D7C31BC0 CRC64;  
 Query Match 58.3%; Score 14; DB 1; Length 225;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LRFDSQTKSIFEQE 14  
 DB 34 LRFDSQTKSIFEQE 47

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RESULT 8
CD9_PIG
ID CD9_PIG STANDARD; PRT; 225 AA.
AC QW03;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE CD9 antigen.
GN Name=CD9;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
TISSUE=Smooth muscle;
RX PubMed=14610355; DOI=10.1159/000074170;
RA Yubero N., Jimenez-Marín A., Yerle M., Morera L., Barbancho M.J.,
RA Lilanes D., Garrido J.J.;
RT "Molecular cloning, expression pattern and chromosomal mapping of pig
RT CD9 antigen.";
RL Cytogenet. Genome Res. 101:143-146(2003).
CC -!- FUNCTION: Involved in platelet activation and aggregation.
CC -!- REGULATION: paraneural junction formation. Required for gamete
CC fusion. Involved in cell adhesion, cell motility and tumor
CC metastasis (By similarity).
CC -!- SUBUNIT: Forms both disulfide-linked homodimers and higher
CC homooligomers as well as heterooligomers with other members of the
CC tetraspanin family. Associates with CR2/CD21 and with PTGFRN/CD9p1
CC (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- PTM: Phosphorylated on tyrosine following B-cell activation (By
CC similarity).
CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AY072785; AAL69966.1; -; mRNA.
CC GO; GO:0005887; C:integral to plasma membrane; ISS.
CC GO; GO:0005515; P:protein binding; ISS.
CC GO; GO:0007155; P:cell adhesion; ISS.
CC GO; GO:0006928; P:cell motility; ISS.
CC GO; GO:0007342; P:fusion of sperm to egg plasma membrane; ISS.
CC GO; GO:0030913; P:paxanodal junction formation; ISS.
CC GO; GO:0030168; P:platelet activation; ISS.
CC InterPro; IPR000301; Transmem 4.
CC Pfam; PF00335; Tetraspanin; 1.
CC PRINTS; PR00259; TMFOUR.
CC PROSITE; PS00421; TM4_1; 1.
CC
CC Antigen; Cell adhesion; Fertilization; Glycoprotein; Lipoprotein;
CC Palmitate; Phosphorylation; Transmembrane.
FT INIT_MET 0 0 By similarity.
FT TOPO_DOM 1 11 Cytoplasmic (potential).
FT TRANSMEM 12 32 Potential.
FT TOPO_DOM 33 52 Extracellular (potential).
FT TRANSMEM 53 73 Potential.
FT TOPO_DOM 74 84 Cytoplasmic (potential).
FT TRANSMEM 85 108 Potential.
FT TOPO_DOM 109 192 Extracellular (potential).
FT TRANSMEM 193 218 Potential.
FT TOPO_DOM 219 225 Cytoplasmic (potential).
FT LIPID 8 8 S-palmitoyl cysteine (By similarity).
FT LIPID 75 75 S-palmitoyl cysteine (By similarity).
FT LIPID 76 76 S-palmitoyl cysteine (By similarity).
FT LIPID 84 84 S-palmitoyl cysteine (By similarity).
FT LIPID 215 215 S-palmitoyl cysteine (By similarity).

RESULT 9
Q8MJ48_PIG PRELIMINARY; PRT; 226 AA.
AC Q8MJ48;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transmembrane protein CD9.
GN Name=CD9;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Heinz M., Huang C.A., Emery D.W., Giovino M.A., LeGuern A.,
RA Kurilla-Mahon B., Theodore P., Arn J.S., Sykes M., Mulligan R.C.,
RA Down J.D., Sachs D.H., Goodell M.A.;
RT "Use of CD9 Expression to Enrich for Porcine Hematopoietic
RT Progenitors.";
RL Exp. Hematol. 0:0-0(2002).
DR EMBL; AF525029; AAM81376.1; -; mRNA.
DR HSP; P60033; IG80.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR000301; Transmem 4.
DR Pfam; PF00335; Tetraspanin; 1.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM4_1; 1.
DR Transmembrane.
SQ SEQUENCE 226 AA; 25127 MW; 885C244477F95C23 CRC64;

Query Match 58.3%; Score 14; DB 1; Length 226;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSQTSIFEQE 14
DB 35 LRFDSQTSIFEQE 48

RESULT 10
CD9_FELCA STANDARD; PRT; 225 AA.
AC P40239;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE CD9 antigen.
GN Name=CD9;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC Felinae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX PubMed=7753050; DOI=10.1016/0161-5890(95)00008-3;
RA Willett B.J., Neil J.C.;
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RT "cDNA cloning and eukaryotic expression of feline CD9." ;
RL Mol. Immunol. 32:417-423(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA].
RA Morikawa S.;
RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Involved in platelet activation and aggregation.
CC Regulates paranodal junction formation. Required for gamete
CC fusion. Involved in cell adhesion, cell motility and tumor
CC metastasis (By similarity).
CC SUBUNIT: Forms both disulfide-linked homodimers and higher
CC homooligomers as well as heterooligomers with other members of the
CC tetraspanin family. Associates with CR2/CD21 and with PTGFRN/CD9P1
CC (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- PTM: Phosphorylated on tyrosine following B-cell activation (By
CC similarity).
CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; L35275; AAA92867.1; -; mRNA.
DR EMBL; D30786; BAA06452.1; -; mRNA.
DR GO; GO:0005887; C:integral to plasma membrane; ISS.
DR GO; GO:0005515; F:protein binding; ISS.
DR GO; GO:0007155; P:cell adhesion; ISS.
DR GO; GO:0006928; P:cell motility; ISS.
DR GO; GO:0007342; P:fusion of sperm to egg plasma membrane; ISS.
DR GO; GO:0030913; P:paranodal junction formation; ISS.
DR GO; GO:0030168; P:platelet activation; ISS.
DR InterPro; IPR000301; Transmem_4.
DR Pfam; PF00335; Tetraspannin; 1.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM4_1, 1.
KW Antigen; Cell adhesion; Fertilization; Lipoprotein; Palmitate;
KW Phosphorylation; Transmembrane.
FT INIT MET 0 0 By similarity.
FT TOPO_DOM 1 11 Cytoplasmic (Potential).
FT TRANSMEM 12 32 Potential.
FT TOPO_DOM 33 52 Extracellular (Potential).
FT TRANSMEM 53 73 Potential.
FT TOPO_DOM 74 84 Cytoplasmic (Potential).
FT TRANSMEM 85 108 Potential.
FT TOPO_DOM 109 192 Extracellular (Potential).
FT TRANSMEM 193 218 Potential.
FT TOPO_DOM 219 225 Cytoplasmic (Potential).
FT LIPID 8 8 S-palmitoyl cysteine (By similarity).
FT LIPID 75 75 S-palmitoyl cysteine (By similarity).
FT LIPID 76 76 S-palmitoyl cysteine (By similarity).
FT LIPID 84 84 S-palmitoyl cysteine (By similarity).
FT LIPID 215 215 S-palmitoyl cysteine (By similarity).
FT LIPID 216 216 S-palmitoyl cysteine (By similarity).
FT CONFLICT 82 82 S -> Y (in Ref. 2).
SQ SEQUENCE 225 AA; 24927 MW; 5A049774501B03B3 CRC64;

Query Match 54.2%; Score 13; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSQTKSIFPQ 13
DB 34 LRFDSQTKSIFPQ 46
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RESULT 11
Q8AV92.PETMA
ID Q8AV92.PETMA PRELIMINARY; PRT; 228 AA.
AC Q8AV92;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)

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DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CD9-like protein.
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
OX NCBI_TaxID=7757;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Typhlosolis;
RX MEDLINE=23295056; PubMed=12391333; DOI=10.1073/pnas.212527699;
RA Uinuk-Ool T., Mayer W.E., Sato A., Dongak R., Cooper M.D., Klein J.;
RT "Lamprey lymphocyte-like cells express homologs of genes involved in
RT immunologically relevant activities of mammalian lymphocytes." ;
RL Proc. Natl. Acad. Sci. U.S.A. 99:14356-14361(2002).
DR EMBL; AY152677; AAG64299.1; -; mRNA.
DR HSSP; P60033; 1G8Q.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR000301; Transmem_4.
DR Pfam; PF00335; Tetraspannin; 1.
DR PRINTS; PR00259; TMFOUR.
SQ SEQUENCE 228 AA; 25331 MW; DDB0EAA31E98B935 CRC64;

Query Match 33.3%; Score 8; DB 2; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSQTK 8
DB 35 LRFDSQTK 42
|||||
|||||

RESULT 12
Q6GOE5.XENLA
ID Q6GOE5.XENLA PRELIMINARY; PRT; 228 AA.
AC Q6GOE5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE MGC80123 protein.
GN Name=MGC80123;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences." ;
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;

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RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
RA Richardson P.;  
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
RT initiative.";  
RL Dev. Dyn. 225:384-391(2002).  
RN [3]  
RN NUCLEOTIDE SEQUENCE.  
RP TISSUE=Spleen;  
RC Klein S., Gerhard D.S.;  
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
RL EMBL; BC072800; AAH72800.1; -, mRNA.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR InterPro; IPR000301; Transmem 4.  
DR Pfam; PF00335; Tetraspanin; I.  
DR PRINTS; PR00259; TMFOUR.  
DR PROSITE; PS00421; TM\_1; 1.  
SQ SEQUENCE 228 AA; 25155 MW; 9A826DEC2D9980A2 CRC64;  
  
Query Match 33.3%; Score 8; DB 2; Length 228;  
Best Local Similarity 100.0%; Pred. No. 2.6;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 LRFDSQTK 8  
Db 35 LRFDSQTK 42  
  
RESULT 13  
Q56F04\_9CAUD  
ID Q56F04\_9CAUD PRELIMINARY; PRT; 607 AA.  
AC Q56F04;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Gp60plus39.  
GN Name=Gp60plus39; ORFNames=PHG31p7;  
OS Aeromonas phage 31.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.  
OX NCBI\_TaxID=321023;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Nolan J.M., Petrov V., Bertrand C., Krisch H.M., Karam J.D.;  
RT "Comparative analysis of the Aeromonas bacteriophage 31 genome.";  
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY962392; AAX63496.1; -, Genomic DNA.  
SQ SEQUENCE 607 AA; 68086 MW; E772C3DD1FA916D7 CRC64;  
  
Query Match 33.3%; Score 8; DB 2; Length 607;  
Best Local Similarity 100.0%; Pred. No. 6.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 LRFDSQTK 8  
Db 323 LRFDSQTK 330  
  
RESULT 14  
Q6U9U5\_9CAUD  
ID Q6U9U5\_9CAUD PRELIMINARY; PRT; 607 AA.  
AC Q6U9U5;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Topoisomerase II large subunit.  
GN Name=Gp60plus39;  
OS Bacteriophage 44RR2.8t.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;  
OC T4-like viruses.  
OX NCBI\_TaxID=115987;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Nolan J.M., Petrov V., Bertrand C., Krisch H.M., Karam J.D.;

RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY375531; AAQ81326.1; -, Genomic DNA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.  
DR GO; GO:0006265; F:DNA topological change; IEA.  
DR InterPro; IPR003594; ATP bd ATPase.  
DR InterPro; IPR011558; DNA gyrase B.  
DR InterPro; IPR011241; DNA topoisom.  
DR Pfam; PF00204; DNA gyraseB; 1.  
DR PRINTS; PR00418; HATPase c; 1.  
DR ProDom; PD149633; DNA\_gyrase\_B; 1.  
DR SMART; SM00433; TOP2c; 1.  
KW ATP-binding; Isomerase; Nucleotide-binding; Topoisomerase.  
SQ SEQUENCE 607 AA; 68074 MW; AFDACD841EA8ADD1 CRC64;  
  
Query Match 33.3%; Score 8; DB 2; Length 607;  
Best Local Similarity 100.0%; Pred. No. 6.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 LRFDSQTK 8  
Db 323 LRFDSQTK 330  
  
RESULT 15  
Q76XL0\_9CAUD  
ID Q76XL0\_9CAUD PRELIMINARY; PRT; 607 AA.  
AC Q76XL0;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Topoisomerase II large subunit.  
OS Enterobacteria phage RB49.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;  
OC T4-like viruses.  
OX NCBI\_TaxID=50948;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=97250366; PubMed=9096222; DOI=10.1006/jmbi.1996.0867;  
RA Monod C., Repolla F., Kutateladze M., Tetart F., Krisch H.M.;  
RT "The genome of the pseudo T-even bacteriophages, a diverse group that  
RT resembles T4.";  
RL J. Mol. Biol. 267:237-249(1997).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=21062343; PubMed=11092834; DOI=10.1146/annurev.genet.34.1.439;  
RA Ang D., Keppel F., Klein G., Richardson A., Georgopoulos C.;  
RT "Genetic analysis of bacteriophage-encoded co-chaperonins.";  
RL Annu. Rev. Genet. 34:439-456(2000).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=21972795; PubMed=11976309;  
DOI=10.1128/JB.184.10.2789-2804.2002;  
RA Desplats C., Dez C., Tetart F., Eleaume H., Krisch H.M.;  
RT "Snapshot of the genome of the pseudo-T-even bacteriophage RB49.";  
RL J. Bacteriol. 184:2789-2804(2002).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RA Ang D., Richardson A., Mayer M.P., Keppel F., Krisch H.,  
RA Georgopoulos C.;  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RA Desplats C., Dez C., Tetart F., Eleaume H., Krisch H.M.;  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP NUCLEOTIDE SEQUENCE.  
RA Desplats C., Dez C., Tetart F., Eleaume H., Krisch H.M.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP NUCLEOTIDE SEQUENCE.  
RA Tetart F., Desplats C., Kutateladze M., Monod C., Ackermann H.-W.,

RA Krisch H.M.;  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
RN [8]  
RP NUCLEOTIDE SEQUENCE.  
RA Krisch H.M.;  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
RN [9]  
RP NUCLEOTIDE SEQUENCE.  
RA Zhao L., Tetart F., Krisch H.M., Arisaka F.;  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
RN [10]  
RP NUCLEOTIDE SEQUENCE.  
RA Thiemer C.A., Desplats C., Dez C., Tetart F., Eleaume H., Krisch H.M.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
RN [11]  
RP NUCLEOTIDE SEQUENCE.  
RA Krisch H.M.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
RN [12]  
RP NUCLEOTIDE SEQUENCE.  
RA Desplats C., Krisch H.M.;  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
RN [13]  
RP NUCLEOTIDE SEQUENCE.  
RA Letarov A.V., Krisch H.M., Tetart P.;  
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
RN [14]  
RP NUCLEOTIDE SEQUENCE.  
RA Bertrand C., Petrov V., Nolan J., Letarov A., Desplats C., Chin D.,  
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
RN [15]  
RP NUCLEOTIDE SEQUENCE.  
RA Karam J.D., Krisch H.M.;  
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
RN [16]  
RP NUCLEOTIDE SEQUENCE.  
RA EMBL; AY343333; AAL15132.2; -; Genomic\_DNA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.  
DR GO; GO:0006265; P:DNA topological change; IEA.  
DR InterPro; IPR003594; ATP bd ATPase.  
DR InterPro; IPR011558; DNA\_gyrase\_B.  
DR InterPro; IPR001241; DNA\_topoisomII.  
DR Pfam; PF00204; DNA\_gyraseB; 1.  
DR Pfam; PF02518; HATPase\_c; 1.  
DR PRINTS; PR00418; TPI2FAMILY.  
DR ProDom; PD149633; DNA\_gyrase\_B; 1.  
DR SMART; SM00387; HATPase\_c; 1.  
DR SMART; SM00433; TOP2c; 1.  
KW ATP-binding; Isomerase; Nucleotide-binding; Topoisomerase.  
SQ SEQUENCE 607 AA; 68461 MW; 3A6C4B35C7E66AFF CRC64;

Query Match 33.3%; Score 8; DB 2; Length 607;  
Best Local Similarity 100.0%; Pred.No. 6.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSQTK 8  
Db |||||  
323 LRFDSQTK 330

Search completed: January 20, 2006, 17:44:14  
Job time : 57.2308 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2006, 17:03:51 ; Search time 133.704 Seconds  
(without alignments)  
124.876 Million cell updates/sec

Title: US-10-619-323-4

Perfect score: 207

Sequence: 1 KDEPQRÉTLKAIHYALNCCGLAGVQFISDICPKDV 38

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- A\_Geneseq\_21.\*
- 1: Geneseq1980s.\*
  - 2: Geneseq1990s.\*
  - 3: Geneseq2000s.\*
  - 4: Geneseq2001s.\*
  - 5: Geneseq2002s.\*
  - 6: Geneseq2003as.\*
  - 7: Geneseq2003bs.\*
  - 8: Geneseq2004s.\*
  - 9: Geneseq2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	207	100.0	38	ADJ57561	Adj57561 Human CD9
2	207	100.0	227	AAR86834	Aar86834 Human CD9
3	207	100.0	227	ABB78366	Abb78366 Amino aci
4	207	100.0	227	AAE14636	Aae14636 Human CD9
5	207	100.0	227	ABU05057	Abu05057 Human exp
6	207	100.0	227	ABU05060	Abu05060 Human exp
7	207	100.0	227	ABW00436	Abw00436 Human CD9
8	207	100.0	227	ADK69862	Adk69862 Human CD9
9	207	100.0	227	ADI19366	Adi19366 Human CD9
10	207	100.0	227	AEA99005	Aea99005 Human CD9
11	207	100.0	228	AAR27525	Aar27525 Metastasi
12	207	100.0	228	ABBA4581	Abba4581 Human wou
13	207	100.0	228	ABU05059	Abu05059 Human exp
14	207	100.0	228	ABU05052	Abu05052 Human exp
15	207	100.0	228	ABU05048	Abu05048 Human exp
16	207	100.0	228	ABU05056	Abu05056 Human exp
17	207	100.0	228	ABU05049	Abu05049 Human exp
18	207	100.0	228	ABU05050	Abu05050 Human exp
19	207	100.0	228	ABU05053	Abu05053 Human exp
20	207	100.0	228	ABW01519	Abw01519 Protein #
21	207	100.0	228	ADD99037	Add99037 TAr278. 1
22	207	100.0	228	ADG32002	Adg32002 Human hom
23	207	100.0	228	ADJ57558	Adj57558 Human CD9
24	207	100.0	228	ADL26782	Adl26782 Human CD9

25	207	100.0	228	8	ADL82853	Adl82853 Human PRO
26	207	100.0	228	8	ADP23088	Adp23088 PRO polyp
27	207	100.0	228	8	ADR73450	Adr73450 Human CD9
28	207	100.0	228	9	ADV70263	Adv70263 Tumor-ass
29	207	100.0	228	9	ADV97163	Adv97163 Human CD9
30	207	100.0	228	9	ADY19604	Ady19604 PRO polyp
31	207	100.0	228	9	ADY14362	Ady14362 PRO polyp
32	207	100.0	228	9	AEB98450	Aeb98450 Human CD9
33	207	100.0	275	3	AAB43936	Aab43936 Human can
34	207	100.0	275	4	AAG75156	Aag75156 Human col
35	207	100.0	275	6	ABU05055	Abu05055 Human exp
36	207	100.0	275	6	ABU05054	Abu05054 Human exp
37	201	97.1	79	2	AAW35851	Aaw35851 Human CD9
38	201	97.1	79	6	ABU05058	Abu05058 Human exp
39	191	92.3	226	7	ADB85281	Adb85281 Rat G9 su
40	187	90.3	454	4	ABG14067	Abg14067 Novel hum
41	167	80.7	226	4	ABB44580	Abb44580 Mouse wou
42	167	80.7	226	5	ABB57234	Abb57234 Mouse isc
43	167	80.7	226	9	ADV25799	Adv25799 Mouse CD9
44	167	80.7	226	9	AEA55045	Aea55045 Mouse CD9
45	128	61.8	30	6	ABU05051	Abu05051 Human exp

ALIGNMENTS

RESULT 1

ADJ57561

ID ADJ57561 standard; protein; 38 AA.

AC ADJ57561;

DT 06-MAY-2004 (first entry)

DE Human CD9 fibronectin-binding domain polypeptide fragment.

XX Human; CD9; antithrombotic; antiarteriosclerotic; vasotropic;

KW haemostatic; angiogenic; cytostatic.

XX Homo sapiens.

XX WO2004007685-A2.

XX 22-JAN-2004.

PF 14-JUL-2003; 2003WO-US022050.

PR 12-JUL-2002; 2002US-0395864P.

XX (UYTE-) UNIV TENNESSEE RES FOUND.

PI Jennings LK, Longhurst CM, Cook GA, Bao J, Zhang C, White MM;

PI Crosseno JT, Lu Y;

DR WPI; 2004-122924/12.

XX Interfering with CD9 binding to fibronectin by binding a fibronectin-binding domain of the CD9 protein or polypeptide, useful in treating thrombosis, atherosclerosis, restenosis, bleeding disorders, angiogenesis and cancers.

PS Claim 7; SEQ ID NO 4; 126pp; English.

XX The present sequence is that of a polypeptide fragment from the fibronectin-binding domain of human CD9 ADJ57558. The peptide, or an antibody that binds to it, is used in claimed methods for: interfering with CD9 binding to fibronectin; modifying adhesion, motility or spreading of a CD9-expressing cell on fibronectin; inhibiting proliferation or survival of CD9-expressing cells; modifying pericellular fibronectin matrix assembly; modifying invasiveness of a cell through a collagen and/or laminin matrix; and modifying cell-to-cell interaction. The methods are based on the finding that increased CD9 expression is implicated in (i) decreased adhesiveness of cells to extracellular matrix

CC (via alpha5-beta-1 integrin) and/or decreased cell invasiveness and/or  
 CC decreased pericellular fibronectin matrix assembly, and/or (ii) increased  
 CC cell motility, spreading, proliferation, cell survival against apoptosis,  
 CC and/or cell-to-cell contacts. Conditions or disease states involving  
 CC proliferation or survival of CD9-expressing cells can be treated, e.g.  
 CC thrombosis, atherosclerosis, vein graft failure, restenosis, transplant  
 CC arteriopathy, bleeding disorders, angiogenesis, and primary and  
 CC metastatic cancers including breast cancer, prostate cancer, colon  
 CC cancer, melanoma, ovarian cancer, neuroblastoma, glioma and glioblastoma.  
 XX Sequence 38 AA;

Query Match 100.0%; Score 207; DB 8; Length 38;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-22;  
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETLLKAIHYALNCCGLAGGVQFISDICKPKDV 38  
 DB 1 KDEPQRETLLKAIHYALNCCGLAGGVQFISDICKPKDV 38

RESULT 2  
 AAR86834  
 ID AAR86834 standard; protein; 227 AA.  
 AC AAR86834;

DT 12-JUL-1996 (first entry)

DE Human CD9 sequence.

XX CD9 antigen; stimulated T cell; antibody; ligand; proliferation;  
 KW monoclonal antibody; ES5.2D8; 27 kD accessory protein; epitope;  
 KW immune response; cancer; infectious disease; growth factor.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Modified-site 51 /note= "Potential N-linked glycosylation site"  
 FT Modified-site 52 /note= "Potential N-linked glycosylation site"  
 FT Domain 111..194 /note= "Extracellular domain"  
 FT Domain 195..220 /note= "Transmembrane domain"  
 FT Domain 221..227 /note= "Cytoplasmic domain"

PN W09533823-A1.

XX 14-DEC-1995.

XX 01-DEC-1994; 94MO-US013782.

PR 03-JUN-1994; 94US-00253751.

PR 03-JUN-1994; 94US-00253964.

XX (USNA ) US SEC OF NAVY.

PA (UNMI ) UNIV MICHIGAN.

PA (REPK ) REPLIGEN CORP.

PA (DAND ) DANA FARBER CANCER INST INC.

XX June CH, Thompson CB, Nabel G, Gray GS, Rennert PD, Freeman GJ;

DR WPI; 1996-040230/04.

XX Selectively inducing CD8 positive T cell proliferation - by activating  
 PT the T cells and stimulating CD9 cell surface ligand, useful for  
 PT immuno:therapy of, e.g. cancer.

XX Example 10; Page 38-39; 79pp; English.

CC This sequence represents CD9 from the surface of stimulated T cells. The  
 CC antigen at residues 31-37 of human CD9 (see AAR86832) is bound by an  
 CC antibody or other ligand to stimulate the T cell population to  
 CC proliferate and expand leading to a 100- to 10000-fold increase in cell  
 CC number compared to the original population. The antigenic sequence fits  
 CC the generic sequence given in AAR86827. This epitope is recognised by the  
 CC monoclonal antibody (MAb) ES5.2D8. CD9 is a 27 kD accessory protein found  
 CC on activated T cells. The epitope was recognised by screening a phage  
 CC display library. Selective proliferation of an antigen-specific T cell  
 CC population is useful in cases where the immune response is to be up  
 CC regulated, e.g. in the treatment of cancer or infectious diseases. By  
 CC causing proliferation of the T cell population by stimulating T cell  
 CC epitope removes the need for exogenous growth factors or accessory cells  
 XX Sequence 227 AA;

Query Match 100.0%; Score 207; DB 2; Length 227;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-21;  
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETLLKAIHYALNCCGLAGGVQFISDICKPKDV 38  
 DB 134 KDEPQRETLLKAIHYALNCCGLAGGVQFISDICKPKDV 171

RESULT 3

ABE78366

ID ABB78366 standard; protein; 227 AA.

AC ABB78366;

DT 16-DEC-2002 (first entry)

DE Amino acid sequence of CD9.

XX T cell; T cell proliferation; infectious disease; cancer; immunotherapy;  
 KW immunotherapy; CD9.

OS Homo sapiens.

PN US2002115214-A1.

PD 22-AUG-2002.

PF 26-JAN-1996; 96US-00592711.

PR 23-NOV-1988; 88US-00275433.

PR 07-APR-1992; 92US-00864805.

PR 07-APR-1992; 92US-00864807.

PR 07-APR-1992; 92US-00864866.

PR 04-JUN-1993; 93US-00073223.

PR 03-JUN-1994; 94US-00253964.

PR 10-MAR-1995; 95US-00403253.

PR 04-MAY-1995; 95US-00435816.

XX (JUNE/) JUNE C H.

PA (THOM/) THOMPSON C B.

PA (NABEL/) NABEL G J.

PA (GRAY/) GRAY G S.

PA (RENN/) RENNERT P D.

PI June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;

XX WPI; 2002-712476/77.

XX Inducing a population of T cells to proliferate, by activating population  
 PT of T cells and stimulating an accessory molecule on the surface of the T  
 PT cells with a ligand which binds the accessory molecule.

XX Example 10; Page 25; 88pp; English.

CC The specification describes method for inducing a population of T cells  
 CC to proliferate. The method involves activating population of T cells,

CC stimulating an accessory molecule on T cell surface with a ligand  
 CC protein) which binds the molecule, to induce proliferation of T cells,  
 CC monitoring proliferation of T cells in response to continuing exposure to  
 CC the ligand, and reactivating and restimulating T cells when rate of  
 CC proliferation has decreased to induce further proliferation of the cells.  
 CC The method is useful for inducing proliferation of T cells, for use in  
 CC treatment of infectious disease, cancer and immunotherapy. The method  
 CC allows for the expansion of a population of T cells in numbers sufficient  
 CC to reconstitute an individual's total CD4+ or CD8+ T cell population.  
 CC The resulting T cell population can be genetically transduced and used  
 CC for immunotherapy or can be used in methods of in vitro analyses of  
 CC infectious agents. A population of tumour-infiltrating lymphocytes can be  
 CC obtained from an individual afflicted with cancer and the T cells  
 CC stimulated to proliferate to sufficient numbers. The resulting T cell  
 CC population can be genetically transduced to express tumour necrosis  
 CC factor (TNF) or other factor and restored to the individual. CD4+ T cells  
 CC expanded by this method are useful in the treatment of HIV infection in  
 CC an individual. The present sequence represents CD9, an antigen present on  
 CC the surface of activated T cells  
 XX

SQ Sequence 227 AA;

Query Match 100.0%; Score 207; DB 5; Length 227;

Best Local Similarity 100.0%; Pred. No. 3.8e-21;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAIHYALNCCGLAGVGFQFISDICKPKDV 38

DB 134 KDEPQRETLKAIHYALNCCGLAGVGFQFISDICKPKDV 171

RESULT 4

AAE14636

ID AAE14636 standard; protein; 227 AA.

XX AAE14636;

DT 16-JUL-2002 (first entry)

DE Human CD9 antigen.

XX T cell; CD3; accessory molecule; CD28; cancer; infectious disease;  
 KW immunotherapy; human immunodeficiency virus; HIV infection; cytokine;  
 KW human; CD9 antigen.

XX Homo sapiens.

XX US6352694-B1.

XX 05-MAR-2002.

XX 10-MAR-1995; 95US-00403253.

XX 03-JUN-1994; 94US-00253964.

XX (GEMY ) GENETICS INST INC.

XX (UNMI ) UNIV MICHIGAN.

PI June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;

XX WPI; 2002-314696/35.

XX Inducing T cell population to proliferate, useful in cancer therapy,  
 PT comprises activating T cells by contacting T cells in vitro with  
 PT immobilized anti-CD3 antibody and stimulating accessory molecule on T  
 PT cell surface.

XX Example 10; Col 42; 71pp; English.

XX The invention relates to a method of inducing T cell population to  
 CC proliferate for use in therapy comprising activating T cells by  
 CC contacting T cells in vitro with anti-CD3 antibody which is immobilised  
 CC on solid phase surface, and stimulating accessory molecule on T cell

CC surface in vitro with anti-CD28 antibody, or stimulatory form of natural  
 CC ligand for CD28 such as B7-1 or B7-2. The method is useful for inducing a  
 CC population of T cells to proliferate in sufficient numbers for use in  
 CC therapy e.g., for treating cancer or an infectious disease. The method  
 CC can be used to selectively expand the population of CD28<sup>+</sup>, CD4<sup>+</sup>, CD8<sup>+</sup>,  
 CC CD28RA<sup>+</sup> or CD28RO<sup>+</sup> T cells for immunotherapy. The T cell population  
 CC resulting by the method can be genetically transduced and used for  
 CC immunotherapy or can be used for in vitro analysis of infectious agents  
 CC such as human immunodeficiency virus (HIV). Proliferation of a population  
 CC of CD4<sup>+</sup> T cells obtained from an individual infected with HIV can be  
 CC achieved and the cells rendered resistant to HIV infection. Following the  
 CC expansion of the T cells to sufficient numbers, the expanded T cells are  
 CC restored to the individual. Also CD4<sup>+</sup> T cells expanded by the above  
 CC mentioned is useful for treating HIV infection in an individual. A  
 CC population of tumour-infiltrating lymphocytes can be obtained from an  
 CC individual afflicted with cancer and the T cells stimulated to  
 CC proliferate to sufficient numbers and restored to the individual. The  
 CC supernatants from cultures of T cells expanded from above mentioned  
 CC method are useful as a rich source of cytokines and can be used to  
 CC sustain T cells in vivo or ex vivo. Stimulating and expanding a  
 CC population of antigen specific T cells are useful in therapeutic  
 CC conditions where it is desirable to upregulate an immune response. The T  
 CC cell proliferation occurs in the absence of exogenous growth factors or  
 CC accessory cells. The present sequence is human CD9 antigen which is  
 CC expressed on surface of activated T cells  
 XX

SQ Sequence 227 AA;

Query Match 100.0%; Score 207; DB 5; Length 227;

Best Local Similarity 100.0%; Pred. No. 3.8e-21;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAIHYALNCCGLAGVGFQFISDICKPKDV 38

DB 134 KDEPQRETLKAIHYALNCCGLAGVGFQFISDICKPKDV 171

RESULT 5

ABU05057

ID ABU05057 standard; protein; 227 AA.

XX ABU05057;

XX 29-JAN-2003 (first entry)

XX Human expressed protein tag (EPT) #1723.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
 KW protease; protease inhibitor; transporter; cytoskeletal protein;  
 KW receptor; transcription factor; cancer; MHC;  
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX Homo sapiens.

XX WO200278524-A2.

XX 10-OCT-2002.

XX 28-MAR-2002; 2002WO-US009671.

XX 28-MAR-2001; 2001US-0279495P.

XX 21-MAY-2001; 2001US-0292544P.

XX 08-AUG-2001; 2001US-0310801P.

XX 01-OCT-2001; 2001US-0326370P.

XX 04-DEC-2001; 2001US-0336780P.

XX 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCOS INC.

XX Chiciz RM, Tomlinson AJ, Urban RG;

XX WPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.  
XX Example 2; SEQ ID NO 1723; 134pp; English.  
XX The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX Sequence 227 AA;  
SQ

Query Match 100.0%; Score 207; DB 6; Length 227;  
Best Local Similarity 100.0%; Pred. No. 3.8e-21;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETAKAIHYALNCCGLAGGVEQFTSDICPKDV 38  
|||||  
Db 134 KDEPQRETAKAIHYALNCCGLAGGVEQFTSDICPKDV 171  
|||||

RESULT 6  
ABU05060  
ID ABU05060 standard; protein; 227 AA.  
XX AC ABU05060;  
XX DT 29-JAN-2003 (first entry)  
XX DE Human expressed protein tag (EPT) #1726.  
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
XX OS Homo sapiens.  
XX PN WO200278524-A2.  
XX PD 10-OCT-2002.  
XX PF 28-MAR-2002; 2002WO-US0095671.  
XX PR 28-MAR-2001; 2001US-0279495P.  
PR 21-MAY-2001; 2001US-0292544P.  
PR 08-AUG-2001; 2001US-0310801P.  
PR 01-OCT-2001; 2001US-0326370P.  
PR 04-DEC-2001; 2001US-0336780P.  
PR 20-FEB-2002; 2002US-0358985P.  
XX PA (ZYCO-) ZYCOS INC.  
XX PI Chicx RM, Tomlinson AJ, Urban RG;  
XX WPI; 2003-040607/03.  
DR

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.  
XX Example 2; SEQ ID NO 1726; 134pp; English.  
XX The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX Sequence 227 AA;  
SQ

Query Match 100.0%; Score 207; DB 6; Length 227;  
Best Local Similarity 100.0%; Pred. No. 3.8e-21;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETAKAIHYALNCCGLAGGVEQFTSDICPKDV 38  
|||||  
Db 134 KDEPQRETAKAIHYALNCCGLAGGVEQFTSDICPKDV 171  
|||||

RESULT 7  
ABW00436  
ID ABW00436 standard; protein; 227 AA.  
XX AC ABW00436;  
XX DT 15-JAN-2004 (first entry)  
XX DE Human CD9 antigenic protein.  
XX KW HIV infection; human immunodeficiency virus; therapy; antigen; human.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
FT Domain 111..194  
FT /note= "Extracellular domain"  
FT Domain 195..220  
FT /note= "Transmembrane domain"  
FT Domain 221..227  
FT /note= "Cytoplasmic domain"  
XX US2003099643-A1.  
XX PD 29-MAY-2003.  
XX PF 08-JUL-1999; 99US-00350202.  
XX PR 23-NOV-1988; 88US-00275433.  
PR 22-NOV-1989; 89WO-US005304.  
PR 07-APR-1992; 92US-00864805.  
PR 07-APR-1992; 92US-00864807.  
PR 07-APR-1992; 92US-00864866.  
PR 04-JUN-1993; 93US-00073223.  
PR 03-JUN-1994; 94US-00253694.  
PR 10-MAR-1995; 95US-00403253.

XX (JUNE/) JUNE C H.  
 PA (THOM/) THOMPSON C B.  
 PA (NABEL/) NABEL G J.  
 PA (GRAY/) GRAY G S.  
 PA (RENN/) RENNERT P D.  
 XX

June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;  
 WPI; 2003-801206/75.

XX Treating HIV infection in individual by isolating T cells from  
 PT leukocytes, contacting T cells with anti-CD3 antibody for T cell  
 PT proliferation, separating antibody from T cells, monitoring proliferation  
 PT of T cells.  
 XX

XX Example 10; Page 23; Opp; English.

XX The present invention relates to a novel method of treating human  
 CC immunodeficiency virus (HIV) infection in an individual. The method  
 CC involves isolating population of CD4 T cells from leukocytes, contacting  
 CC population of CD4+ T cells with an anti-CD3 antibody for stimulating T  
 CC cell proliferation, separating antibody from T cells, monitoring  
 CC proliferation of T cells, restimulating T cells with antibody and  
 CC restoring T cells to individual. The present sequence is human CD9  
 CC antigenic protein. This sequence is used to illustrate the method of the  
 CC invention  
 XX

SQ Sequence 227 AA;  
 Query Match 100.0%; Score 207; DB 7; Length 227;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-21;  
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAIHYALNCCGLAGGVEQFISDICPKKDV 38  
 DB 134 KDEPQRETLKAIHYALNCCGLAGGVEQFISDICPKKDV 171  
 |||||

RESULT 8  
 ADK69862  
 ID ADK69862 standard; protein; 227 AA.  
 XX  
 AC ADK69862;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Human CD9 protein.  
 XX  
 KW CD28-associated signal; immunotherapy; infectious disease; cancer;  
 KW leukopheresis; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6534055-B1.  
 XX  
 PD 18-MAR-2003.  
 XX  
 PF 04-MAY-1995; 95US-00435816.  
 XX  
 PR 07-APR-1992; 92US-00864805.  
 PR 07-APR-1992; 92US-00864807.  
 PR 07-APR-1992; 92US-00864866.  
 PR 04-JUN-1993; 93US-00073223.  
 PR 03-JUN-1994; 94US-00253964.  
 PR 10-MAR-1995; 95US-00403253.  
 XX  
 PA (GEMY ) GENETICS INST INC.  
 XX  
 PI June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;  
 XX WPI; 2003-531074/50.  
 XX

PT Expanding T cell populations, useful for preparing renewable sources of T  
 PT cells (e.g. CD4+) for immunotherapy or diagnostics, by stimulating a CD28  
 PT -associated signal on the surface of the cells with an anti-CD28  
 PT antibody, B7-1 or B7-2.  
 XX  
 PS Example 10; SEQ ID NO 6; 82pp; English.

XX The invention relates to a method for expanding a population of T cells  
 CC to about 100-100000-fold over the original T cell population, or to about  
 CC 10 log 10 to 12 log 12. The method comprises stimulating a CD28-  
 CC associated signal on the surface of the T cells with agent comprising an  
 CC anti-CD28 antibody, B7-1 or B7-2. The method is useful for inducing a  
 CC population of T cells (e.g. CD4+, CD28+, CD8+, CD28RA+ or CD28RO+ T  
 CC cells) to proliferate. The method is particularly useful for preparing a  
 CC renewable source of CD4+ T cells. The expanded T cell population can be  
 CC genetically transduced, and used for immunotherapy to treat a variety of  
 CC human diseases (e.g. infectious diseases or cancer), or used in  
 CC diagnostic protocols. T cells were obtained from leukopheresis of a  
 CC normal donor, and purified with FICOLL density gradient centrifugation,  
 CC followed by magnetic immunobead sorting. The present sequence is CD9 used  
 CC in the exemplification of the invention.  
 XX

SQ Sequence 227 AA;  
 Query Match 100.0%; Score 207; DB 7; Length 227;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-21;  
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAIHYALNCCGLAGGVEQFISDICPKKDV 38  
 DB 134 KDEPQRETLKAIHYALNCCGLAGGVEQFISDICPKKDV 171  
 |||||

RESULT 9  
 ADI19366  
 ID ADI19366 standard; protein; 227 AA.  
 XX  
 AC ADI19366;  
 XX  
 DT 15-APR-2004 (first entry)  
 XX  
 DE Human CD9 protein.  
 XX  
 KW T cell; immunotherapy; therapy; HIV infection; cancer;  
 KW infectious disease; cytostatic; antimicrobial; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2004001829-A1.  
 XX  
 PD 01-JAN-2004.  
 XX  
 PF 17-MAR-2003; 2003US-00390330.  
 XX  
 PR 23-NOV-1989; 88US-00275433.  
 PR 22-NOV-1989; 89WO-US005304.  
 PR 07-APR-1992; 92US-00864805.  
 PR 07-APR-1992; 92US-00864807.  
 PR 07-APR-1992; 92US-00864866.  
 PR 04-JUN-1993; 93US-00073223.  
 PR 03-JUN-1994; 94US-00253964.  
 PR 10-MAR-1995; 95US-00403253.  
 PR 04-MAY-1995; 95US-00435816.  
 XX  
 PA (JUNE/) JUNE C H.  
 PA (THOM/) THOMPSON C B.  
 PA (NABEL/) NABEL G J.  
 PA (GRAY/) GRAY G S.  
 PA (RENN/) RENNERT P D.  
 XX  
 PI June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;  
 XX WPI; 2004-061648/06.  
 XX

XX Inducing a population of T cells to proliferate, for immunotherapy or  
 PT treating HIV infection, cancer or infectious disease, comprises  
 PT activating a population of T cells and stimulating an accessory molecule  
 PT on the surface of the T cells.

XX Example 10; SEQ ID NO 6; 80pp; English.

XX The invention relates to a method for inducing a population of T cells to  
 CC proliferate. The method comprising activating a population of T cells,  
 CC and stimulating an accessory molecule on the surface of the T cells with  
 CC a ligand that binds the accessory molecule. The invention is useful for  
 CC immunotherapy, for treating HIV infection, cancer or infectious disease,  
 CC or in diagnostic applications. The present sequence is human CD9 protein.

XX Sequence 227 AA;

Query Match 100.0%; Score 207; DB 8; Length 227;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-21; Indels 0; Gaps 0;  
 Matches 38; Conservative 0; Mismatches 0;

QY 1 KDEPQRETILKAHYALNCCGLAGGVQFISDIPCCKDV 38  
 |||||  
 Db 134 KDEPQRETILKAHYALNCCGLAGGVQFISDIPCCKDV 171

RESULT 10

AEA89005  
 ID AEA89005 standard; protein; 227 AA.

AC AEA89005;

DT 25-AUG-2005 (first entry)

DE Human CD9 antigenic protein, SEQ ID NO: 6.

KW Cell therapy; immune stimulation; immunotherapy; diagnosis;  
 KW infectious disease; antimicrobial; infection; cancer; cytostatic;  
 KW neoplasia; CD9; antigen.

OS Homo sapiens.

PN US6905681-B1.

PD 14-JUN-2005.

PF 08-JUL-1999; 99US-00349915.

PR 03-JUN-1994; 94US-00253964.

PR 10-MAR-1995; 95US-00403253.

XX (GEMY ) GENETICS INST INC.

PA (UNMI ) UNIV MICHIGAN.

PA (USNA ) US SEC OF NAVY.

XX June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;

XX WPI; 2005-464777/47.

XX Ex vivo proliferation of T cell population for use in therapy, involves  
 PT contacting population of T cells with surface having anti-CD3 antibody  
 PT and anti-CD28 antibody for activating T cells and stimulating activated T  
 PT cells, respectively.

XX Example 10; SEQ ID NO 6; 76pp; English.

XX The present invention relates to a method of including ex vivo  
 CC proliferation of a population of T cells to sufficient numbers for use in  
 CC therapy. The method involves contacting population of T cells with  
 CC surface having anti-CD3 antibody and anti-CD28 antibody for activating T  
 CC cells and stimulating activated T cells, respectively. The invention is  
 CC useful for treating cancer and infectious disease and also useful in cell  
 CC therapy. The present sequence is the human CD9 antigenic protein. This

CC sequence is bound by an ES5.2D8 monoclonal antibody, which is to be used  
 CC to stimulate a CD8+ T cell population.

XX Sequence 227 AA;

Query Match 100.0%; Score 207; DB 9; Length 227;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-21; Indels 0; Gaps 0;  
 Matches 38; Conservative 0; Mismatches 0;

QY 1 KDEPQRETILKAHYALNCCGLAGGVQFISDIPCCKDV 38  
 |||||

Db 134 KDEPQRETILKAHYALNCCGLAGGVQFISDIPCCKDV 171

RESULT 11

AAR27525

ID AAR27525 standard; protein; 228 AA.

AC AAR27525;

DT 25-MAR-2003 (revised)

DT 05-MAR-1993 (first entry)

DE Metastasis controlling peptide.

KW M31-15 monoclonal antibody; cancer cell motility; prophylaxis; treatment;  
 KW lung; glioblastoma.

OS Homo sapiens.

PN EP508417-A2.

PD 14-OCT-1992.

PF 09-APR-1992; 92EP-00106093.

PR 12-APR-1991; 91JP-00079996.

PR 17-APR-1991; 91JP-00085396.

PR 07-FEB-1992; 92JP-00022321.

XX (TAKE ) TAKEDA CHEM IND LTD.

PA (MIYA/) MIYAKE M.

XX Ikeyama S, Koyama M, Senoo M, Miyake M;

XX WPI; 1992-341723/42.

DR N-PSDB; AAQ29182.

XX New monoclonal antibody M31-15 specific for metastasis-controlling  
 PT peptide - useful for treating and preventing cancer and metastasis.

XX Claim 7; Fig 4; 3app; English.

XX The sequence is that of a cancer cell surface protein which is capable of  
 CC suppressing the motility of cancer cells. It is specifically recognised  
 CC by the monoclonal (Mab) antibody M31-15 which is useful for suppressing  
 CC cancer metastasis. The polypeptide and Mab M31-15 are therefore useful in  
 CC the prophylaxis and treatment of cancer, e.g. lung, glioblastoma and  
 CC other metastatic cancers. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 228 AA;

Query Match 100.0%; Score 207; DB 2; Length 228;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-21;  
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETILKAHYALNCCGLAGGVQFISDIPCCKDV 38  
 |||||

Db 135 KDEPQRETILKAHYALNCCGLAGGVQFISDIPCCKDV 172

RESULT 12

ABB44581

```
ID ABB44581 standard; protein; 228 AA.
XX
AC ABB44581;
XX
DT 25-JAN-2002 (first entry)
XX
DE Human wound healing related polypeptide SEQ ID NO 38.
XX
XX Human; mouse; vulnery; dermatological; skin disorder; wound healing;
KW gene therapy.
XX
XX Homo sapiens.
XX
XX CA2325226-A1.
XX
XX 17-MAY-2001.
XX
XX 16-NOV-2000; 2000CA-02325226.
XX
XX 17-NOV-1999; 99DE-01055349.
XX
XX 17-DEC-1999; 99US-0172511P.
XX
XX 20-JUN-2000; 2000DE-01030149.
XX
XX (SWIT-) SWITCH BIOTECH AG.
XX
XX Regenhogen J, Wolf E, Goppelt A, Werner S, Halle J;
XX WPI; 2001-433142/47.
XX
XX Use of novel polypeptide or its variant or nucleic acid encoding the
PT polypeptide for diagnosing and/or preventing and/or treating skin
PT disorders and/or treatment in wound healing or for identifying active
PT substances.
XX
XX Disclosure; Page 193-194; 265pp; English.
XX
XX The invention relates to the use of a polypeptide (ABB44544-ABB44601,
CC ABB44606-ABB44623) or its variant or encoding nucleic acid (ABA81990-
CC ABA81995, ABA82016-ABA82032) with vulnerary and/or dermatological
CC activity for the diagnosis, prevention and treatment of skin disorders
CC and treatment in wound healing or for the identification of
CC pharmacologically active substances. The nucleic acids are useful in gene
CC therapy. Note: The printed sequence listing for this specification was
CC incomplete, terminating part way through SEQ ID NO 106. The remaining
CC data was obtained from EPO data for an equivalent patent (EP1114862)
XX
XX Sequence 228 AA;
SQ
Query Match 100.0%; Score 207; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 3.8e-21;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAIHYALNCCGLAGGVQFISDICPKKDV 38
DB 135 KDEPQRETLKAIHYALNCCGLAGGVQFISDICPKKDV 172

RESULT 13
ABU05059
ID ABU05059 standard; protein; 228 AA.
XX
AC ABU05059;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1725.
XX
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX

ID ABB44581 standard; protein; 228 AA.
XX
AC ABB44581;
XX
DT 25-JAN-2002 (first entry)
XX
DE Human wound healing related polypeptide SEQ ID NO 38.
XX
XX Human; mouse; vulnery; dermatological; skin disorder; wound healing;
KW gene therapy.
XX
XX Homo sapiens.
XX
XX CA2325226-A1.
XX
XX 17-MAY-2001.
XX
XX 16-NOV-2000; 2000CA-02325226.
XX
XX 17-NOV-1999; 99DE-01055349.
XX
XX 17-DEC-1999; 99US-0172511P.
XX
XX 20-JUN-2000; 2000DE-01030149.
XX
XX (SWIT-) SWITCH BIOTECH AG.
XX
XX Regenhogen J, Wolf E, Goppelt A, Werner S, Halle J;
XX WPI; 2001-433142/47.
XX
XX Use of novel polypeptide or its variant or nucleic acid encoding the
PT polypeptide for diagnosing and/or preventing and/or treating skin
PT disorders and/or treatment in wound healing or for identifying active
PT substances.
XX
XX Disclosure; Page 193-194; 265pp; English.
XX
XX The invention relates to the use of a polypeptide (ABB44544-ABB44601,
CC ABB44606-ABB44623) or its variant or encoding nucleic acid (ABA81990-
CC ABA81995, ABA82016-ABA82032) with vulnerary and/or dermatological
CC activity for the diagnosis, prevention and treatment of skin disorders
CC and treatment in wound healing or for the identification of
CC pharmacologically active substances. The nucleic acids are useful in gene
CC therapy. Note: The printed sequence listing for this specification was
CC incomplete, terminating part way through SEQ ID NO 106. The remaining
CC data was obtained from EPO data for an equivalent patent (EP1114862)
XX
XX Sequence 228 AA;
SQ
Query Match 100.0%; Score 207; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 3.8e-21;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAIHYALNCCGLAGGVQFISDICPKKDV 38
DB 135 KDEPQRETLKAIHYALNCCGLAGGVQFISDICPKKDV 172

RESULT 14
ABU05052
ID ABU05052 standard; protein; 228 AA.
XX
AC ABU05052;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1718.
XX
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX

OS Homo sapiens.
XX
XX WO200278524-A2.
XX
XX 10-OCT-2002.
XX
XX 28-MAR-2002; 2002WO-US009671.
XX
XX 28-MAR-2001; 2001US-0279495P.
XX
XX 21-MAY-2001; 2001US-0292544P.
XX
XX 08-AUG-2001; 2001US-0310801P.
XX
XX 01-OCT-2001; 2001US-0326370P.
XX
XX 04-DEC-2001; 2001US-0336780P.
XX
XX 20-FEB-2002; 2002US-0358985P.
XX
XX (ZYCO-) ZYCOS INC.
XX
XX Chicx RM, Tomlinson AJ, Urban RG;
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 1725; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 228 AA;
SQ
Query Match 100.0%; Score 207; DB 6; Length 228;
Best Local Similarity 100.0%; Pred. No. 3.8e-21;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAIHYALNCCGLAGGVQFISDICPKKDV 38
DB 135 KDEPQRETLKAIHYALNCCGLAGGVQFISDICPKKDV 172

RESULT 14
ABU05052
ID ABU05052 standard; protein; 228 AA.
XX
AC ABU05052;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1718.
XX
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
```

```

OS Homo sapiens.
XX WO200278524-A2.
XX 10-OCT-2002.
XX
XX 28-MAR-2002; 2002WO-US009671.
XX
XX 28-MAR-2001; 2001US-0279495P.
XX 21-MAY-2001; 2001US-0292544P.
XX 08-AUG-2001; 2001US-0310801P.
XX 01-OCT-2001; 2001US-0326370P.
XX 04-DEC-2001; 2001US-0336780P.
XX 20-FEB-2002; 2002US-0358985P.
XX
XX (ZYCO-) ZYCOS INC.
XX
XX Chiciz RM, Tomlinson AJ, Urban RG;
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.
XX
XX Example 2; SEQ ID NO 1718; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and
XX polynucleotides are particularly useful for treating or preventing
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX lymphoma or leukaemia. These are also useful for screening agents for
XX treating the above mentioned diseases. This sequence represents an
XX expressed protein tag (EPT) isolated from human tissue for translational
XX profiling. Note: This sequence does not appear in the printed
XX specification but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 228 AA;
XX
XX Query Match 100.0%; Score 207; DB 6; Length 228;
XX Best Local Similarity 100.0%; Pred. No. 3.8e-21;
XX Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 KDEPQRETAKAIHYALNCCGLAGGVEQFISDICPKKDV 38
DB 135 KDEPQRETAKAIHYALNCCGLAGGVEQFISDICPKKDV 172

RESULT 15
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ID ABU05048 standard; protein; 228 AA.
XX
XX AC ABU05048;
XX
XX DT 29-JAN-2003 (first entry)
XX
XX DE Human expressed protein tag (EPT) #1714.
XX
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX KW protease; protease inhibitor; transporter; cytoskeletal protein;
XX KW receptor; transcription factor; cancer; MHC;
XX KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX

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Search completed: January 20, 2006, 17:16:06  
Job time : 133.704 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2006, 17:10:37 ; Search time 26.7407 Seconds  
(without alignments)  
117.486 Million cell updates/sec

Title: US-10-619-323-4

Perfect score: 207  
Sequence: 1 KDSFQRETLKAIHYALNCCGLAGVQFISDIPCKDV 38

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	207	100.0	227	1	US-08-253-751-6
3	207	100.0	227	1	US-08-453-925-6
4	207	100.0	227	2	US-08-403-253A-6
5	207	100.0	227	2	US-08-435-816A-6
6	207	100.0	227	2	US-09-350-202-6
7	207	100.0	227	2	US-08-592-711-6
8	207	100.0	227	2	US-09-349-915B-6
9	207	100.0	228	1	US-08-408-222B-1
10	201	97.1	79	2	US-08-630-172-8
11	201	97.1	79	2	US-09-375-419-8
12	157	75.8	29	1	US-08-254-493-5
13	157	75.8	29	1	US-08-408-222B-5
14	54	26.1	542	2	US-09-583-110-4474
15	54	26.1	546	2	US-09-107-433-3368
16	53.5	25.8	343	1	US-08-454-196-6
17	53.5	25.8	343	1	US-08-286-819A-4
18	53.5	25.8	343	2	US-08-980-357-4
19	53.5	25.8	343	2	US-09-064-033-6
20	53.5	25.8	343	2	US-09-291-046-6
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25	52	25.1	416	2	US-09-252-991A-28499
26	52	25.1	422	2	US-09-252-991A-22959
27	51.5	24.9	547	2	US-08-461-722-2

28 51.5 24.9 547 2 US-08-336-251-2 Sequence 2, Appli  
29 51.5 24.9 547 2 US-09-468-041-2 Sequence 2, Appli  
30 51.5 24.9 547 4 PCT-US94-06362-2 Sequence 2, Appli  
31 51.5 24.9 548 1 US-08-467-822-32 Sequence 32, Appli  
32 51.5 24.9 548 2 US-09-472-971-3 Sequence 3, Appli  
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36 51 24.6 1836 2 US-10-162-012-24 Sequence 24, Appli  
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38 50.5 24.4 764 2 US-07-741-453A-60 Sequence 60, Appli  
39 50 24.2 29 1 US-08-254-493-6 Sequence 6, Appli  
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43 50 24.2 434 2 US-10-759-277-2 Sequence 2, Appli  
44 50 24.2 434 2 US-09-930-440C-4 Sequence 4, Appli  
45 50 24.2 462 2 US-09-248-796A-14397 Sequence 14397, A

#### ALIGNMENTS

RESULT 1  
US-08-254-493-1  
; Sequence 1, Application US/08254493  
; Patent No. 5439886  
; GENERAL INFORMATION:  
; APPLICANT: IKEYAMA, SHUICHI  
; APPLICANT: KOYAMA, MASARU  
; APPLICANT: MIYAKE, MASAYUKI  
; APPLICANT: SENOO, MASAHARU  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND  
; TITLE OF INVENTION: PRODUCTION THEREOF  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
; STREET: 130 WATER STREET  
; CITY: BOSTON  
; STATE: MASSACHUSETTS  
; COUNTRY: US  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/254,493  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/865552  
; FILING DATE: 09-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 0799996-1991  
; FILING DATE: 12-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 085396-1991  
; FILING DATE: 17-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 0223321-1992  
; FILING DATE: 07-FEB-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: RESNICK, DAVID S.  
; REGISTRATION NUMBER: 34235  
; REFERENCE/DOCKET NUMBER: 41777  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 523-3400  
; TELEFAX: (617) 523-6440  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:

; LENGTH: 227 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-254-493-1

Query Match 100.0%; Score 207; DB 1; Length 227;  
Best Local Similarity 100.0%; Pred. No. 3.8e-23;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAIHYALNCCGLAGGVEQFISD1CPKDV 38  
|||||  
Db 134 KDEPQRETLKAIHYALNCCGLAGGVEQFISD1CPKDV 171

## RESULT 2

US-08-253-751-6  
; Sequence 6, Application US/08253751

; Patent No. 5858358

; GENERAL INFORMATION:

; APPLICANT: June, Carl H.

; APPLICANT: Thompson, Craig B.

; APPLICANT: Nabel, Gary J.

; APPLICANT: Gray, Gary S.

; APPLICANT: Rennert, Paul D.

; APPLICANT: Freeman, Gordon J.

; TITLE OF INVENTION: METHODS FOR SELECTIVELY STIMULATING

; TITLE OF INVENTION: PROLIFERATION OF T-CELLS

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 STATE STREET, SUITE 510

; CITY: BOSTON

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII TEXT

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/253,751

; FILING DATE: 3 JUNE 1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/073,223

; FILING DATE: 4 JUNE 1993

; APPLICATION NUMBER: US 08/200,947

; FILING DATE: 23 FEB 1994

; APPLICATION NUMBER: US 07/864,805

; FILING DATE: 7 APR 1992

; APPLICATION NUMBER: US 08/247,505

; FILING DATE: 23 MAY 1994

; APPLICATION NUMBER: US 07/864,866

; FILING DATE: 7 APR 1992

; APPLICATION NUMBER: 08/218,155

; FILING DATE: 25 MAR 1994

; APPLICATION NUMBER: US 07/864,807

; FILING DATE: 7 APR 1992

; APPLICATION NUMBER: US 07/902,467

; FILING DATE: 16 JUNE 1992

; APPLICATION NUMBER: US 07/275,433

; FILING DATE: 23 NOV 1988

; ATTORNEY/AGENT INFORMATION:

; NAME: MANDRAGOURAS, AMY E.

; REGISTRATION NUMBER: 36,207

; REFERENCE/DOCKET NUMBER: RPI-002CPB

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 227-7400

; TELEFAX: (617) 227-5941

; INFORMATION FOR SEQ ID NO: 6:

; LENGTH: 227 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-253-751-6

Query Match 100.0%; Score 207; DB 1; Length 227;  
Best Local Similarity 100.0%; Pred. No. 3.8e-23;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAIHYALNCCGLAGGVEQFISD1CPKDV 38  
|||||  
Db 134 KDEPQRETLKAIHYALNCCGLAGGVEQFISD1CPKDV 171

## RESULT 3

US-08-453-925-6

; Sequence 6, Application US/08453925

; Patent No. 5883223

; GENERAL INFORMATION:

; APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.

; APPLICANT: Gray, Gary S., Rennert, Paul D., Freeman, Gordon J.

; TITLE OF INVENTION: METHODS FOR SELECTIVELY STIMULATING

; TITLE OF INVENTION: PROLIFERATION OF T-CELLS

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 STATE STREET, SUITE 510

; CITY: BOSTON

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII TEXT

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/453,925

; FILING DATE: 30 MAY 1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/253,751

; FILING DATE: 3 JUNE 1994

; APPLICATION NUMBER: US 08/073,223

; FILING DATE: 4 JUNE 1993

; APPLICATION NUMBER: US 08/200,947

; FILING DATE: 23 FEB 1994

; APPLICATION NUMBER: US 07/864,805

; FILING DATE: 7 APR 1992

; APPLICATION NUMBER: US 08/247,505

; FILING DATE: 23 MAY 1994

; APPLICATION NUMBER: US 07/864,866

; FILING DATE: 7 APR 1992

; APPLICATION NUMBER: 08/218,155

; FILING DATE: 25 MAR 1994

; APPLICATION NUMBER: US 07/864,807

; FILING DATE: 7 APR 1992

; APPLICATION NUMBER: US 07/902,467

; FILING DATE: 16 JUNE 1992

; APPLICATION NUMBER: US 07/275,433

; FILING DATE: 23 NOV 1988

; ATTORNEY/AGENT INFORMATION:

; NAME: MANDRAGOURAS, AMY E.

; REGISTRATION NUMBER: 36,207

; REFERENCE/DOCKET NUMBER: RPI-002CPB

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 227-7400

; TELEFAX: (617) 227-5941

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 227 amino acids

; TYPE: amino acid

; TOPOLOGY: linear



US-08-435-816A-6

Query Match 100.0%; Score 207; DB 2; Length 227;  
Best Local Similarity 100.0%; Pred. No. 3.8e-23;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAIHYALNCCGLAGGVEQFISDICKPKDV 38  
|||||  
Db 134 KDEPQRETLKAIHYALNCCGLAGGVEQFISDICKPKDV 171

## RESULT 6

US-09-350-202-6  
; Sequence 6, Application US/09350202  
; Patent No. 6887466  
; GENERAL INFORMATION:  
; APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.  
; APPLICANT: Gray, Gary S., Rennert, Paul D.  
; TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/350,202  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/403,253  
; FILING DATE: March 10, 1995  
; APPLICATION NUMBER: US 08/253,964  
; FILING DATE: 3 JUNE 1994  
; APPLICATION NUMBER: US 08/073,223  
; FILING DATE: 4 JUNE 1993  
; APPLICATION NUMBER: US 08/200,947  
; FILING DATE: 23 FEB 1994  
; APPLICATION NUMBER: US 07/864,805  
; FILING DATE: 7 APR 1992  
; APPLICATION NUMBER: US 08/247,505  
; FILING DATE: 23 MAY 1994  
; APPLICATION NUMBER: US 07/864,866  
; FILING DATE: 7 APR 1992  
; APPLICATION NUMBER: US 08/218,155  
; FILING DATE: 25 MAR 1994  
; APPLICATION NUMBER: US 07/864,807  
; FILING DATE: 7 APR 1992  
; APPLICATION NUMBER: US 07/902,467  
; FILING DATE: 16 JUNE 1992  
; APPLICATION NUMBER: US 07/275,433  
; FILING DATE: 23 NOV 1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mandragouras, Amy E.  
; REGISTRATION NUMBER: 36,207  
; REFERENCE/DOCKET NUMBER: RPI-002CP2  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 742-4214  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 227 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-350-202-6

Query Match 100.0%; Score 207; DB 2; Length 227;  
Best Local Similarity 100.0%; Pred. No. 3.8e-23;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAIHYALNCCGLAGGVEQFISDICKPKDV 38  
|||||  
Db 134 KDEPQRETLKAIHYALNCCGLAGGVEQFISDICKPKDV 171

## RESULT 7

US-08-592-711-6  
; Sequence 6, Application US/08592711  
; Patent No. 6905680  
; GENERAL INFORMATION:  
; APPLICANT: June, Carl H.  
; APPLICANT: Thompson, Craig B.  
; APPLICANT: Nabel, Gary J.  
; APPLICANT: Gray, Gary S.  
; APPLICANT: Rennert, Paul D.  
; TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/592,711  
; FILING DATE: 26-JAN-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/435,816  
; FILING DATE: 4-MAY-1995  
; APPLICATION NUMBER: US 08/403,253  
; FILING DATE: 10-MARCH-1995  
; APPLICATION NUMBER: US 08/253,964  
; FILING DATE: 3-JUNE-1994  
; APPLICATION NUMBER: US 08/073,223  
; FILING DATE: 4-JUNE-1993  
; APPLICATION NUMBER: US 08/200,947  
; FILING DATE: 23-FEB-1994  
; APPLICATION NUMBER: US 07/864,805  
; FILING DATE: 7-APR-1992  
; APPLICATION NUMBER: US 08/247,505  
; FILING DATE: 23-MAY-1994  
; APPLICATION NUMBER: US 07/864,866  
; FILING DATE: 7-APR-1992  
; APPLICATION NUMBER: US 08/218,155  
; FILING DATE: 25-MAR-1994  
; APPLICATION NUMBER: US 07/864,807  
; FILING DATE: 7-APR-1992  
; APPLICATION NUMBER: US 07/902,467  
; FILING DATE: 16-JUNE-1992  
; APPLICATION NUMBER: US 07/275,433  
; FILING DATE: 23-NOV-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mandragouras, Amy E.  
; REGISTRATION NUMBER: 36,207  
; REFERENCE/DOCKET NUMBER: RPI-002CP4  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 227 amino acids  
; TYPE: amino acid

; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-08-592-711-6

Query Match 100.0%; Score 207; DB 2; Length 227;  
Best Local Similarity 100.0%; Pred. No. 3.8e-23;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEPQRETAKAIHYALNCCGLAGGVEQFISDICPKDV 38  
Db 134 KDEPQRETAKAIHYALNCCGLAGGVEQFISDICPKDV 171

## RESULT 8

US-09-349-915B-6

; Sequence 6, Application US/09349915B

; Patent No. 6905681

; GENERAL INFORMATION:

; APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.

; Gray, Gary S., Rennert, Paul D.

; TITLE OF INVENTION: Methods For Selectively Stimulating

; Proliferation Of T-Cells

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: HALE AND DORR LLP

; STREET: 60 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/349,915B

; FILING DATE: 01-Aug-2000

; CLASSIFICATION: &lt;Unknown&gt;

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/403,253

; FILING DATE: March 10, 1995

; APPLICATION NUMBER: US 08/253,964

; FILING DATE: 3 JUNE 1994

; APPLICATION NUMBER: US 08/073,223

; FILING DATE: 4 JUNE 1993

; APPLICATION NUMBER: US 08/200,947

; FILING DATE: 23 FEB 1994

; APPLICATION NUMBER: US 07/864,805

; FILING DATE: 7 APR 1992

; APPLICATION NUMBER: US 08/247,505

; FILING DATE: 23 MAY 1994

; APPLICATION NUMBER: US 07/864,866

; FILING DATE: 7 APR 1992

; APPLICATION NUMBER: US 08/218,155

; FILING DATE: 25 MAR 1994

; APPLICATION NUMBER: US 07/864,807

; FILING DATE: 7 APR 1992

; APPLICATION NUMBER: US 07/902,467

; FILING DATE: 16 JUNE 1992

; APPLICATION NUMBER: US 07/275,433

; FILING DATE: 23 NOV 1988

; ATTORNEY/AGENT INFORMATION:

; NAME: Suparcho, Colleen

; REGISTRATION NUMBER: 39,850

; REFERENCE/DOCKET NUMBER: 36119-125 (US10)

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 526-6564

; TELEFAX: (617) 526-5000

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 227 amino acids

; TYPE: amino acid

; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-349-915B-6

Query Match 100.0%; Score 207; DB 2; Length 227;  
Best Local Similarity 100.0%; Pred. No. 3.8e-23;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEPQRETAKAIHYALNCCGLAGGVEQFISDICPKDV 38  
Db 134 KDEPQRETAKAIHYALNCCGLAGGVEQFISDICPKDV 171

## RESULT 9

US-08-408-222B-1

; Sequence 1, Application US/08408222B

; Patent No. 5776727

; GENERAL INFORMATION:

; APPLICANT: Ikeyama, Shuichi

; APPLICANT: Koyama, Masaru

; APPLICANT: Miyake, Masayuki

; APPLICANT: Senoo, Masaharu

; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: Dike, Bronstein, Roberts &amp; Cushman

; STREET: 130 Water Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/408,222B

; FILING DATE: 22-MAR-1995

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/254,493

; FILING DATE: 06-JUN-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP-079996-1991

; FILING DATE: 12-APR-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP-085396-1991

; FILING DATE: 14-APR-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP-022321-1992

; FILING DATE: 07-FEB-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Resnick, David S.

; REGISTRATION NUMBER: 34,235

; REFERENCE/DOCKET NUMBER: 41777-DIV

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-523-3400

; TELEFAX: 617-523-6440

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 228 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: internal

; ORIGINAL SOURCE:

; US-08-408-222B-1

Query Match 100.0%; Score 207; DB 1; Length 228;  
Best Local Similarity 100.0%; Pred. No. 3.8e-23;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAIHYALNCCGLAGVGEQFISDICKPKDV 38  
|||||  
Db 135 KDEPQRETLKAIHYALNCCGLAGVGEQFISDICKPKDV 172

## RESULT 10

US-08-630-172-8  
; Sequence 8, Application US/08630172  
; Patent No. 6060054  
; GENERAL INFORMATION:  
; APPLICANT: Staerz, Uwe  
; TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T  
; TITLE OF INVENTION: LYMPHOCYTE VETO  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS: 41  
; ADDRESSEE: Sheridan Ross & McIntosh  
; STREET: 1700 Lincoln Street, 35th Floor  
; CITY: Denver  
; STATE: Colorado  
; COUNTRY: U.S.  
; ZIP: 80203  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/630,172  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Connell, Gary J.  
; REGISTRATION NUMBER: 32,020  
; REFERENCE/DOCKET NUMBER: 2879-36  
; TELEPHONE: (303) 863-9700  
; TELEFAX: (303) 863-0223  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 79 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-630-172-8

Query Match 97.1%; Score 201; DB 2; Length 79;  
Best Local Similarity 97.4%; Pred. No. 8.7e-23;  
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAIHYALNCCGLAGVGEQFISDICKPKDV 38  
|||||  
Db 23 KDEPQRETLKAIHYALNCCGLAGVGEQFISDICKPKDV 60

## RESULT 11

US-09-375-419-8  
; Sequence 8, Application US/09375419  
; Patent No. 626490  
; GENERAL INFORMATION:  
; APPLICANT: Staerz, Uwe  
; TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T  
; TITLE OF INVENTION: LYMPHOCYTE VETO  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS: 41  
; ADDRESSEE: Sheridan Ross & McIntosh  
; STREET: 1700 Lincoln Street, 35th Floor  
; CITY: Denver  
; STATE: Colorado  
; COUNTRY: U.S.

; ZIP: 80203  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/375,419  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/630,172  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Connell, Gary J.  
; REGISTRATION NUMBER: 32,020  
; REFERENCE/DOCKET NUMBER: 2879-36  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (303) 863-9700  
; TELEFAX: (303) 863-0223  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 79 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-375-419-8

Query Match 97.1%; Score 201; DB 2; Length 79;  
Best Local Similarity 97.4%; Pred. No. 8.7e-23;  
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAIHYALNCCGLAGVGEQFISDICKPKDV 38  
|||||  
Db 23 KDEPQRETLKAIHYALNCCGLAGVGEQFISDICKPKDV 60

## RESULT 12

US-08-254-493-5  
; Sequence 5, Application US/08254493  
; Patent No. 5439886  
; GENERAL INFORMATION:  
; APPLICANT: IKEYAMA, SHUICHI  
; APPLICANT: KOYAMA, MASARU  
; APPLICANT: MIYAKE, MASAYUKI  
; APPLICANT: SENOO, MASAHARU  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND  
; TITLE OF INVENTION: PRODUCTION THEREOF  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
; STREET: 130 WATER STREET  
; CITY: BOSTON  
; STATE: MASSACHUSETTS  
; COUNTRY: US  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/254,493  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/865552  
; FILING DATE: 09-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 0799996-1991  
; FILING DATE: 12-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 085396-1991

; FILING DATE: 17-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 022321-1992  
; FILING DATE: 07-FEB-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: RESNICK, DAVID S.  
; REGISTRATION NUMBER: 34235  
; REFERENCE/DOCKET NUMBER: 41777  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 523-3400  
; TELEFAX: (617) 523-6440  
; TELEX: 200291 STEE UR  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 29 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-254-493-5

Query Match 75.8%; Score 157; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 1.2e-16;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QRETLKAIHYALNCCGLAGGVEQFISDIC 33  
DB 1 QRETLKAIHYALNCCGLAGGVEQFISDIC 29

RESULT 13  
US-08-408-222B-5  
; Sequence 5, Application US/08408222B  
; Patent No. 5776727  
; GENERAL INFORMATION:  
; APPLICANT: Ikeyama, Shuichi  
; APPLICANT: Koyama, Masaru  
; APPLICANT: Miyake, Masauyuki  
; APPLICANT: Senoo, Masaharu  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pike, Bronstein, Roberts & Cushman  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/408,222B  
; FILING DATE: 22-MAR-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/254,493  
; FILING DATE: 06-JUN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP-079996-1991  
; FILING DATE: 12-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP-085396-1991  
; FILING DATE: 14-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP-022321-1992  
; FILING DATE: 07-FEB-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Resnick, David S.  
; REGISTRATION NUMBER: 34,235  
; REFERENCE/DOCKET NUMBER: 41777-DIV

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-523-3400  
; TELEFAX: 617-523-6440  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 29 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-408-222B-5

Query Match 75.8%; Score 157; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 1.2e-16;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QRETLKAIHYALNCCGLAGGVEQFISDIC 33  
DB 1 QRETLKAIHYALNCCGLAGGVEQFISDIC 29

RESULT 14  
US-09-583-110-4474  
; Sequence 4474, Application US/09583110  
; Patent No. 6699703  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al.  
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus  
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics  
; FILE REFERENCE: PATH00-07A  
; CURRENT APPLICATION NUMBER: US/09/583,110  
; CURRENT FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/107,433  
; PRIOR FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: US 60/085,131  
; PRIOR FILING DATE: 1998-05-12  
; PRIOR APPLICATION NUMBER: US 60/051,553  
; PRIOR FILING DATE: 1997-07-02  
; NUMBER OF SEQ ID NOS: 5322  
; SEQ ID NO 4474  
; LENGTH: 542  
; TYPE: PRT  
; ORGANISM: Streptococcus pneumoniae  
US-09-583-110-4474

Query Match 26.1%; Score 54; DB 2; Length 542;  
Best Local Similarity 35.5%; Pred. No. 14;  
Matches 11; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAIHYALNCCGLAGGVEQFISD 31  
DB 390 KDAQSQDFMQAVSYQLNEVGKNEVVQITSD 420

RESULT 15  
US-09-107-433-3368  
; Sequence 3368, Application US/09107433  
; Patent No. 6800744  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID  
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE  
; THERAPEUTICS  
; NUMBER OF SEQUENCES: 5206  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02354  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD-ROM ISO9660  
; COMPUTER: <Unknown>

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/ OPERATING SYSTEM: <Unknown>
/ SOFTWARE: <Unknown>
/ CURRENT APPLICATION DATA:
/   APPLICATION NUMBER: US/09/107,433
/   FILING DATE: 30-Jun-1998
/ PRIOR APPLICATION DATA:
/   APPLICATION NUMBER: 60/ 085131
/   FILING DATE: May 12, 1998
/   APPLICATION NUMBER: 60/051553
/   FILING DATE: July 2, 1997
/ ATTORNEY/AGENT INFORMATION:
/   NAME: Ariniello, Pamela Deneke
/   REGISTRATION NUMBER: 40,489
/   REFERENCE/DOCKET NUMBER: CTC-011
/ TELECOMMUNICATION INFORMATION:
/   TELEPHONE: (781)893-5007
/   TELEFAX: (781)893-8277
/ INFORMATION FOR SEQ ID NO: 3368:
/   SEQUENCE CHARACTERISTICS:
/     LENGTH: 546 amino acids
/     TYPE: amino acid
/     TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: YES
/ ORIGINAL SOURCE:
/   ORGANISM: Streptococcus pneumoniae
/ FEATURE:
/   NAME/KEY: misc feature
/   LOCATION: (B) LOCATION 1...546
/ SEQUENCE DESCRIPTION: SEQ ID NO: 3368:
US-09-107-433-3368

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Query Match      26.1%; Score 54; DB 2; Length 546;
Best Local Similarity 35.5%; Pred. No. 14;
Matches 11; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

QY      1 KDEPQRETLKATHYALNCCGLAGGVQFI SD 31
Db      394 KDQASQDFWQVSVYQLNEVGKNEVVQITSD 424

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Search completed: January 20, 2006, 17:23:44  
 Job time : 27.7407 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2006, 17:11:18 ; Search time 76.4691 Seconds  
(without alignments)  
207.633 Million cell updates/sec

Title: US-10-619-323-4

Perfect score: 207

Sequence: 1 KDEPQRETLKAIHYALNCCGLAGGVQFISDICPKKDV 38

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA\_Main:  
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2: /cgn2\_6/prodata/1/pubpaa/US08\_PUBCOMB.pap:  
3: /cgn2\_6/prodata/1/pubpaa/US09\_PUBCOMB.pap:  
4: /cgn2\_6/prodata/1/pubpaa/US10A\_PUBCOMB.pap:  
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6: /cgn2\_6/prodata/1/pubpaa/US11\_PUBCOMB.pap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	207	100.0	38	US-10-619-323-4	Sequence 4, Appli
2	207	100.0	227	US-08-592-711-6	Sequence 6, Appli
3	207	100.0	227	US-09-183-055-6	Sequence 6, Appli
4	207	100.0	227	US-09-350-202-6	Sequence 6, Appli
5	207	100.0	227	US-10-390-330-6	Sequence 6, Appli
6	207	100.0	227	US-10-473-127-1723	Sequence 1723, Ap
7	207	100.0	227	US-10-473-127-1726	Sequence 1726, Ap
8	207	100.0	228	US-10-156-136-39	Sequence 39, Appl
9	207	100.0	228	US-10-331-496A-41	Sequence 41, Appl
10	207	100.0	228	US-10-619-323-1	Sequence 1, Appli
11	207	100.0	228	US-10-794-899-97	Sequence 97, Appl
12	207	100.0	228	US-10-473-127-1714	Sequence 1714, Ap
13	207	100.0	228	US-10-473-127-1715	Sequence 1715, Ap
14	207	100.0	228	US-10-473-127-1716	Sequence 1716, Ap
15	207	100.0	228	US-10-473-127-1718	Sequence 1718, Ap
16	207	100.0	228	US-10-473-127-1719	Sequence 1719, Ap
17	207	100.0	228	US-10-473-127-1722	Sequence 1722, Ap
18	207	100.0	228	US-10-473-127-1725	Sequence 1725, Ap
19	207	100.0	228	US-10-789-378-18	Sequence 18, Appl
20	207	100.0	228	US-10-482-029-144	Sequence 144, App
21	207	100.0	228	US-10-852-335A-187	Sequence 187, App
22	207	100.0	228	US-11-041-419-39	Sequence 39, Appl
23	207	100.0	275	US-09-925-301-1381	Sequence 1381, Ap
24	207	100.0	275	US-10-106-698-5930	Sequence 5930, Ap
25	207	100.0	275	US-10-473-127-1720	Sequence 1720, Ap
26	207	100.0	275	US-10-473-127-1721	Sequence 1721, Ap
27	201	97.1	79	US-10-473-127-1724	Sequence 1724, Ap

28	191	92.3	226	4	US-10-205-194-162	Sequence 162, App
29	187	90.3	454	5	US-10-450-763-44426	Sequence 44426, A
30	128	61.8	30	5	US-10-473-127-1717	Sequence 1717, Ap
31	105	50.7	209	4	US-10-106-698-6825	Sequence 6825, Ap
32	103	49.8	74	4	US-10-425-115-240878	Sequence 240878, A
33	60.5	29.2	96	4	US-10-425-115-216442	Sequence 216442, A
34	60	29.0	22	4	US-10-619-323-7	Sequence 7, Appli
35	58	28.0	217	4	US-10-437-963-109106	Sequence 109106, A
36	56	27.1	198	4	US-10-424-599-266302	Sequence 266302, A
37	55	26.6	64	4	US-10-424-599-171926	Sequence 171926, A
38	55	26.6	373	6	US-11-097-143-15411	Sequence 15411, A
39	54.5	26.3	943	4	US-10-282-122A-48512	Sequence 48512, A
40	54	26.1	546	5	US-10-617-320-3368	Sequence 3368, Ap
41	53.5	25.8	151	5	US-10-488-074-56	Sequence 56, Appl
42	53.5	25.8	200	5	US-10-488-074-40	Sequence 40, Appl
43	53.5	25.8	343	4	US-10-186-886-23	Sequence 23, Appl
44	53.5	25.8	343	5	US-10-952-915-4	Sequence 4, Appli
45	53.5	25.8	2296	5	US-10-952-915-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1

US-10-619-323-4  
; Sequence 4, Application US/10619323  
; Publication No. US20040136985A1  
; GENERAL INFORMATION:  
; APPLICANT: Jennings, Lisa K.  
; APPLICANT: Longhurst, Celia M.  
; APPLICANT: Cook, George A.  
; APPLICANT: Bao, Jianxiong  
; APPLICANT: Zhang, Chunxiang  
; APPLICANT: White, Melanie M.  
; APPLICANT: Croseno, Jr., Joseph T.  
; APPLICANT: Lu, Yi  
; TITLE OF INVENTION: METHODS OF MODIFYING BEHAVIOR OF CD9-EXPRESSING CELLS  
; FILE REFERENCE: 20609/241  
; CURRENT APPLICATION NUMBER: US/10/619,323  
; CURRENT FILING DATE: 2003-07-14  
; PRIOR APPLICATION NUMBER: 60/395,864  
; PRIOR FILING DATE: 2002-07-12  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: CD9 peptide  
US-10-619-323-4

Query Match 100.0%; Score 207; DB 4; Length 38;  
Best Local Similarity 100.0%; Pred. No. 2.4e-22;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KDEPQRETLKAIHYALNCCGLAGGVQFISDICPKKDV 38  
DB 1 KDEPQRETLKAIHYALNCCGLAGGVQFISDICPKKDV 38

RESULT 2

US-08-592-711-6  
; Sequence 6, Application US/08592711  
; Publication No. US20020115214A1  
; GENERAL INFORMATION:  
; APPLICANT: June, Carl H.  
; APPLICANT: Thompson, Craig B.  
; APPLICANT: Nabel, Gary J.  
; APPLICANT: Gray, Gary S.  
; APPLICANT: Rennett, Paul D.  
; TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells  
; NUMBER OF SEQUENCES: 14

;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: LAHIVE & COCKFIELD  
;/ STREET: 60 State Street  
;/ CITY: Boston  
;/ STATE: Massachusetts  
;/ COUNTRY: USA  
;/ ZIP: 02109  
;/  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/592,711  
;/ FILING DATE: 26-JAN-1996  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: US 08/435,816  
;/ FILING DATE: 4-MAY-1995  
;/ APPLICATION NUMBER: US 08/403,253  
;/ FILING DATE: 10-MARCH-1995  
;/ APPLICATION NUMBER: US 08/253,964  
;/ FILING DATE: 3-JUNE-1994  
;/ APPLICATION NUMBER: US 08/073,223  
;/ FILING DATE: 4-JUNE-1993  
;/ APPLICATION NUMBER: US 08/200,947  
;/ FILING DATE: 23-FEB-1994  
;/ APPLICATION NUMBER: US 07/864,805  
;/ FILING DATE: 7-APR-1992  
;/ APPLICATION NUMBER: US 08/247,505  
;/ FILING DATE: 23-MAY-1994  
;/ APPLICATION NUMBER: US 07/864,866  
;/ FILING DATE: 7-APR-1992  
;/ APPLICATION NUMBER: US 08/218,155  
;/ FILING DATE: 25-MAR-1994  
;/ APPLICATION NUMBER: US 07/864,807  
;/ FILING DATE: 7-APR-1992  
;/ APPLICATION NUMBER: US 07/902,467  
;/ FILING DATE: 16-JUNE-1992  
;/ APPLICATION NUMBER: US 07/275,433  
;/ FILING DATE: 23-NOV-1988  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Mandragouras, Amy E.  
;/ REGISTRATION NUMBER: 36,207  
;/ REFERENCE/DOCKET NUMBER: RPI-002CP4  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (617) 227-7400  
;/ TELEFAX: (617) 227-5941  
;/ INFORMATION FOR SEQ ID NO: 6:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 227 amino acids  
;/ TYPE: amino acid  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: protein  
;/ US-08-592-711-6

Query Match 100.0%; Score 207; DB 2; Length 227;  
Best Local Similarity 100.0%; Pred. No. 1.7e-21;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAIHYALNCCGLAGGVEQFISDICKPKDV 38  
Db 134 KDEPQRETLKAIHYALNCCGLAGGVEQFISDICKPKDV 171

## RESULT 3

US-09-183-055-6  
; Sequence 6, Application US/09183055  
; Publication No. US20020076407A1  
; GENERAL INFORMATION:  
; APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.  
; APPLICANT: Gray, Gary S., Rennert, Paul D.  
; TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells

;/ NUMBER OF SEQUENCES: 14  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: HALE AND DORR LLP  
;/ STREET: 60 State Street  
;/ CITY: Boston  
;/ STATE: Massachusetts  
;/ COUNTRY: USA  
;/ ZIP: 02109  
;/  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/09/183,055  
;/ FILING DATE: 30-Oct-1998  
;/ CLASSIFICATION: <Unknown>  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: US 08/403,253  
;/ FILING DATE: March 10, 1995  
;/ APPLICATION NUMBER: US 08/253,964  
;/ FILING DATE: 3 JUNE 1994  
;/ APPLICATION NUMBER: US 08/073,223  
;/ FILING DATE: 4 JUNE 1993  
;/ APPLICATION NUMBER: US 08/200,947  
;/ FILING DATE: 23 FEB 1994  
;/ APPLICATION NUMBER: US 07/864,805  
;/ FILING DATE: 7 APR 1992  
;/ APPLICATION NUMBER: US 08/247,505  
;/ FILING DATE: 23 MAY 1994  
;/ APPLICATION NUMBER: US 07/864,866  
;/ FILING DATE: 7 APR 1992  
;/ APPLICATION NUMBER: US 08/218,155  
;/ FILING DATE: 25 MAR 1994  
;/ APPLICATION NUMBER: US 07/864,807  
;/ FILING DATE: 7 APR 1992  
;/ APPLICATION NUMBER: US 07/902,467  
;/ FILING DATE: 16 JUNE 1992  
;/ APPLICATION NUMBER: US 07/275,433  
;/ FILING DATE: 23 NOV 1988  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Superko, Colleen  
;/ REGISTRATION NUMBER: 39,850  
;/ REFERENCE/DOCKET NUMBER: 36119-125US8  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (617) 526-6564  
;/ TELEFAX: (617) 526-5000  
;/ INFORMATION FOR SEQ ID NO: 6:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 227 amino acids  
;/ TYPE: amino acid  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: protein  
;/ SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
;/ US-09-183-055-6

Query Match 100.0%; Score 207; DB 3; Length 227;  
Best Local Similarity 100.0%; Pred. No. 1.7e-21;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAIHYALNCCGLAGGVEQFISDICKPKDV 38  
Db 134 KDEPQRETLKAIHYALNCCGLAGGVEQFISDICKPKDV 171

## RESULT 4

US-09-350-202-6  
; Sequence 6, Application US/09350202  
; Publication No. US20030099643A1  
; GENERAL INFORMATION:  
; APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.  
; APPLICANT: Gray, Gary S., Rennert, Paul D.  
; TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells

NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/350,202  
FILING DATE: 3 JUNE 1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/403,253  
FILING DATE: March 10, 1995  
APPLICATION NUMBER: US 08/253,964  
FILING DATE: 3 JUNE 1994  
APPLICATION NUMBER: US 08/073,223  
FILING DATE: 4 JUNE 1993  
APPLICATION NUMBER: US 08/200,947  
FILING DATE: 23 FEB 1994  
APPLICATION NUMBER: US 07/864,805  
FILING DATE: 7 APR 1992  
APPLICATION NUMBER: US 08/247,505  
FILING DATE: 23 MAY 1994  
APPLICATION NUMBER: US 07/864,866  
FILING DATE: 7 APR 1992  
APPLICATION NUMBER: US 08/218,155  
FILING DATE: 25 MAR 1994  
APPLICATION NUMBER: US 07/864,807  
FILING DATE: 7 APR 1992  
APPLICATION NUMBER: US 07/902,467  
FILING DATE: 16 JUNE 1992  
APPLICATION NUMBER: US 07/275,433  
FILING DATE: 23 NOV 1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: RPI-002CP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 742-4214  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 227 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-350-202-6

Query Match 100.0%; Score 207; DB 3; Length 227;  
Best Local Similarity 100.0%; Pred. No. 1.7e-21;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETAKAIHYALNCCGLAGGVQFISDICPKKDV 38  
Db 134 KDEPQRETAKAIHYALNCCGLAGGVQFISDICPKKDV 171

RESULT 5  
US-10-390-330-6  
Sequence 6, Application US/10390330  
Publication No. US20040001829A1  
GENERAL INFORMATION:  
APPLICANT: June, Carl H.  
APPLICANT: Thompson, Craig B.  
APPLICANT: Nabel, Gary J.  
APPLICANT: Gray, Gary S.

APPLICANT: Rennett, Paul D.  
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation  
OF T-Cells  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/390,330  
FILING DATE: March 17, 2003  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/435,816A  
FILING DATE: May 4, 1995  
CLASSIFICATION:  
APPLICATION NUMBER: US 08/403,253  
FILING DATE: 10 MARCH 1995  
APPLICATION NUMBER: US 08/253,964  
FILING DATE: 3 JUNE 1994  
APPLICATION NUMBER: US 08/073,223  
FILING DATE: 4 JUNE 1993  
APPLICATION NUMBER: US 08/200,947  
FILING DATE: 23 FEB 1994  
APPLICATION NUMBER: US 07/864,805  
FILING DATE: 7 APR 1992  
APPLICATION NUMBER: US 08/247,505  
FILING DATE: 23 MAY 1994  
APPLICATION NUMBER: US 07/864,866  
FILING DATE: 7 APR 1992  
APPLICATION NUMBER: US 08/218,155  
FILING DATE: 25 MAR 1994  
APPLICATION NUMBER: US 07/864,807  
FILING DATE: 7 APR 1992  
APPLICATION NUMBER: US 07/902,467  
FILING DATE: 16 JUNE 1992  
APPLICATION NUMBER: US 07/275,433  
FILING DATE: 23 NOV 1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: RPI-002CP3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 227 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-10-390-330-6

Query Match 100.0%; Score 207; DB 4; Length 227;  
Best Local Similarity 100.0%; Pred. No. 1.7e-21;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETAKAIHYALNCCGLAGGVQFISDICPKKDV 38  
Db 134 KDEPQRETAKAIHYALNCCGLAGGVQFISDICPKKDV 171

RESULT 6  
US-10-473-127-1723  
Sequence 1723, Application US/10473127

Publication No. US20040236091A1  
GENERAL INFORMATION:  
APPLICANT: Zycos Inc.  
TITLE OF INVENTION: TRANSLATIONAL PROFILING  
FILE REFERENCE: 08191-026W01  
CURRENT APPLICATION NUMBER: US/10/473,127  
CURRENT FILING DATE: 2003-09-26  
PRIOR APPLICATION NUMBER: 60/279,495  
PRIOR FILING DATE: 2001-03-28  
PRIOR APPLICATION NUMBER: 60/292,544  
PRIOR FILING DATE: 2001-05-21  
PRIOR APPLICATION NUMBER: 60/310,801  
PRIOR FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: 60/326,370  
PRIOR FILING DATE: 2001-10-01  
PRIOR APPLICATION NUMBER: 60/336,780  
PRIOR FILING DATE: 2001-12-04  
PRIOR APPLICATION NUMBER: 60/358,985  
PRIOR FILING DATE: 2002-02-20  
NUMBER OF SEQ ID NOS: 2041  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1723  
LENGTH: 227  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-473-127-1723

Query Match 100.0%; Score 207; DB 5; Length 227;  
Best Local Similarity 100.0%; Pred. No. 1.7e-21;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETALKAIHYALNCCGLAGGVEQFISDICPKKDV 38  
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DB 134 KDEPQRETALKAIHYALNCCGLAGGVEQFISDICPKKDV 171

RESULT 7  
US-10-473-127-1726  
Sequence 1726, Application US/10473127  
Publication No. US20040236091A1  
GENERAL INFORMATION:  
APPLICANT: Zycos Inc.  
TITLE OF INVENTION: TRANSLATIONAL PROFILING  
FILE REFERENCE: 08191-026W01  
CURRENT APPLICATION NUMBER: US/10/473,127  
CURRENT FILING DATE: 2003-09-26  
PRIOR APPLICATION NUMBER: 60/279,495  
PRIOR FILING DATE: 2001-03-28  
PRIOR APPLICATION NUMBER: 60/292,544  
PRIOR FILING DATE: 2001-05-21  
PRIOR APPLICATION NUMBER: 60/310,801  
PRIOR FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: 60/326,370  
PRIOR FILING DATE: 2001-10-01  
PRIOR APPLICATION NUMBER: 60/336,780  
PRIOR FILING DATE: 2001-12-04  
PRIOR APPLICATION NUMBER: 60/358,985  
PRIOR FILING DATE: 2002-02-20  
NUMBER OF SEQ ID NOS: 2041  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1726  
LENGTH: 227  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-473-127-1726

Query Match 100.0%; Score 207; DB 5; Length 227;  
Best Local Similarity 100.0%; Pred. No. 1.7e-21;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETALKAIHYALNCCGLAGGVEQFISDICPKKDV 38  
|||||  
DB 134 KDEPQRETALKAIHYALNCCGLAGGVEQFISDICPKKDV 171

RESULT 8  
US-10-156-136-39  
Sequence 39, Application US/10156136  
Publication No. US20030129696A1  
GENERAL INFORMATION:  
APPLICANT: NI, et al.  
TITLE OF INVENTION: Polynucleotides and Polypeptides Encoding Receptors  
NUMBER OF SEQUENCES: 63  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Ave  
CITY: Rockville  
STATE: MD  
COUNTRY: US  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/10/156,136  
FILING DATE: 29-May-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/010,146  
FILING DATE: <Unknown>  
APPLICATION NUMBER: WO US98/00959  
FILING DATE: 21-JAN-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: A. Anders Brookes  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PF354PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8439  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 228 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
US-10-156-136-39

Query Match 100.0%; Score 207; DB 4; Length 228;  
Best Local Similarity 100.0%; Pred. No. 1.7e-21;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETALKAIHYALNCCGLAGGVEQFISDICPKKDV 38  
|||||  
DB 135 KDEPQRETALKAIHYALNCCGLAGGVEQFISDICPKKDV 172

RESULT 9  
US-10-331-496A-41  
Sequence 41, Application US/10331496A  
Publication No. US20030228305A1  
GENERAL INFORMATION:  
APPLICANT: FRANTZ, GRETCHEN  
APPLICANT: HILLAN, KENNETH J.  
APPLICANT: PHILLIPS, HEIDI S.  
APPLICANT: POLAKIS, PAUL  
APPLICANT: SMITH, VICTORIA  
APPLICANT: SPENCER, SUSAN D.  
APPLICANT: WILLIAMS, P. MICKEY  
APPLICANT: WU, THOMAS D.  
APPLICANT: ZHANG, ZEMIN  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND

```
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5014R1-PCT
; CURRENT APPLICATION NUMBER: US/10/331,496A
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 60/345,444
; PRIOR FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: US 60/351,885
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 60/360,066
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: US 60/362,004
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/366,869
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: US 60/366,284
; PRIOR FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: US 60/368,679
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 95
; SEQ ID NO 41
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-331-496A-41

Query Match 100.0%; Score 207; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.7e-21;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETAKAIHYALNCCGLAGGVEQFISDICKKDV 38
|||||
DB 135 KDEPQRETAKAIHYALNCCGLAGGVEQFISDICKKDV 172

RESULT 10
US-10-619-323-1
; Sequence 1, Application US/10619323
; Publication No. US20040136985A1
; GENERAL INFORMATION:
; APPLICANT: Jennings, Lisa K.
; APPLICANT: Longhurst, Celia M.
; APPLICANT: Cook, George A.
; APPLICANT: Bao, Jianxiong
; APPLICANT: Zhang, Chunxiang
; APPLICANT: White, Melanie M.
; APPLICANT: Crossno, Jr., Joseph T.
; APPLICANT: Lu, Yi
; TITLE OF INVENTION: METHODS OF MODIFYING BEHAVIOR OF CD9-EXPRESSING CELLS
; FILE REFERENCE: 20609/241
; CURRENT APPLICATION NUMBER: US/10/619,323
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: 60/395,864
; PRIOR FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-619-323-1

Query Match 100.0%; Score 207; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.7e-21;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETAKAIHYALNCCGLAGGVEQFISDICKKDV 38
|||||
DB 135 KDEPQRETAKAIHYALNCCGLAGGVEQFISDICKKDV 172

; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5014R1-PCT
; CURRENT APPLICATION NUMBER: US/10/331,496A
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 60/345,444
; PRIOR FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: US 60/351,885
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 60/360,066
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: US 60/362,004
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/366,869
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: US 60/366,284
; PRIOR FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: US 60/368,679
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 95
; SEQ ID NO 41
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-331-496A-41

Query Match 100.0%; Score 207; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.7e-21;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETAKAIHYALNCCGLAGGVEQFISDICKKDV 38
|||||
DB 135 KDEPQRETAKAIHYALNCCGLAGGVEQFISDICKKDV 172

RESULT 11
US-10-794-899-97
; Sequence 97, Application US/10794899
; Publication No. US20040146516A1
; GENERAL INFORMATION:
; APPLICANT: Utah Ventures
; TITLE OF INVENTION: Lumen-Exposed Molecules and Methods Targeted Delivery
; FILE REFERENCE: 27110-715
; CURRENT APPLICATION NUMBER: US/10/794,899
; CURRENT FILING DATE: 2004-03-05
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 97
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-794-899-97

Query Match 100.0%; Score 207; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.7e-21;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETAKAIHYALNCCGLAGGVEQFISDICKKDV 38
|||||
DB 135 KDEPQRETAKAIHYALNCCGLAGGVEQFISDICKKDV 172

RESULT 12
US-10-473-127-1714
; Sequence 1714, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows version 4.0
; SEQ ID NO 1714
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1714

Query Match 100.0%; Score 207; DB 5; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.7e-21;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETAKAIHYALNCCGLAGGVEQFISDICKKDV 38
|||||
DB 135 KDEPQRETAKAIHYALNCCGLAGGVEQFISDICKKDV 172

RESULT 13
US-10-473-127-1715
; Sequence 1715, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
```

```
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1715
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1715
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Query Match 100.0%; Score 207; DB 5; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.7e-21;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETLLKAIHYALNCCGLAGGVEQFISDICPKKDV 38
|||||
Db 135 KDEPQRETLLKAIHYALNCCGLAGGVEQFISDICPKKDV 172
```

## RESULT 14

```
US-10-473-127-1716
; Sequence 1716, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1716
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1716
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```
Query Match 100.0%; Score 207; DB 5; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.7e-21;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETLLKAIHYALNCCGLAGGVEQFISDICPKKDV 38
|||||
Db 135 KDEPQRETLLKAIHYALNCCGLAGGVEQFISDICPKKDV 172
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## RESULT 15

```
US-10-473-127-1718
; Sequence 1718, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1718
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1718

Query Match 100.0%; Score 207; DB 5; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.7e-21;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETLLKAIHYALNCCGLAGGVEQFISDICPKKDV 38
|||||
Db 135 KDEPQRETLLKAIHYALNCCGLAGGVEQFISDICPKKDV 172

Search completed: January 20, 2006, 17:26:38
Job time : 77.4691 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:16:18 ; Search time 6.5679 Seconds  
(without alignments)  
58.632 Million cell updates/sec

Title: US-10-619-323-4

Perfect score: 207

Sequence: 1 KDEPQRETLKAHYALNCCGLAGGVEQFISDIPCKKDV 38

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 70606 seqs, 10133881 residues

Total number of hits satisfying chosen parameters: 70606

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications\_AA\_New.\*
- 1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pbp.\*
  - 2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pbp.\*
  - 3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pbp.\*
  - 4: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pbp.\*
  - 5: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pbp.\*
  - 6: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pbp.\*
  - 7: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pbp.\*
  - 8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pbp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	207	100.0	228	6	US-10-821-234-1266
2	51	24.6	287	6	US-10-467-657-2768
3	50	24.2	434	7	US-11-123-013-4
4	46	22.2	207	6	US-10-467-657-8262
5	46	22.2	273	6	US-10-793-626-728
6	45.5	22.0	78	6	US-10-467-657-3038
7	45	21.7	212	7	US-11-124-368A-320
8	45	21.7	254	7	US-11-124-368A-318
9	45	21.7	303	5	US-09-978-360A-763
10	45	21.7	508	6	US-10-467-657-3444
11	43.5	21.0	391	6	US-10-467-657-5988
12	43.5	21.0	1071	6	US-10-467-657-1654
13	43	20.8	122	6	US-10-467-657-606
14	43	20.8	154	6	US-10-821-234-1469
15	43	20.8	432	7	US-11-084-624-20
16	43	20.8	2340	7	US-11-052-554A-171
17	42.5	20.5	425	7	US-11-037-243-92
18	42.5	20.5	798	6	US-10-770-726-64
19	42.5	20.5	1767	7	US-11-052-554A-372
20	42	20.3	269	6	US-10-995-561-535
21	42	20.3	278	7	US-11-009-658-8
22	42	20.3	303	6	US-10-995-561-534
23	42	20.3	1400	6	US-10-821-234-1045
24	41.5	20.0	366	6	US-10-524-647-126
25	41.5	20.0	371	6	US-10-467-962B-41

ALIGNMENTS

RESULT 1

US-10-821-234-1266  
; Sequence 1266, Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Andarmani, Susan  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
; FILE REFERENCE: 821A  
; CURRENT APPLICATION NUMBER: US/10/821,234  
; PRIOR FILING DATE: 2004-04-07  
; PRIOR APPLICATION NUMBER: US 60/462,047  
; NUMBER OF SEQ ID NOS: 1704  
; SOFTWARE: pt\_seq\_genes Version 1.0  
; SEQ ID NO 1266  
; LENGTH: 228  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-821-234-1266

Query Match 100.0%; Score 207; DB 6; Length 228;  
Best Local Similarity 100.0%; Pred. No. 5.7e-24;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAHYALNCCGLAGGVEQFISDIPCKKDV 38  
DB 135 KDEPQRETLKAHYALNCCGLAGGVEQFISDIPCKKDV 172

RESULT 2

US-10-467-657-2768  
; Sequence 2768, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON Spa  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12

```

; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2768
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2768

```

Query Match 24.6%; Score 51; DB 6; Length 287;  
Best Local Similarity 44.0%; Pred. No. 2.1;  
Matches 11; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

Qy	3	EPQRETLKAIHYALNCCGLAGVEQ	27
		:           :	
Db	205	EPSRQLSKQAHYALQTEGLQNALAQ	229

RESULT 3  
US-11-123-013-4  
Sequence 4, Application US/11123013  
Publication No. US20050287637A1  
GENERAL INFORMATION:  
APPLICANT: Betenbaugh, Michael J.  
APPLICANT: Lawrence, Shawn J.  
APPLICANT: Lee, Yuan C.  
APPLICANT: Coleman, Timothy A.  
TITLE OF INVENTION: Engineering Intracellular Sialylation Pathways  
FILE REFERENCE: 03940077bp  
CURRENT APPLICATION NUMBER: US/11/123, 013  
CURRENT FILING DATE: 2005-05-06  
PRIOR APPLICATION NUMBER: US 60/122,582  
PRIOR FILING DATE: 1999-03-02  
PRIOR APPLICATION NUMBER: US 60/169,624  
PRIOR FILING DATE: 1999-12-08  
PRIOR APPLICATION NUMBER: US 60/227,579  
PRIOR FILING DATE: 2000-08-25  
PRIOR APPLICATION NUMBER: US 09/516,793  
PRIOR FILING DATE: 2000-03-01  
PRIOR APPLICATION NUMBER: US 09/930,440  
PRIOR FILING DATE: 2001-08-16  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 4  
LENGTH: 434  
TYPE: DNA

Query Match 24.2%; Score 50; DB 7; Length 434;  
Best Local Similarity 37.5%; Pred. No. 4.7;  
Matches 9; Conservative 3; Mismatches 12; Indels

Qy	10	KAIHYALNCCGLAGGVEQFISDIC	33
		:	
D <sub>b</sub>	399	KAVGYICKNGRGGAIREFAEHIC	422

```

RESULT 4
US-10-467-657-8262
; Sequence 8262, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 8262
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8262

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Query Match      22.2%; Score 46; DB 6; Length 207;
Best Local Similarity 36.0%; Pred. No. 8.2;
Matches 9; Conservative 4; Mismatches 12; Indels 0; Gaps 0;
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**Qy**      14 YALNCCGLAGVEQFISDICPKOV 38  
          : ||| :| :|| |  
**Db**     136 FAQNCA DLSGSFQFCRFILDDSDI 160

```

RESULT 5
US-10-793-626-728
; Sequence 728, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 728
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-728

```

Query Match 22.2%; Score 46; DB 6; Length 273;  
Best Local Similarity 34.1%; Pred. No. 11;  
Matches 14; Conservative 6; Mismatches 11; Indels 10; Gaps 2

Qy 8 TLKAIH---YALNCCGLAGV-----EQFISDIPCQDV 38  
| | | | | : | | | | : | | : | :  
Dd 185 TYKAIHACKTYNVNRLIVAGVSNKGLRNALSEACKKEGI 225

RESULT 6  
US-10-467-657-3038  
; Sequence 3038, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SPA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia





```

; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1654
; LENGTH: 1071
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1654

Query Match          21.0%; Score 43.5; DB 6; Length
Best Local Similarity 35.7%; Pred. No. 1.2e+02;
Matches 15; Conservative 8; Mismatches 10; Indels

QY 1 KDEPQRETLKAIHYALNCCGLAG-----GVGEFISDICKP 35
Db      800 QDEIRRTQ-KAMAYALGVVGLMNVQFAVDGV-VFVLEVNPR 839

RESULT 13
US-10-467-657-606
; Sequence 606, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 606
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-606

Query Match          20.8%; Score 43; DB 6; Length 1
Best Local Similarity 50.0%; Pred. No. 13;
Matches 9; Conservative 3; Mismatches 6; Indels

QY 20 GLAGGVRFQFISDICKPKD 37
Db      25 GFDGGVEQFDNDRHKRRD 42

RESULT 14
US-10-821-234-1469
; Sequence 1469, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment o
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234

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Search completed: January 20, 2006, 17:27:02  
Job time : 6.5679 secs

**This Page Blank (uspto)**

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2006, 17:06:32 ; Search time 26.7407 Seconds  
(without alignments)  
136.729 Million cell updates/sec

Title: US-10-619-323-4

Perfect score: 207

Sequence: 1 KDEPQRETLKAIHYALNCCGLAGVQRFISDICPKKDV 38

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80:\*  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	207	100.0	228	1 A40402	CD9 antigen [valid
2	202	97.6	228	1 A42929	CD9 antigen - gree
3	191	92.3	226	1 S39262	CD9 antigen - rat
4	167	80.7	226	2 I49589	antigen - mouse
5	151	72.9	226	1 JX0221	CD9 antigen - bovi
6	56.5	27.3	172	2 T26914	hypothetical prote
7	56.5	27.3	203	2 T22537	hypothetical prote
8	56	27.1	363	2 S62537	probable RNA 3'-te
9	55	26.6	302	2 S78509	heterodisulfide re
10	54	26.1	302	2 D69118	heterodisulfide re
11	54	26.1	342	2 A98021	hypothetical prote
12	53.5	25.8	343	1 CES0VM	vancomycin resist
13	53.5	25.8	764	2 JCS643	thyroid stimulat
14	52.5	25.4	548	2 B84932	60 kD chaperonin [
15	52.5	25.4	548	2 B42281	symbionin syml - p
16	52.5	25.4	1651	2 F88750	protein vit-6 [imp
17	52	25.1	894	2 B96557	probable receptor
18	52	25.1	933	2 A31930	cytotactin - chick
19	51.5	24.9	544	2 B82048	chaperonin, 60 kD
20	51.5	24.9	548	1 BVRCGL	chaperonin groEL -
21	51.5	24.9	548	2 B86110	hypothetical prote
22	51.5	24.9	548	2 AE1045	GroEL protein [imp
23	51.5	24.9	548	2 D81938	chaperonin GroEL [
24	51	24.6	290	2 D81938	probable RNA polym
25	51	24.6	290	2 G81166	RNA polymerase sig
26	51	24.6	306	2 B70304	dihydroorotase den
27	51	24.6	336	2 D64621	hypothetical prote
28	51	24.6	560	2 T46189	calcium-dependent
29	51	24.6	644	2 S39356	transcription fact

## ALIGNMENTS

### RESULT 1

A40402

CD9 antigen (validated) - human

N;Alternate names: motility-related protein-1

C;Species: Homo sapiens (man)

C;Date: 06-Dec-1991 #sequence revision 07-Jul-1995 #text\_change 09-Jul-2004

C;Accession: A46123; A40402; JH0555; A39029; S10564

R;Rubinstein, E.; Benoit, P.; Billard, M.; Plaisance, S.; Prenant, M.; Uzan, G.; Bouche

Genomics 16, 132-138, 1993

A;Title: Organization of the human CD9 gene.

A;Reference number: A46123; MUID:93252369; PMID:8486348

A;Accession: A46123

A;Molecule type: DNA

A;Residues: 1-228 <LAN>

A;Cross-references: UNIPROT:P21926; UNIPARC:UPI000003B45A; GB:S60489; NID:G300112; PIDN

A;Experimental source: leukocyte

A;Note: sequence extracted from NCBI backbone (NCBIN:131318, NCBIN:131326, NCBIN:131328

R;Lanza, P.; Wolf, D.; Fox, C.P.; Kieffer, N.; Seyer, J.M.; Fried, V.A.; Coughlin, S.R.

J. Biol. Chem. 266, 10638-10645, 1991

A;Title: cDNA cloning and expression of platelet p24/CD9. Evidence for a new family of

A;Reference number: A40402; MUID:91244846; PMID:2037603

A;Accession: A40402

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-228 <LAN>

A;Cross-references: UNIPARC:UPI000003B45A; GB:L34068; GB:M61880; NID:G508495; PIDN:AAA5

A;Note: parts of this sequence, including the amino end of the mature protein, were con

R;Miya, M.; Koyama, M.; Seno, M.; Ikeyama, S.

J. Exp. Med. 174, 1347-1354, 1991

A;Title: Identification of the motility-related protein (MRP-1), recognized by monoclon

A;Reference number: JH0555; MUID:92078843; PMID:1720807

A;Accession: JH0555

A;Molecule type: mRNA

A;Residues: 1-228 <MIY>

A;Cross-references: UNIPARC:UPI000003B45A; GB:X60111; NID:G34768; PIDN:CAA42708.1; PID:

A;Experimental source: breast carcinoma

A;Note: this protein has the epitope defined by cell motility-inhibiting monoclonal ant

R;Bouchaix, C.; Benoit, P.; Frachet, P.; Billard, M.; Worthington, R.E.; Gagnon, J.; U

J. Biol. Chem. 266, 117-122, 1991

A;Title: Molecular cloning of the CD9 antigen. A new family of cell surface proteins.

A;Reference number: A39029; MUID:91093112; PMID:1840589

A;Accession: A39029

A;Molecule type: mRNA

A;Residues: 1-8,'S',10-66,'A',68-193,195-228 <BOU>

A;Cross-references: UNIPARC:UPI000017414B; GB:M38690

A;Note: parts of this sequence, including the amino end of the mature protein, were con

R;Higashihara, M.; Takahata, K.; Yatomi, Y.; Nakahara, K.; Kurokawa, K.

FEBS Lett. 264, 270-274, 1990

A;Title: Purification and partial characterization of CD9 antigen of human platelets.

A;Reference number: S10564; MUID:90292223; PMID:2358073

A;Accession: S10564

A;Molecule type: protein

probable phytoene  
DNA-binding protei  
major single-stran  
sodium channel alp  
sodium channel alp  
sodium channel alp  
sodium channel alp  
D-alanine-D-alanin  
thyrotropin recept  
vitellogenin vit-6  
probable RNA methy  
probable enzyme yg  
yGCA protein - Esc  
heat shock protein  
probable DNA relax  
tral protein - Esc

```
A:Residues: 2-8 'X', 10-21 <HIG>
A:Cross-references: UNIPARC:UPI000017414C
C:Genetics:
A:Gene: GDB:CD9; MIC3
A:Cross-references: GDB:120582; OMIM:143030
A:Map position: 12p13-12p13
C:Superfamily: CD9 antigen
C:Keywords: glycoprotein; transmembrane protein
F:2-228/Product: CD9 antigen #status experimental <MAT>
F:2-11/Domain: intracellular #status predicted <CY1>
F:12-35/Domain: transmembrane #status predicted <TM1>
F:36-55/Domain: extracellular #status predicted <EX1>
F:56-82/Domain: transmembrane #status predicted <TM2>
F:83-86/Domain: intracellular #status predicted <CY2>
F:87-111/Domain: transmembrane #status predicted <TM3>
F:112-194/Domain: extracellular #status predicted <EX2>
F:195-221/Domain: transmembrane #status predicted <TM4>
F:222-228/Domain: intracellular #status predicted <CY3>
F:53/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      100.0%; Score 207; DB 1; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.2e-20;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KDEPQRETLLKAIHYALNCCGLAGGVQFISDTCPKKDV 38
Db      135 KDEPQRETLLKAIHYALNCCGLAGGVQFISDTCPKKDV 172

RESULT 2
A42929
CD9 antigen - green monkey
N/Alternate names: 27K diphtheria toxin receptor-associated protein DRAP27
C:Species: Cercopithecus aethiops (green monkey, grivet)
C:Date: 01-Oct-1992 #sequence_revision 09-Aug-1996 #text_change 09-Jul-2004
A:Accession: A42929
R:Mitamura, T.; Iwamoto, R.; Umata, T.; Yomo, T.; Urabe, I.; Tsunooka, M.; Mekada, E.
J. Cell Biol. 118, 1389-1399, 1992
A:Title: The 27-kD diphtheria toxin receptor-associated protein (DRAP27) from vero cells
epitopes on toxin-sensitive cells.
A:Reference number: A42929; MUID:92394967; PMID:1522113
A:Accession: A42929
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-228 <MIT>
A:Cross-references: UNIPROT:P30409; UNIPARC:UPI000016C3B8; GB:D10726; NID:9218565; PIDN:
A:Superfamily: CD9 antigen
C:Keywords: glycoprotein; transmembrane protein
F:2-228/Product: CD9 antigen #status predicted <MAT>
F:2-11/Domain: intracellular #status predicted <CY1>
F:12-35/Domain: transmembrane #status predicted <TM1>
F:36-55/Domain: extracellular #status predicted <EX1>
F:56-82/Domain: transmembrane #status predicted <TM2>
F:83-86/Domain: intracellular #status predicted <CY2>
F:87-111/Domain: transmembrane #status predicted <TM3>
F:112-194/Domain: extracellular #status predicted <EX2>
F:195-221/Domain: transmembrane #status predicted <TM4>
F:222-228/Domain: intracellular #status predicted <CY3>
F:52,53/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      97.6%; Score 202; DB 1; Length 228;
Best Local Similarity 97.4%; Pred. No. 5.9e-20;
Matches 37; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KDEPQRETLLKAIHYALNCCGLAGGVQFISDTCPKKDV 38
Db      135 KDEPQRETLLKAIHYALNCCGLAGGVQFISDTCPKKDV 172

RESULT 3
S39262
CD9 antigen - rat
N/Alternate names: platelet cell surface glycoprotein
```

```
C:Species: Rattus norvegicus (Norway rat)
C:Date: 06-Jan-1995 #sequence_revision 09-Aug-1996 #text_change 09-Jul-2004
A:Accession: I56562; S39262
R:Kaprielian, Z.; Cho, K.O.; Hadjiargyrou, M.; Patterson, P.H.
J. Neurosci. 15, 562-573, 1995
A:Title: CD9, a major platelet cell surface glycoprotein, is a ROCA antigen and is expressed
in the developing rat brain.
A:Reference number: I56562; MUID:95123481; PMID:7823164
A:Accession: I56562
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-226 <RES>
A:Cross-references: UNIPROT:P40241; UNIPARC:UPI00001708C6; EMBL:X76489; NID:g434314; PIDN:
A:Genetics:
C:Superfamily: CD9 antigen
C:Keywords: glycoprotein; transmembrane protein
F:2-11/Domain: intracellular #status predicted <CY1>
F:12-35/Domain: transmembrane #status predicted <TM1>
F:36-53/Domain: extracellular #status predicted <EX1>
F:54-80/Domain: transmembrane #status predicted <TM2>
F:81-84/Domain: intracellular #status predicted <CY2>
F:85-109/Domain: transmembrane #status predicted <TM3>
F:110-192/Domain: extracellular #status predicted <EX2>
F:193-219/Domain: transmembrane #status predicted <TM4>
F:220-226/Domain: intracellular #status predicted <CY3>
F:50/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      92.3%; Score 191; DB 1; Length 226;
Best Local Similarity 92.1%; Pred. No. 1.8e-18;
Matches 35; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 KDEPQRETLLKAIHYALNCCGLAGGVQFISDTCPKKDV 38
Db      133 KDEPQRETLLKAIHYALNCCGLAGGVQFISDTCPKKDV 170

RESULT 4
I49589
antigen - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
A:Accession: I49589
R:Rubinstein, E.; Billard, M.; Plaisance, S.; Prenant, M.; Boucheix, C.
Thromb. Res. 71, 377-383, 1993
A:Title: Molecular cloning of the mouse equivalent of CD9 antigen.
A:Reference number: I49589; MUID:94054345; PMID:8236164
A:Accession: I49589
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-226 <RES>
A:Cross-references: UNIPROT:P40240; UNIPARC:UPI0000003E37; GB:L08115; NID:g388911; PIDN:
C:Superfamily: CD9 antigen

Query Match      80.7%; Score 167; DB 2; Length 226;
Best Local Similarity 78.9%; Pred. No. 3.4e-15;
Matches 30; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      1 KDEPQRETLLKAIHYALNCCGLAGGVQFISDTCPKKDV 38
Db      133 KDEPQRETLLKAIHYALNCCGLAGGVQFISDTCPKKQL 170

RESULT 5
JX0221
CD9 antigen - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 09-Oct-1992 #sequence_revision 09-Aug-1996 #text_change 09-Jul-2004
A:Accession: JX0221
R:Martin-Alonso, J.M.; Hernando, N.; Ghosh, S.; Coca-Prados, M.
J. Biochem. 112, 63-67, 1992
A:Title: Molecular cloning of the bovine CD9 antigen from ocular ciliary epithelial cells.
A:Reference number: JX0221; MUID:93054422; PMID:1339429
A:Accession: JX0221
```

A;Map position: 4  
A;Introns: 22/3; 83/3; 116/3

Query Match            27.3%; Score 56.5; DB 2; Length 203;  
Best Local Similarity    45.8%; Pred. No. 3.5;  
Matches    11; Conservative     4; Mismatches    8; Indels    1; Gaps    1;

QY      6 RETLKAIHYALNCCGLAGGVGEQFI 29  
     : ||| : | |||| | ||| :  
Db      107 KNTLWDVHTSLKCG-ANGCEDFL 129

RESULT 8  
S62537  
probable RNA 3'-terminal phosphate cyclase - fission yeast (*Schizosaccharomyces pombe*)  
C;Species: Schizosaccharomyces pombe  
C;Date: 16-May-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C;Accession: S62537; T37595  
R;Devlin, K.; Odell, C.; Churcher, C.M.  
submitted to the EMBL Data Library, November 1995  
A;Reference number: S62532  
A;Accession: S62537  
A>Status: preliminary  
A:Molecule type: DNA  
A;Residues: 1-363 <DEV>  
A;Cross-references: UNIPROT:Q09870; UNIPARC:UPI000013346E; EMBL:Z66568; NID:g1052518; F:  
R;Devlin, K.; Odell, C.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.  
submitted to the EMBL Data Library, November 1995  
A;Reference number: Z21727  
A;Accession: T37595  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A;Residues: 1-363 <DE2>  
A;Cross-references: UNIPARC:UPI000013346E; EMBL:Z66568; PIDN:CAA91501.1; GSPDB:GN00066  
A;Experimental source: strain 972h-; cosmid c12g12  
C;Genetics:  
A;Gene: SPAC12G12.06c  
A;Map position: 1L  
C;Superfamily: hypothetical protein YOL010w

Query Match            27.1%; Score 56; DB 2; Length 363;  
Best Local Similarity    40.0%; Pred. No. 7.1;  
Matches    12; Conservative     2; Mismatches    16; Indels    0; Gaps    0;

QY      7 ETLLKAHYNLCCLAGGVGFSDICPKK 36  
     : ||| : | |||| | ||| :  
Db      248 ETWKGSYAEHCAGEGPEDVGSCFAKK 277

RESULT 9  
S78509  
heterodisulfide reductase (EC 1.97.1.-) chain B - Methanobacterium thermoautotrophicum  
N;Alternate names: heterodisulfide reductase 36k chain  
C;Species: Methanobacterium thermoautotrophicum  
C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004  
C;Accession: S78509; S41205  
R;Hedderich, R.; Koch, J.; Linder, D.; Thauer, R.K.  
Eur. J. Biochem. 225, 253-261, 1994  
A;Title: The heterodisulfide reductase from Methanobacterium thermoautotrophicum contains  
A;Reference number: S48720; MUID:95010113; PMID:7925445  
A;Accession: S78509  
A;Molecule type: DNA  
A;Residues: 1-302 <HEd>  
A;Cross-references: UNIPROT:Q50755; UNIPARC:UPI000006298D; EMBL:X81133; NID:g600449; PIR:  
R;Setzke, E.; Hedderich, R.; Heiden, S.; Thauer, R.K.  
Eur. J. Biochem. 220, 139-148, 1994  
A;Title: H(2): heterodisulfide oxidoreductase complex from Methanobacterium thermoauto  
A;Reference number: S41204; MUID:94164153; PMID:8119281  
A;Accession: S41205  
A:Molecule type: protein  
A;Residues: 1-27 <SET>  
A;Cross-references: UNIPARC:UPI0000178FD2

A:Experimental source: strain Marburg	
C:Genetics: hdrB	
C:Complex: membrane-associated complex; holoenzyme is the hydrogen:heterodisulfide oxidoreductase (EC 1.1.2.99.-) and a F420-non-reducing-hydrogenase (EC 1.1.2.99.-) subcomplex; each of the subcomplexes is a F420-non-reducing-hydrogenase (EC 1.1.2.99.-) subcomplex; each of the subcomplexes is a F420-non-reducing-hydrogenase (EC 1.1.2.99.-) subcomplex	
C:Function: A:Description: heterodisulfide reductase	
C:Superfamily: Acidianus ambivalens succinate dehydrogenase chain C	
C:Keywords: membrane-associated complex; oxidoreductase	
Query Match 26.6%; Score 55; DB 2; Length 302;	
Best Local Similarity 30.2%; Pred. No. 8.2;	
Matches 13; Conservative 6; Mismatches 12; Indels 12; Gaps 2;	
QY 2 DEPORETL-----KAIHY--ALNCCGLAGGVEQFISDI 32	
DB 165 DNPERTILDELVEVTGAKSVYKDKMCCGAGGVRSDLDV 207	
RESULT 10	
D69118	
heterodisulfide reductase (EC 1.97.1.-) chain B - Methanobacterium thermoautotrophicum (strain Marburg)	
C:Species: Methanobacterium thermoautotrophicum	
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004	
C:Accession: D69118	
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Liu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiawani, N.; Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.	
J. Bacteriol. 179, 7135-7155, 1997	
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: function	
A:Reference number: A69000; MUID:98037514; PMID:93711463	
A:Accession: D69118	
A>Status: preliminary; nucleic acid sequence not shown; translation not shown	
A:Molecule type: DNA	
A:Residues: 1-302 <MTH>	
A:Cross-references: UNIPROT:Q27907; UNIPARC:UPI00000665F1; GB:AE000940; GB:AE000666; NID:1000000000	
A:Experimental source: strain Delta H	
C:Genetics:	
A:Gene: MTH1879	
C:Superfamily: Acidianus ambivalens succinate dehydrogenase chain C	
C:Keywords: membrane-associated complex; oxidoreductase	
Query Match 26.1%; Score 54; DB 2; Length 302;	
Best Local Similarity 30.2%; Pred. No. 11;	
Matches 13; Conservative 6; Mismatches 12; Indels 12; Gaps 2;	
QY 2 DEPORETL-----KAIHY--ALNCCGLAGGVEQFISDI 32	
DB 165 DNPERTILDELVEVTGAKSVYKDKMCCGAGGVRSDLDV 207	
RESULT 11	
A98021	
hypothetical protein appA [imported] - Streptococcus pneumoniae (strain R6)	
C:Species: Streptococcus pneumoniae	
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004	
C:Accession: A98021	
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M, Y. P.; Sun, P.M.; Winkler, M.E.	
J. Bacteriol. 183, 5709-5717, 2001	
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.	
A:Reference number: A97872; MUID:21429245; PMID:11544234	
A:Accession: A98021	
A>Status: preliminary	
A:Molecule type: DNA	
A:Residues: 1-542 <KUR>	
A:Cross-references: UNIPROT:Q8DPF2; UNIPARC:UPI00000E35F9; GB:AE007317; PIDN:AAK99997.1;	
C:Genetics:	
A:Gene: appA	
Query Match 26.1%; Score 54; DB 2; Length 542;	

Best Local Similarity 35.5%; Pred. No. 20;	
Matches 11; Conservative 7; Mismatches 13; Indels 0; Gaps 0;	
QY 1 KDEPQRETLKAIHYALNCCGLAGGVEQFISD 31	
DB 390 KQASQDFMQAVSYQLNEVGINKNEVVQITSD 420	
RESULT 12	
CSOVM	
vancomycin resistance protein vana - Enterococcus faecium plasmid pIP816	
C:Species: Enterococcus faecium	
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004	
C:Accession: S12254; A38812	
R:Dutka-Malen, S.; Molinas, C.; Arthur, M.; Courvalin, P.	
Mol. Gen. Genet. 224, 364-372, 1990	
A:Title: The VANA glycopeptide resistance protein is related to D-alanyl-D-alanine ligase	
A:Reference number: S12254; MUID:91094773; PMID:2266943	
A:Accession: S12254	
A:Molecule type: DNA	
A:Residues: 1-343 <DUL>	
A:Cross-references: UNIPROT:P25051; UNIPARC:UPI00000013A3; EMBL:X56895; NID:G43335; PIDN:1000000000	
A:Accession: A38812	
A:Molecule type: protein	
A:Residues: 1-9 <DUL>	
A:Cross-references: UNIPARC:UPI0000149858	
C:Comment: This protein can complement mutations of D-alanine-D-alanine ligase.	
C:Genetics:	
A:Gene: vana	
A:Genome: Plasmid	
C:Superfamily: D-alanine-D-alanine ligase	
C:Keywords: antibiotic resistance	
F:1-343/Product: vana glycopeptide resistance protein #status experimental <MAT>	
Query Match 25.8%; Score 53.5; DB 1; Length 343;	
Best Local Similarity 50.0%; Pred. No. 15;	
Matches 13; Conservative 4; Mismatches 8; Indels 1; Gaps 1;	
QY 6 RRTLKAIHYALNCCGLAGGVEQFISD 31	
DB 273 QETAKKIYKALGCRGLA-RVDMFLQD 297	
RESULT 13	
JC5643	
thyroid stimulating hormone receptor precursor - sheep	
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)	
C:Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 09-Jul-2004	
C:Accession: JC5643	
R:Bockmann, J.; Winter, C.; Witkowski, W.; Kreutz, M.R.; Boeckers, T.M.	
Biochem. Biophys. Res. Commun. 238, 173-178, 1997	
A:Title: Cloning and expression of a brain-derived TSH receptor.	
A:Reference number: JC5643; MUID:97445147; PMID:9299474	
A:Accession: JC5643	
A:Molecule type: mRNA	
A:Residues: 1-764 <BOC>	
A:Cross-references: UNIPROT:P56495; UNIPARC:UPI0000137760; GB:Y13434; NID:G2462632; PIDN:1000000000	
A:Note: the sequences of residues 4-7 and 8-17, 4136-439 and 440-449 are interchanged in the original sequence	
C:Comment: This receptor belongs to the guanine nucleotide binding protein (G-protein) coupled receptor family	
C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat	
F:1-21/Domain: signal sequence #status predicted <SIG>	
F:22-764/Product: thyroid stimulating hormone receptor #status predicted <MAT>	
F:179-200/Domain: leucine-rich alpha-2-glycoprotein repeat	
F:303-382/Domain: extracellular #status predicted <EXC>	
F:416-439/Domain: transmembrane #status predicted <TM1>	
F:451-474/Domain: transmembrane #status predicted <TM2>	
F:495-518/Domain: transmembrane #status predicted <TM3>	
F:538-561/Domain: transmembrane #status predicted <TM4>	
F:581-604/Domain: transmembrane #status predicted <TM5>	
F:627-650/Domain: transmembrane #status predicted <TM6>	
F:661-684/Domain: transmembrane #status predicted <TM7>	



Query Match 25.8%; Score 53.5; DB 2; Length 764;  
Best Local Similarity 41.7%; Pred. No. 32;  
Matches 15; Conservative 3; Mismatches 11; Indels 7; Gaps 3;  
QY 4 PORETLKAI--HYALNCCGLAGGVEQFISDICPKKD 37  
DB 373 PORETLQAFDNHYDYTVCC--GGSEEMV--CTPKSD 403

## RESULT 14

B84932  
60 KD chaperonin [imported] - Buchnera sp. (strain APS)  
C;Species: Buchnera sp.  
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 23-Mar-2001  
C;Accession: B84932  
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.  
Nature 407, 81-86, 2000  
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A  
A;Reference number: A84930; MUID:20445173; PMID:10993077  
A;Accession: B84932  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-548 <STO>  
A;Cross-references: UNIPARC:UPI000005E41D; GB:AP000398; GSPDB:GN00144  
A;Experimental source: strain APS  
C;Genetics:  
A;Gene: mopA; BU019  
C;Superfamily: chaperonin groEL

Query Match 25.4%; Score 52.5; DB 2; Length 548;  
Best Local Similarity 34.3%; Pred. No. 32;  
Matches 12; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY 3 EPORETLKATHYALNCCGLAGGVEQFISDICPKKD 37  
DB 495 DPTKVTRSALQYAASVAGLMTTTCMVTDL-PKED 528

## RESULT 15

B42281  
symbionin symL - pea aphid  
C;Species: Acyrthosiphon pisum (pea aphid)  
C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 26-Aug-1999  
C;Accession: B42281; S70753; S24481  
R;Ohtaka, C.; Nakamura, H.; Ishikawa, H.  
J. Bacteriol. 174, 1869-1874, 1992  
A;Title: Structures of chaperonins from an intracellular symbiont and their functional e  
A;Reference number: A42281; MUID:92193273; PMID:1347769  
A;Accession: B42281  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-548 <OHT>  
A;Cross-references: UNIPARC:UPI000005E41D; EMBL:X61150; NID:g5658; PIDN:CAA43460.1; PID:  
A;Note: Sequence extracted from NCBI backbone (NCBIN:88668, NCBIP:88674)  
R;Ohtaka, C.; Ishikawa, H.  
J. Mol. Evol. 36, 121-126, 1993  
A;Title: Accumulation of adenine and thymine in a groE-homologous operon of an intracell  
A;Reference number: S70752; MUID:93164272; PMID:8433382  
A;Accession: S70753  
A;Status: preliminary; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-548 <OH2>  
A;Cross-references: UNIPARC:UPI000005E41D; EMBL:X61150; NID:g5658; PIDN:CAA43460.1; PID:  
C;Genetics:  
A;Gene: symL  
C;Superfamily: chaperonin groEL  
C;Keywords: molecular chaperone

Query Match 25.4%; Score 52.5; DB 2; Length 548;  
Best Local Similarity 34.3%; Pred. No. 32;  
Matches 12; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY 3 EPORETLKATHYALNCCGLAGGVEQFISDICPKKD 37

Db 495 DPTKVTRSALQYAASVAGLMTTTCMVTDL-PKED 528  
Search completed: January 20, 2006, 17:22:36  
Job time : 27.7407 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:05:21 ; Search time 144.494 Seconds  
(without alignments)  
185.545 Million cell updates/sec

Title: US-10-619-323-4  
Perfect score: 207

Sequence: 1 KDEPQRETLKAIHYALNCCGLAGGVQFISDIPKKDV 38

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Uniprot\_05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	207	100.0	227	1	P21926 homo sapien
2	207	100.0	227	1	Q5J7W6 homo sapien
3	202	97.6	227	1	P30409 cercopithec
4	194	93.7	225	1	P40239 felis silve
5	191	92.3	225	1	P40241 rattus norv
6	179	86.5	226	2	Q8MJ48 sus scrofa
7	168	81.2	225	1	Q8WNG3 sus scrofa
8	167	80.7	225	1	P40240 mus musculu
9	151	72.9	225	1	P30932 bos taurus
10	127	61.4	228	2	Q6GQ85 XENLA
11	120	58.0	224	2	Q91BC9 CHICK
12	100	48.3	228	2	Q6DKM9 XENLA
13	95	45.9	227	2	Q7ZUH9 BRARE
14	94	45.4	227	2	Q6NWG7 BRARE
15	92	44.4	227	2	Q61QH7 BRARE
16	89	43.0	192	2	Q56CY1 HUMAN
17	88	42.5	246	2	Q6P0W1 BRARE
18	80	38.6	227	2	Q4REW0 TETNG
19	77	37.2	236	2	Q7ZTR5 XENLA
20	74	35.7	230	2	Q8AYJ0 SALSA
21	72.5	35.0	237	2	Q6P351 XENTR
22	72	34.8	230	2	Q8AXJ1 ONCMY
23	71.5	34.5	237	2	Q6DCU4 XENLA
24	66	31.9	546	2	Q4YD19 PLABE
25	66	31.9	813	2	Q6IMB9 9APIC
26	64	30.9	236	2	Q9DD57 BRARE
27	64	30.9	236	2	Q6PUL1 BRARE
28	59	28.5	126	2	Q6DT38 9NOCA
29	58	28.0	767	2	Q8AAF9 BACTN
30	57.5	27.8	2424	2	Q4UB39 THEAN
31	57	27.5	199	2	Q4JWS2 CORJK

32	57	27.5	818	2	Q4XS13 PLACH	Q4xs13 plasmodium
33	56.5	27.3	228	2	Q8AV92 PETMA	Q8av92 petromyzon
34	56.5	27.3	230	2	Q20707 CAEEL	Q20707 caenorhabdi
35	56.5	27.3	235	2	Q4S1G3 TETNG	Q4s1g3 tetraodon n
36	56.5	27.3	241	2	Q62466 CAEEL	Q62466 caenorhabdi
37	56.5	27.3	1090	2	Q6CTA6 KJULA	Q6cta6 kluyveromyc
38	56	27.1	108	2	Q4UU38 XANCP	Q4uu38 xanthomonas
39	56	27.1	108	2	Q8P9P4 XANCP	Q8p9p4 xanthomonas
40	56	27.1	249	1	Q5TTA9 ANOGA	Q5tta9 anopheles g
41	56	27.1	363	1	RCL1 SCHPO	Q09870 schizosacch
42	55.5	26.8	87	2	Q8XKJ7 CLOPE	Q8xkj7 clostridium
43	55	26.6	256	2	Q7ZUI6 BRARE	Q7zui6 brachydanio
44	55	26.6	256	2	Q4SA96 TETNG	Q4sa96 tetraodon n
45	55	26.6	302	1	HDRB METTM	Q50755 methanobact

#### ALIGNMENTS

RESULT 1					
CD9_HUMAN					
ID	CD9_HUMAN	STANDARD;	PRT;	227	AA.
AC	P21926; Q96ES4;				
DT	01-MAY-1991 (Rel. 18, Created)				
DT	01-APR-1993 (Rel. 25, Last sequence update)				
DT	13-SEP-2005 (Rel. 48, Last annotation update)				
DE	CD9 antigen (p24) (Leukocyte antigen MIC3) (Motility-related protein)				
DE	(MRP-1) (Tetrapanin-29) (TSPAN-29);				
GN	Name=CD9; Synonyms=MIC3, TSPAN29;				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;				
OC	Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 1-4.				
RX	MEDLINE=91093112; PubMed=1840589;				
RA	Boucheix C., Benoit P., Frachet P., Billard M., Worthington R.E.,				
RA	Gagnon J., Uzan G.;				
RT	"Molecular cloning of the CD9 antigen. A new family of cell surface				
RT	proteins.";				
RL	J. Biol. Chem. 266:117-122 (1991).				
RN	[2]				
RP	NUCLEOTIDE SEQUENCE [MRNA], AND PARTIAL PROTEIN SEQUENCE.				
RX	MEDLINE=9124846; PubMed=2037603;				
RA	Lanza F., Wolf D., Fox C.F., Kieffer N., Seyer J.M., Fried V.A.,				
RA	Coughlin S.R., Phillips D.R., Jennings L.K.;				
RT	"cDNA cloning and expression of platelet p24/CD9. Evidence for a new				
RT	family of multiple membrane-spanning proteins.";				
RL	J. Biol. Chem. 266:10638-10645 (1991).				
RN	[3]				
RP	NUCLEOTIDE SEQUENCE.				
RX	MEDLINE=92078843; PubMed=1720807; DOI=10.1084/jem.174.6.1347;				
RA	Miyake M., Koyama M., Seno M., Ikegama S.;				
RT	"Identification of the motility-related protein (MRP-1), recognized by				
RT	monoclonal antibody M31-15, which inhibits cell motility.";				
RL	J. Exp. Med. 174:1347-1354 (1991).				
RN	[4]				
RP	NUCLEOTIDE SEQUENCE [GENOMIC DNA].				
RX	TISSUE=Leukocyte;				
RC	MEDLINE=93252369; PubMed=8486348;				
RX	Rubinstein E., Benoit P., Billard M., Plaisance S., Prenant M.,				
RA	Uzan G., Boucheix C.;				
RT	"Organization of the human CD9 gene.";				
RL	Genomics 16:132-138 (1993).				
RN	[5]				
RP	NUCLEOTIDE SEQUENCE [GENOMIC DNA].				
RA	Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O.,				
RA	Rajkumar N., Yi Q., Nickerson D.A.;				
RT	"SeattleSNPs, NHLBI HL6682 program for genomic applications, UW-				
RT	FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";				
RL	Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.				
RN	[6]				

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RC TISSUE=Ovary;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg K.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalil D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [7]  
 RP PROTEIN SEQUENCE OF 1-20.  
 RC TISSUE=Platelet;  
 RX MEDLINE=90292223; PubMed=2358073; DOI=10.1016/0014-5793(90)80265-K;  
 RA Higashihara M., Takahata K., Yatomi Y., Nakahara K., Kurokawa K.;  
 RT "Purification and partial characterization of CD9 antigen of human  
 RT platelets.";  
 RL FEBS Lett. 264:270-274(1990).  
 RN [8]  
 RP ROLE IN CELL MOTILITY AND METASTASIS.  
 RX PubMed=8478605; DOI=10.1084/jem.177.5.1231;  
 RA Ikegama S., Koyama M., Yamako M., Saeada R., Miyake M.;  
 RT "Suppression of cell motility and metastasis by transfection with  
 RT human motility-related protein (MRP-1/CD9) DNA.";  
 RL J. Exp. Med. 177:1231-1237(1993).  
 RN [9]  
 RP ROLE IN CELL ADHESION.  
 RX PubMed=7511626;  
 RA Masellis-Smith A., Shaw A.R.;  
 RT "CD9-regulated adhesion. Anti-CD9 monoclonal antibody induce pre-B  
 RT cell adhesion to bone marrow fibroblasts through de novo recognition  
 RT of fibronectin.";  
 RL J. Immunol. 152:2768-2777(1994).  
 RN [10]  
 RP ROLE IN GAMETE FUSION.  
 RX PubMed=14575715; DOI=10.1016/j.bbrc.2003.09.196;  
 RA Higginbottom A., Takahashi Y., Bolling L., Coonrod S.A., White J.M.,  
 RA Partridge L.J., Monk P.N.;  
 RT "Structural requirements for the inhibitory action of the CD9 large  
 RT extracellular domain in sperm/oocyte binding and fusion.";  
 RL Biochem. Biophys. Res. Commun. 311:208-214(2003).  
 RN [11]  
 RP SUBUNIT.  
 RX PubMed=14556650; DOI=10.1042/BJ20031037;  
 RA Kovalenko O.V., Yang X., Kolesnikova T.V., Hemler M.E.;  
 RT "Evidence for specific tetraspanin homodimers: inhibition of  
 RT palmitoylation makes cysteine residues available for cross-linking.";  
 RL Biochem. J. 377:407-417(2004).  
 RN [12]  
 RP PHOSPHORYLATION.  
 RX MEDLINE=93327758; PubMed=7687539;  
 RA Chalupny N.J., Kanner S.B., Schieven G.L., Wee S., Gilliland L.K.,  
 RA Aruffo A., Ledbetter J.A.;  
 RT "Tyrosine phosphorylation of CD19 in pre-B and mature B cells.";  
 RL EMBO J. 12:2691-2696(1993).  
 RN [13]  
 RP PALMITOYLATION, AND MUTAGENESIS OF CVS-8; CVS-77; CVS-78; CVS-86;  
 RP CVS-217 AND CVS-218.  
 RX PubMed=11959120; DOI=10.1016/S0014-5793(02)02522-X;  
 RA Charrin S., Manie S., Oualid M., Billard M., Boucheix C.,  
 RA Rubinstein E.;  
 RT "Differential stability of tetraspanin/tetraspanin interactions: role  
 RT of palmitoylation.";  
 RL FEBS Lett. 516:139-144(2002).  
 RN [14]  
 RP INTERACTION WITH PTGFRN.  
 RX MEDLINE=21216740; PubMed=11278880; DOI=10.1074/jbc.M011297200;  
 RA Charrin S., Le Naour F., Oualid M., Billard M., Faure G., Hanash S.M.,  
 RA Boucheix C., Rubinstein E.;  
 RT "The major CD9 and CD81 molecular partner. Identification and  
 RT characterization of the complexes.";  
 RL J. Biol. Chem. 276:14329-14337(2001).  
 CC -!- FUNCTION: Involved in platelet activation and aggregation.  
 CC Regulates paranodal junction formation. Required for gamete  
 CC metastasis.  
 CC -!- SUBUNIT: Forms both disulfide-linked homodimers and higher  
 CC homooligomers as well as heterooligomers with other members of the  
 CC tetraspanin family. Associates with CR2/CD21 and with  
 CC PTGFRN/CD9P1.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- TISSUE SPECIFICITY: Expressed by a variety of hematopoietic and  
 CC epithelial cells.  
 CC -!- PTM: Protein exists in three forms with molecular masses between  
 CC 22 and 27 kDa, and is known to carry covalently linked fatty  
 CC acids.  
 CC -!- PTM: Phosphorylated on tyrosine following B-cell activation.  
 CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.

DR PROSITE; PS00421; TW4.1; 1.  
 KW Antigen; Cell adhesion; Direct protein sequencing; Fertilization;  
 Query Match 100.0%; Score 207; DB 1; Length 227;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-21;  
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAIHYALNCCGLAGGVEQFISDIPCKDV 38  
 |||  
 134 KDEPQRETLKAIHYALNCCGLAGGVEQFISDIPCKDV 171

RESULT 2  
 Q5J7W6 HUMAN  
 ID Q5J7W6 HUMAN PRELIMINARY; PRT; 228 AA.  
 AC Q5J7W6;  
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
 DE Growth-inhibiting gene 2 protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RZ NUCLEOTIDE SEQUENCE.  
 RA Kim J.W.;  
 RT "Identification of a human growth inhibition gene 2 (GIC2).";  
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
 RE EMBL: A1423720; AAS00483.1; -; mRNA.  
 SQ SEQUENCE 228 AA; 25416 MW; F683333E0C20611D8 CRC64;

Query Match 100.0%; Score 207; DB 2; Length 228;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-21;  
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAIHYALNCCGLAGGVEQFISDIPCKDV 38  
 |||  
 135 KDEPQRETLKAIHYALNCCGLAGGVEQFISDIPCKDV 172

RESULT 3  
 CD9 CERAE  
 ID CD9 CERAE STANDARD; PRT; 227 AA.  
 AC P30409;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE CD9 antigen (27 kDa diphtheria toxin receptor-associated protein) (DRAP27).  
 GN Name=CD9;  
 OS Cercopithecus aethiops (Green monkey) (Grivet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 OC Cercopitheidae; Cercopithecinae; Cercopithecus.  
 OX NCBI\_TaxID=9534;  
 RN [1]  
 RZ NUCLEOTIDE SEQUENCE [mRNA].  
 RA Mitamura T., Iwanoto R., Unata T., Yomo T., Urabe I., Tsuneoka M.,  
 RE MEDLINE=92394967; PubMed=1522113; DOI=10.1083/jcb.118.6.1389;  
 RT Mekada E.;  
 RT "The 27-kD diphtheria toxin receptor-associated protein (DRAP27) from  
 vero cells is the monkey homologue of human CD9 antigen: expression of  
 DRAP27 elevates the number of diphtheria toxin receptors on toxin-  
 sensitive cells.";  
 RL J. Cell Biol. 118:1389-1399(1992).  
 CC -!- FUNCTION: Involved in platelet activation and aggregation.  
 CC Regulates paranodal junction formation. Required for gamete  
 CC fusion. Involved in cell adhesion, cell motility and tumor  
 CC metastasis (By similarity).  
 CC -!- FUNCTION: Expression of DRAP27 elevates the number of diphtheria  
 CC toxin receptors on toxin-sensitive cells.

```

RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX PubMed:7753050; DOI=10.1016/0161-5890(95)00008-3;
RA Willett B.J., Neil J.C.;
RT "cDNA cloning and eukaryotic expression of feline CD9.";
RL Mol. Immunol. 32:417-423(1995).
RN [2]
RP IMMUNE SEQUENCE [MRNA].
RA Morikawa S.;
RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Involved in platelet activation and aggregation.
CC Regulates paranodal junction formation. Required for gamete
CC fusion. Involved in cell adhesion, cell motility and tumor
CC metastasis (By similarity).
CC -!- SUBUNIT: Forms both disulfide-linked homodimers and higher
CC homooligomers as well as heterooligomers with other members of the
CC tetraspanin family. Associates with CR2/CD21 and with PTGFRN/CD9p1
CC (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- PTM: Phosphorylated on tyrosine following B-cell activation (By
CC similarity).
CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; L35275; AAA92867.1; -; mRNA.
CC EMBL; D30786; BAA0642.1; -; mRNA.
CC GO; GO:0005887; C:integral to plasma membrane; ISS.
CC GO; GO:0005515; P:protein binding; ISS.
CC GO; GO:0007155; P:cell adhesion; ISS.
CC GO; GO:0006928; P:cell motility; ISS.
CC GO; GO:0007342; P:fusion of sperm to egg plasma membrane; ISS.
CC GO; GO:0030913; P:paranodal junction formation; ISS.
CC GO; GO:0030168; P:platelet activation; ISS.
CC Pfam; PF00335; Tetraspanin; 1.
CC PRINTS; PR00259; TMFOUR.
CC PROSITE; PS00421; TM4 1; 1.
CC Antigen; Cell adhesion; Fertilization; Lipoprotein; Palmitate;
CC Phosphorylation; Transmembrane.
FT INIT_MET 0 0 By similarity.
FT TOPO_DOM 1 11 Cytoplasmic (Potential).
FT TRANSMEM 12 32 Potential.
FT TOPO_DOM 33 52 Extracellular (Potential).
FT TRANSMEM 53 73 Potential.
FT TOPO_DOM 74 84 Cytoplasmic (Potential).
FT TRANSMEM 85 108 Potential.
FT TOPO_DOM 109 192 Extracellular (Potential).
FT TRANSMEM 193 218 Potential.
FT TOPO_DOM 219 225 Cytoplasmic (Potential).
FT LIPID 8 8 S-palmitoyl cysteine (By similarity).
FT LIPID 75 75 S-palmitoyl cysteine (By similarity).
FT LIPID 76 76 S-palmitoyl cysteine (By similarity).
FT LIPID 84 84 S-palmitoyl cysteine (By similarity).
SQ SEQUENCE 225 AA; 24927 MW; 5A049774501B03B3 CRC64;

Query Match 93.7%; Score 194; DB 1; Length 225;
Best Local Similarity 89.5%; Pred. No. 8.6e-20;
Matches 34; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETLKATHYALNCCGLAGGVEQFISDTCPKQDV 38
DB 132 KDEPQRETLKATHYALNCCGLAGGVEQFISDTCPKQDI 169

RESULT 5

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CD9_RAT
ID CD9_RAT STANDARD; PRT; 225 AA.
AC P40241;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE CD9 antigen.
GN Name=CD9;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX STRAIN=Sprague-Dawley; TISSUE=Sciatic nerve;
RX MEDLINE=95123481; PubMed=7823164;
RA Kaprielian Z., Cho K.O., Hadjiargyrou M., Patterson P.H.;
RT "CD9, a major platelet cell surface glycoprotein, is a ROCA antigen
RT and is expressed in the nervous system.";
RL J. Neurosci. 15:562-573(1995).
CC -!- FUNCTION: Involved in platelet activation and aggregation.
CC Regulates paranodal junction formation. Required for gamete
CC fusion. Involved in cell adhesion, cell motility and tumor
CC metastasis (By similarity).
CC -!- SUBUNIT: Forms both disulfide-linked homodimers and higher
CC homooligomers as well as heterooligomers with other members of the
CC tetraspanin family. Associates with CR2/CD21 and with PTGFRN/CD9p1
CC (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in the peripheral nervous system.
CC -!- PTM: Phosphorylated on tyrosine following B-cell activation (By
CC similarity).
CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; X76489; CAA54027.1; -; mRNA.
CC PIR; I56562; S39262.
CC Ensembl; ENSRNOG00000019556; Rattus norvegicus.
CC RGD; 2318; CD9.
CC GO; GO:0005986; C:cell surface; IDA.
CC GO; GO:0005887; C:integral to plasma membrane; ISS.
CC GO; GO:0005515; P:protein binding; IPI.
CC GO; GO:0007155; P:cell adhesion; ISS.
CC GO; GO:0006928; P:cell motility; ISS.
CC GO; GO:0007342; P:fusion of sperm to egg plasma membrane; ISS.
CC GO; GO:0030913; P:paranodal junction formation; ISS.
CC GO; GO:0030168; P:platelet activation; ISS.
CC InterPro; IPR000301; Transmem 4.
CC Pfam; PF00335; Tetraspanin; 1.
CC PRINTS; PR00259; TMFOUR.
CC PROSITE; PS00421; TM4 1; 1.
CC Antigen; Cell adhesion; Fertilization; Glycoprotein; Lipoprotein;
CC Palmitate; Phosphorylation; Transmembrane.
FT INIT_MET 0 0 By similarity.
FT TOPO_DOM 1 11 Cytoplasmic (Potential).
FT TRANSMEM 12 32 Potential.
FT TOPO_DOM 33 52 Extracellular (Potential).
FT TRANSMEM 53 73 Potential.
FT TOPO_DOM 74 84 Cytoplasmic (Potential).
FT TRANSMEM 85 108 Potential.
FT TOPO_DOM 109 192 Extracellular (Potential).
FT TRANSMEM 193 218 Potential.
FT TOPO_DOM 219 225 Cytoplasmic (Potential).
FT LIPID 8 8 S-palmitoyl cysteine (By similarity).
FT LIPID 75 75 S-palmitoyl cysteine (By similarity).
FT LIPID 76 76 S-palmitoyl cysteine (By similarity).
FT LIPID 84 84 S-palmitoyl cysteine (By similarity).

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FT LIPID 215 215 S-palmitoyl cysteine (By similarity).
FT LIPID 216 216 S-palmitoyl cysteine (By similarity).
FT CARBOHYD 49 49 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 225 AA; 25084 MW; 7889619F99A59C9D CRC64;

Query Match 92.3%; Score 191; DB 1; Length 225;
Best Local Similarity 92.1%; Pred. No. 2.4e-19;
Matches 35; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAIHYALNCCGLAGGVEQFISDICKPKDV 38
Db 132 KDEPQRETLKAIHYALNCCGLAGGVEQFISDICKPKDV 169

RESULT 6
Q8MJ48_PIG PRELIMINARY; PRT; 226 AA.
ID Q8MJ48_PIG
AC Q8MJ48;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transmembrane protein CD9.
GN Name:CD9;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Heinz M., Huang C.A., Emery D.W., Giovino M.A., LeGuern A.,
RA Kurilla-Mahon B., Theodore P., Arn J.S., Sykes M., Mulligan R.C.,
RA Down J.D., Sachs D.H., Goodell M.A.;
RT "Use of CD9 Expression to Enrich for Porcine Hematopoietic
RT Progenitors";
RL Exp. Hematol. 0:0-0(2002).
DR EMBL; AF525029; AAM81376.1; -; mRNA.
DR HSP; P60033; I08Q.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR InterPro; IPR000301; Transmem 4.
DR Pfam; PF00335; Tetraspanin; I.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM4_1; 1.
KW Transmembrane.
SQ SEQUENCE 226 AA; 25127 MW; 885C244477F95C23 CRC64;

Query Match 86.5%; Score 179; DB 2; Length 226;
Best Local Similarity 81.6%; Pred. No. 1.4e-17;
Matches 31; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAIHYALNCCGLAGGVEQFISDICKPKDV 38
Db 133 KDEPQRETLKAIHYALDCCGLMGVEQLADICPKQDV 170

RESULT 7
CD9_PIG STANDARD; PRT; 225 AA.
ID CD9_PIG
AC Q8WQJ3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE CD9 antigen.
GN Name:CD9;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE [RNA].
RC Tissue=Smooth muscle;
RX PubMed=14610355; DOI=10.1159/000074170;
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RA Yubero N., Jimenez-Marin A., Yerle M., Morera L., Barbancho M.J.,
RA Llanes D., Garrido J.J.;
RT "Molecular cloning, expression pattern and chromosomal mapping of pig
RT CD9 antigen.";
RL Cytogenet. Genome Res. 101:143-146(2003).
CC -1- FUNCTION: Involved in platelet activation and aggregation.
CC Regulates paranodal junction formation. Required for gamete
CC fusion. Involved in cell adhesion, cell motility and tumor
CC metastasis (By similarity).
CC -1- SUBUNIT: Forms both disulfide-linked homodimers and higher
CC homooligomers as well as heterooligomers with other members of the
CC tetraspanin family. Associates with CR2/CD21 and with PTGFRN/CD9P1
CC (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- PTM: Phosphorylated on tyrosine following B-cell activation (By
CC similarity).
CC -1- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AY027285; AAL68966.1; -; mRNA.
CC GO; GO:0005887; C: integral to plasma membrane; ISS.
CC GO; GO:0005515; P: protein binding; ISS.
CC GO; GO:0007155; P: cell adhesion; ISS.
CC GO; GO:0006928; P: cell motility; ISS.
CC GO; GO:0007342; P: fusion of sperm to egg plasma membrane; ISS.
CC GO; GO:0030913; P: paranodal junction formation; ISS.
CC GO; GO:0030168; P: platelet activation; ISS.
CC InterPro; IPR000301; Transmem 4.
CC Pfam; PF00335; Tetraspanin; I.
CC PRINTS; PR00259; TMFOUR.
CC PROSITE; PS00421; TM4_1; 1.
CC Antigen; Cell adhesion; Fertilization; Glycoprotein; Lipoprotein;
KW Palmitate; Phosphorylation; Transmembrane.
FT INIT MET 0 0 By similarity.
FT TOPO_DOM 1 11 Cytoplasmic (Potential).
FT TRANSMEM 12 32 Potential.
FT TOPO_DOM 33 52 Extracellular (Potential).
FT TRANSMEM 53 73 Potential.
FT TOPO_DOM 74 84 Cytoplasmic (Potential).
FT TRANSMEM 85 108 Potential.
FT TOPO_DOM 109 192 Extracellular (Potential).
FT TRANSMEM 193 218 Potential.
FT TOPO_DOM 219 225 Cytoplasmic (Potential).
FT LIPID 75 75 S-palmitoyl cysteine (By similarity).
FT LIPID 76 76 S-palmitoyl cysteine (By similarity).
FT LIPID 84 84 S-palmitoyl cysteine (By similarity).
FT LIPID 215 215 S-palmitoyl cysteine (By similarity).
FT LIPID 216 216 S-palmitoyl cysteine (By similarity).
FT CARBOHYD 49 49 N-linked (GlcNAc...) (Potential).
FT SEQUENCE 225 AA; 25070 MW; FF280FE39BC11545 CRC64;

Query Match 81.2%; Score 168; DB 1; Length 225;
Best Local Similarity 76.3%; Pred. No. 5.6e-16;
Matches 29; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAIHYALNCCGLAGGVEQFISDICKPKDV 38
Db 132 KDEPQRETLKAIHYALDCCGLMGVEQLADICPKQDV 169

RESULT 8
CD9_MOUSE STANDARD; PRT; 225 AA.
ID CD9_MOUSE
AC P40240;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
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DT	13-SEP-2005 (rel. 48, Last annotation update)	RP	ROLE IN GAMETE FUSION.
DE	CD9 antigen.	RX	PubMed=10700183; DOI=10.1038/73502;
GN	Mouse muscle (Mouse).	RA	Kaji K., Oda S., Shikano T., Ohnuki T., Uematsu Y., Sakagami J.,
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	RA	Tada N., Miyazaki S., Kudo A.,
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;	RT	"The gamete fusion process is defective in eggs of Cd9-deficient
OC	Muroidea; Muridae; Murinae; Mus.	RT	mice.";
OX	NCBI_TaxID=10090;	RL	Nat. Genet. 24:279-282(2000).
RN	[1]	RN	[5]
RP	NUCLEOTIDE SEQUENCE [MRNA].	RN	ROLE IN PARANODAL FORMATION, AND TISSUE SPECIFICITY.
RC	STRAIN=BALB/C; TISSUE=Kidney.	RX	PubMed=14715942; DOI=10.1523/JNEUROSCI.1484-03.2004;
RC	MEDLINE=94054345; PubMed=8236164; DOI=10.1016/0049-3848(93)90162-H;	RA	Ishibashi T., Ding L., Ikenaka K., Inoue Y., Miyado K., Mekada E.,
RX	Rubinstein E., Billard M., Plaisance S., Prenant M., Boucheix C.;	RA	Baba H.;
RA	"Molecular cloning of the mouse equivalent of CD9 antigen.";	RT	"tetraspanin protein CD9 is a novel paranodal component regulating
RT	Thromb. Res. 71:377-383(1993).	RT	paranodal junctional formation.";
RL	[2]	RL	J. Neurosci. 24:96-102(2004).
RN	[2]	RN	[6]
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].	RP	FUNCTION AS RECEPTOR FOR PSG17.
RC	STRAIN=C57BL/6J; TISSUE=Kidney.	RX	PubMed=11805154; DOI=10.1084/jem.20011741;
RX	MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;	RA	Waterhouse R., Ha C., Dveksler G.S.;
RA	Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,	RT	"Murine CD9 is the receptor for pregnancy-specific glycoprotein 17.";
RA	Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,	RL	J. Exp. Med. 195:277-282(2002).
RA	Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,	CC	-!- FUNCTION: Involved in platelet activation and aggregation.
RA	Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,	CC	Regulates paranodal junction formation. Required for gamete
RA	Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,	CC	fusion. Involved in cell adhesion, cell motility and tumor
RA	Blake J.A., Bradt D., Brusic V., Ghothia C., Corbani L.E., Cousins S.,	CC	metastasis. Acts as a receptor for PSG17.
RA	Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,	CC	-!- SUBUNIT: Forms both disulfide-linked homodimers and higher
RA	Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,	CC	homooligomers as well as heterooligomers with other members of the
RA	Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,	CC	tetraspanin family. Associates with CR2/CD21 and with PTCFRN/CD9P1
RA	Kanai A., Kawaji H., Kawasaki Y., Kedzierski R.M., King B.L.,	CC	(By similarity).
RA	Konagaya A., Kurochkin I.V., Lee Y., Lenzhard B., Lyons P.A.,	CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.
RA	Maglott D.R., Malcais L., Marchionni L., McKenzie L., Miki H.,	CC	-!- TISSUE SPECIFICITY: Expressed predominantly in the peripheral
RA	Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,	CC	nervous system.
RA	Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,	CC	-!- PTM: Phosphorylated on tyrosine following B-cell activation (By
RA	Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,	CC	similarity).
RA	Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,	CC	-!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
RA	Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,	CC	This Swiss-Prot entry is copyright. It is produced through a collaboration
RA	Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
RA	Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,	CC	the European Bioinformatics Institute. There are no restrictions on its
RA	Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,	CC	use as long as its content is in no way modified and this statement is not
RA	Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,	CC	removed.
RA	Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,	CC	-----
RA	Hara A., Hashizume M., Imotani K., Ichii Y., Itoh M., Kagawa I.,	CC	EMBL; L08115; AAA37405.1; -; mRNA.
RA	Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,	CC	EMBL; AK002251; BAB21965.1; -; mRNA.
RA	Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,	CC	EMBL; AK012793; BAB28473.1; -; mRNA.
RA	Birney E., Hayashizaki Y.;	CC	EMBL; BC070474; AAH70474.1; -; mRNA.
RT	"Analysis of the mouse transcriptome based on functional annotation of	CC	PIR; I49589; I49589.
RT	60,770 full-length cDNAs.";	CC	Ensembl; ENSMUSG0000030342; Mus musculus.
RL	Nature 420:563-573(2002).	CC	MG1; MG1:88348; Cd9.
RN	[3]	CC	GO; GO:0005887; C:integral to plasma membrane; ISS.
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].	CC	GO; GO:0005886; C:plasma membrane; TAS.
RC	STRAIN=C57BL/6; TISSUE=Brain;	CC	GO; GO:0005515; F:protein binding; IPI.
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;	CC	GO; GO:0007155; P:cell adhesion; ISS.
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	CC	GO; GO:0006928; P:cell motility; ISS.
RA	Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,	CC	GO; GO:0007342; P:fusion of sperm to egg plasma membrane; IDA.
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	CC	GO; GO:0030913; P:paranodal junction formation; IDA.
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	CC	GO; GO:0030169; P:platelet activation; ISS.
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	CC	InterPro; IPR000301; Transmem 4.
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	CC	Pfam; PF00335; Tetraspanin; I.
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,	CC	PRINTS; PR00259; TMSOUR.
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,	CC	PROSITE; PS00421; TM4_1; 1.
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	CC	Antigen; Cell adhesion; Fertilization; Glycoprotein; Lipoprotein;
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	CC	Palmitate; Phosphorylation; Transmembrane.
RA	Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	CC	INIT MET 0 0
RA	Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,	CC	By similarity.
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	CC	TOPO_DOM 1 11
RA	Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,	CC	TRANSMEM 12 32
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,	CC	TOPO_DOM 33 52
RA	Butterfield Y.S.N., Krzywicki M.I., Skalek A.U., Smallos D.E.,	CC	TRANSMEM 53 73
RA	Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;	CC	TOPO_DOM 74 84
RT	"Generation and initial analysis of more than 15,000 full-length human	CC	TRANSMEM 85 108
RT	and mouse cDNA sequences.";	CC	TOPO_DOM 109 192
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	CC	TRANSMEM 193 218
RN	[4]	CC	TOPO_DOM 219 225



FT LIPID 8 8 S-palmitoyl cysteine (By similarity).  
 FT LIPID 75 75 S-palmitoyl cysteine (By similarity).  
 FT LIPID 76 76 S-palmitoyl cysteine (By similarity).  
 FT LIPID 84 84 S-palmitoyl cysteine (By similarity).  
 FT LIPID 215 215 S-palmitoyl cysteine (By similarity).  
 FT LIPID 216 216 S-palmitoyl cysteine (By similarity).  
 FT CARBOHYD 49 49 N-linked (GlcNAc...) (Potential).  
 SQ SEQUENCE 225 AA; 2BBE40B8D7C31BC0 CRC64;  
 Query Match 80.78; Score 167; DB 1; Length 225;  
 Best Local Similarity 78.9%; Pred. No. 7.8e-16;  
 Matches 30; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 KDBPQRETLKAHYALNCCGLAGVEQFISDTCPPKDV 38  
 DB 132 KDBPQRETLKAHYALNCCGLAGVEQFISDTCPPKQL 169  
 RESULT 9  
 CD9\_BOVIN STANDARD; PRT; 225 AA.  
 ID CD9\_BOVIN STANDARD; PRT; 225 AA.  
 AC P30932;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE CD9 antigen.  
 GN Names=CD9;  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 OC Pecora; Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [MRNA].  
 RC TISSUE=Ocular ciliary epithelium;  
 RX MEDLINE=93054422; PubMed=1339429;  
 RA Martin-Alonso J.M., Hernando N., Ghosh S., Coca-Prados M.;  
 RT "Molecular cloning of the bovine CD9 antigen from ocular ciliary  
 epithelial cells";  
 RL J. Biochem. 112:63-67(1992).  
 CC -I- FUNCTION: Involved in platelet activation and aggregation.  
 CC Regulates paranodal junction formation. Required for gamete  
 CC fusion. Involved in cell adhesion, cell motility and tumor  
 CC metastasis (By similarity).  
 CC -I- SUBUNIT: Forms both disulfide-linked homodimers and higher  
 CC homooligomers as well as heterooligomers with other members of the  
 CC tetraspanin family. Associates with CR2/CD21 and with PTCFRN/CD9p1  
 CC (By similarity).  
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -I- PTM: Phosphorylated on tyrosine following B-cell activation (By  
 CC similarity).  
 CC -I- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.  
 CC  
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 CC removed.  
 CC  
 CC EMBL; M81720; AAA30439.1; -; mRNA.  
 CC FR; JX0221; JX0221.  
 CC DR GO; GO:0005887; C:integral to plasma membrane; ISS.  
 CC DR GO; GO:0005155; F:protein binding; ISS.  
 CC DR GO; GO:0007155; P:cell adhesion; ISS.  
 CC DR GO; GO:0006928; P:cell motility; ISS.  
 CC DR GO; GO:0007342; P:fusion of sperm to egg plasma membrane; ISS.  
 CC DR GO; GO:0030913; P:paranodal junction formation; ISS.  
 CC DR GO; GO:0030168; P:platelet activation; ISS.  
 CC InterPro; IPR000301; Transmem 4.  
 CC Pfam; PF00335; Tetraspanin; 1.  
 CC PRINTS; PR00259; TMFOUR.  
 CC DR PROSITE; PS00421; TM4.1; 1.  
 CC Antigen; Cell adhesion; Fertilization; Glycoprotein; Lipoprotein;  
 KW

KW Palmitate; Phosphorylation; Transmembrane.  
 INIT MET 0 0 By similarity.  
 FT TOPO\_DOM 1 11 Cytoplasmic (Potential).  
 FT TRANSMEM 12 32 Potential.  
 FT TOPO\_DOM 33 52 Extracellular (Potential).  
 FT TRANSMEM 53 73 Potential.  
 FT TOPO\_DOM 74 84 Cytoplasmic (Potential).  
 FT TRANSMEM 85 108 Potential.  
 FT TOPO\_DOM 109 192 Extracellular (Potential).  
 FT TRANSMEM 193 218 Potential.  
 FT TOPO\_DOM 219 225 Cytoplasmic (Potential).  
 FT LIPID 8 8 S-palmitoyl cysteine (By similarity).  
 FT LIPID 75 75 S-palmitoyl cysteine (By similarity).  
 FT LIPID 76 76 S-palmitoyl cysteine (By similarity).  
 FT LIPID 84 84 S-palmitoyl cysteine (By similarity).  
 FT LIPID 215 215 S-palmitoyl cysteine (By similarity).  
 FT LIPID 216 216 S-palmitoyl cysteine (By similarity).  
 FT CARBOHYD 49 49 N-linked (GlcNAc...) (Potential).  
 SQ SEQUENCE 225 AA; 25127 MW; ECB67DB91A0858E7 CRC64;  
 Query Match 72.9%; Score 151; DB 1; Length 225;  
 Best Local Similarity 71.1%; Pred. No. 1.7e-13;  
 Matches 27; Conservative 5; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 KDBPQRETLKAHYALNCCGLAGVEQFISDTCPPKDV 38  
 DB 132 KDBPQRETLKAHYALNCCGLAGVEQFISDTCPPKQL 169  
 RESULT 10  
 Q6QGE5\_XENLA PRELIMINARY; PRT; 228 AA.  
 ID Q6QGE5\_XENLA PRELIMINARY; PRT; 228 AA.  
 AC Q6QGE5;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DE MGC80123 protein.  
 GN Name=MGC80123;  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
 OC Xenopodidae; Xenopus; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Spleen;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altshul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S.C., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Spleen;  
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
 RA Richardson P.;

RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
RT initiative.";   
RL Dev. Dyn. 225:384-391(2002).   
RN [3]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Spleen;

RA Klein S., Gerhard D.S.;

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL, BC072800; AAH72800.1; -, mRNA.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR InterPro; IPR000301; Transmem 4.

DR Pfam; PF00335; Tetraspannin; I.

DR PRINTS; PR00259; TMFOUR.

DR PROSITE; PS00421; TM4 1; 1.

SQ SEQUENCE 228 AA; 25155 MW; 9A826DBC2D9980A2 CRC64;

Query Match 61.4%; Score 127; DB 2; Length 228;

Best Local Similarity 55.6%; Pred. No. 5.8e-10;

Matches 20; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 KDEPQRETIKAIHYALNCCGLAGGVEQFISDPCPK 36

DB 134 RDGPKLTKGIHFAMNCCGLAGTIDATLTIDPCPK 169

RESULT 11

Q9IBC9 CHICK

ID Q9IBC9\_CHICK PRELIMINARY; PRT; 224 AA.

AC Q9IBC9;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE CD9 antigen.

OS Name=CD9;

GN Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI\_TaxID=9031;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Spinal cord;

RA Kobayashi T., Mekada E.;

RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL, AB032767; BAA93011.1; -, mRNA.

DR HSSP; P60033; IG8Q.

DR Ensembl; ENSGALG00000017274; Gallus gallus.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR InterPro; IPR000301; Transmem 4.

DR Pfam; PF00335; Tetraspannin; I.

DR PRINTS; PR00259; TMFOUR.

DR PROSITE; PS00421; TM4 1; 1.

SQ SEQUENCE 224 AA; 24969 MW; AE64BDF849516151 CRC64;

Query Match

Best Local Similarity 58.0%; Score 120; DB 2; Length 224;

Matches 20; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 6 RETLKAIHYALNCCGLAGGVEQFISDPCPK 36

DB 136 REILKAFPALNCCGIGTGLEQLQMLMESCCK 166

RESULT 12

Q6DKM9 XENLA

ID Q6DKM9\_XENLA PRELIMINARY; PRT; 228 AA.

AC Q6DKM9;

DT 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE MGCD2181 protein.

GN Name=MGCD2181;

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
OC Xenopodinae; Xenopus; Xenopus.

OX NCBI\_TaxID=8355;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Embryo;

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL, BC072800; AAH72800.1; -, mRNA.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR InterPro; IPR000301; Transmem 4.

DR Pfam; PF00335; Tetraspannin; I.

DR PRINTS; PR00259; TMFOUR.

DR PROSITE; PS00421; TM4 1; 1.

SQ SEQUENCE 228 AA; 25155 MW; 9A826DBC2D9980A2 CRC64;

Query Match 61.4%; Score 127; DB 2; Length 228;

Best Local Similarity 55.6%; Pred. No. 5.8e-10;

Matches 20; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 KDEPQRETIKAIHYALNCCGLAGGVEQFISDPCPK 36

DB 134 RDGPKLTKGIHFAMNCCGLAGTIDATLTIDPCPK 169

RESULT 11

Q9IBC9 CHICK

ID Q9IBC9\_CHICK PRELIMINARY; PRT; 224 AA.

AC Q9IBC9;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE CD9 antigen.

OS Name=CD9;

GN Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI\_TaxID=9031;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Spinal cord;

RA Kobayashi T., Mekada E.;

RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL, AB032767; BAA93011.1; -, mRNA.

DR HSSP; P60033; IG8Q.

DR Ensembl; ENSGALG00000017274; Gallus gallus.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR InterPro; IPR000301; Transmem 4.

DR Pfam; PF00335; Tetraspannin; I.

DR PRINTS; PR00259; TMFOUR.

DR PROSITE; PS00421; TM4 1; 1.

SQ SEQUENCE 224 AA; 24969 MW; AE64BDF849516151 CRC64;

Query Match

Best Local Similarity 58.0%; Score 120; DB 2; Length 224;

Matches 20; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 6 RETLKAIHYALNCCGLAGGVEQFISDPCPK 36

DB 136 REILKAFPALNCCGIGTGLEQLQMLMESCCK 166

RESULT 12

Q6DKM9 XENLA

ID Q6DKM9\_XENLA PRELIMINARY; PRT; 228 AA.

AC Q6DKM9;

DT 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE MGCD2181 protein.

GN Name=MGCD2181;

OS Xenopus laevis (African clawed frog).

OC

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DR

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DR

DR

DR

SQ

Query Match

Best Local Similarity

Matches

QY

DB

RESULT 13

Q7ZUH9 BRARE

ID

AC

DT

DT

DT

DE

GN

OS

OC

OC

OC

OX

RN NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Whole body;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Villalon D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguezes S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Whole body;  
 RX Director MGC Project;  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC049036; AHA9036.1; -; mRNA.  
 DR HSP; P60033; 168Q.  
 DR ENSDARG0000016691; Danio rerio.  
 DR ZFIN; ZDB-GENE-040426-2768; cd91.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR InterPro; IPR000301; Transmem 4.  
 DR Pfam; PF00335; Tetraspannin; 1.  
 DR PRINTS; PR00259; TMPOUR.  
 DR PROSITE; PS00421; TM4\_1; 1.  
 SQ SEQUENCE 227 AA; 24362 MW; A48AEEAA2B74B100 CRC64;  
 Query Match 45.9%; Score 95; DB 2; Length 227;  
 Best Local Similarity 47.2%; Pred. No. 2.8e-05;  
 Matches 17; Conservative 6; Mismatches 13; Indels 0; Gaps 0;  
 QY 2 DEPORETLKAIHYALNCCGLAGVGEQFISDICPKKD 37  
 DB 135 DGPLKETLTAHFSLQCGTGLASDGVSTCPKQE 170  
 RESULT 14  
 Q6NWG7 BRARE  
 ID Q6NWG7 BRARE PRELIMINARY; PRT; 227 AA.  
 AC Q6NWG7  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
 DE Hypothetical protein cd9.  
 GN Names=cd9;  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OC NCBI\_TaxID=7955;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Wild-type; TISSUE=Eye, and Kidney;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Villalon D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguezes S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Whole body;  
 RX Director MGC Project;  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC049036; AHA9036.1; -; mRNA.  
 DR HSP; P60033; 168Q.  
 DR ENSDARG0000016691; Danio rerio.  
 DR ZFIN; ZDB-GENE-040426-2768; cd91.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR InterPro; IPR000301; Transmem 4.  
 DR Pfam; PF00335; Tetraspannin; 1.  
 DR PRINTS; PR00259; TMPOUR.  
 DR PROSITE; PS00421; TM4\_1; 1.  
 SQ SEQUENCE 227 AA; 24362 MW; A48AEEAA2B74B100 CRC64;  
 Query Match 45.9%; Score 95; DB 2; Length 227;  
 Best Local Similarity 47.2%; Pred. No. 2.8e-05;  
 Matches 17; Conservative 6; Mismatches 13; Indels 0; Gaps 0;  
 QY 2 DEPORETLKAIHYALNCCGLAGVGEQFISDICPKKD 37  
 DB 135 DGPLKETLTAHFSLQCGTGLASDGVSTCPKQE 170

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguezes S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Kidney;  
 RX Director MGC Project;  
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC067597; AAH67597.1; -; mRNA.  
 DR ZFIN; ZDB-GENE-030131-1175; cd9.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR InterPro; IPR000301; Transmem 4.  
 DR Pfam; PF00335; Tetraspannin; 1.  
 DR PRINTS; PR00259; TMPOUR.  
 DR PROSITE; PS00421; TM4\_1; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 227 AA; 25116 MW; 26E5BC35F4E63888 CRC64;  
 Query Match 45.4%; Score 94; DB 2; Length 227;  
 Best Local Similarity 37.8%; Pred. No. 3.9e-05;  
 Matches 14; Conservative 11; Mismatches 12; Indels 0; Gaps 0;  
 QY 1 KDEPQRETLKAIHYALNCCGLAGVGEQFISDICPKKD 37  
 DB 134 KQELAKKTLLRFOHGLNCCGPGSGNMQESLDETCPKKE 170  
 RESULT 15  
 Q6IQH7 BRARE  
 ID Q6IQH7 BRARE PRELIMINARY; PRT; 227 AA.  
 AC Q6IQH7  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE CD9 antigen, like.  
 GN Names=cd9;  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OC NCBI\_TaxID=7955;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Embryo;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,



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OM protein - protein search, using sw model

Run on: January 20, 2006, 17:03:51 ; Search time 87.963 Seconds  
(without alignments)  
124.876 Million cell updates/sec

Title: US-10-619-323-5

Perfect score: 132

Sequence: 1 PKKDVLETFVRSKCPDAIKVEFDNK 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_21:\*

- 1: Geneseq1980s:\*
- 2: Geneseq1990s:\*
- 3: Geneseq2000s:\*
- 4: Geneseq2001s:\*
- 5: Geneseq2002s:\*
- 6: Geneseq2003as:\*
- 7: Geneseq2003bs:\*
- 8: Geneseq2004s:\*
- 9: Geneseq2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	132	100.0	25	ADJ57562	Adj57562 Human CD9
2	132	100.0	227	AAR86834	Aar86834 Human CD9
3	132	100.0	227	ABB78366	Abb78366 Amino aci
4	132	100.0	227	AAE14636	Aae14636 Human CD9
5	132	100.0	227	ABU05057	Abu05057 Human exp
6	132	100.0	227	ABU05060	Abu05060 Human exp
7	132	100.0	227	ABW00436	Abw00436 Human CD9
8	132	100.0	227	ADK9862	Adk9862 Human CD9
9	132	100.0	227	ADI19366	Adi19366 Human CD9
10	132	100.0	227	AEA89005	Aea89005 Human CD9
11	132	100.0	228	AAR27525	Aar27525 Metastasi
12	132	100.0	228	ABB44581	Abb44581 Human exp
13	132	100.0	228	ABU05059	Abu05059 Human exp
14	132	100.0	228	ABU05052	Abu05052 Human exp
15	132	100.0	228	ABU05048	Abu05048 Human exp
16	132	100.0	228	ABU05056	Abu05056 Human exp
17	132	100.0	228	ABU05049	Abu05049 Human exp
18	132	100.0	228	ABU05050	Abu05050 Human exp
19	132	100.0	228	ABU05053	Abu05053 Human exp
20	132	100.0	228	ABW01519	Abw01519 Protein #
21	132	100.0	228	ADG89037	Adg89037 TAT278. 1
22	132	100.0	228	ADG32002	Adg32002 Human hom
23	132	100.0	228	ADJ57558	Adj57558 Human CD9
24	132	100.0	228	ADL26782	Adl26782 Human CD9

25	132	100.0	228	8	ADL82853	Adl82853 Human PRO
26	132	100.0	228	8	ADP23088	Adp23088 PRO polyp
27	132	100.0	228	8	ADR73450	Adr73450 Human CD9
28	132	100.0	228	9	ADV70263	Adv70263 Tumor-ass
29	132	100.0	228	9	ADY97163	Ady97163 Human CD9
30	132	100.0	228	9	ADY19604	Ady19604 PRO polyp
31	132	100.0	228	9	ADY14362	Ady14362 PRO polyp
32	132	100.0	228	9	AE98450	Aeb98450 Human can
33	132	100.0	275	3	ABA43936	Aab43936 Human can
34	132	100.0	275	4	AAG75156	Aag75156 Human col
35	132	100.0	275	6	ABU05055	Abu05055 Human exp
36	132	100.0	275	6	ABU05054	Abu05054 Human exp
37	132	100.0	454	4	ABG14067	Abg14067 Novel hum
38	117.5	89.0	79	2	AAW35851	Aaw35851 Human CD9
39	117.5	89.0	79	6	ABU05058	Abu05058 Human exp
40	98	74.2	226	7	ADB85281	Adb85281 Rat G9 su
41	95	72.0	18	8	ADJ57563	Adj57563 Human CD9
42	94	71.2	226	4	ABB44580	Abb44580 Mouse wou
43	94	71.2	226	5	ABB57234	Abb57234 Mouse isc
44	94	71.2	226	9	ADV25799	Adv25799 Mouse CD9
45	94	71.2	226	9	AEA55045	Aea55045 Mouse CD9

#### ALIGNMENTS

##### RESULT 1

ADJ57562

ID ADJ57562 standard; peptide; 25 AA.

AC ADJ57562;

DT 06-MAY-2004 (first entry)

DE Human CD9 fibronectin-binding domain peptide fragment.

Human; CD9; antithrombotic; antiarteriosclerotic; vasototropic;

haemostatic; antiangiogenic; cytostatic.

OS Homo sapiens.

PN WO2004007685-A3.

PD 22-JAN-2004.

PF 14-JUL-2003; 2003WO-US022050.

PR 12-JUL-2002; 2002US-0395864P.

PA (UYTE-) UNIV TENNESSEE RES FOUND.

PI Jennings LK, Longhurst CM, Cook GA, Bao J, Zhang C, White MM;

Crossano JT, Lu Y;

WPI; 2004-122924/12.

Interfering with CD9 binding to fibronectin by binding a fibronectin-binding domain of the CD9 protein or polypeptide, useful in treating thrombosis, atherosclerosis, restenosis, bleeding disorders, angiogenesis and cancers.

Claim 7; SEQ ID NO 5; 126pp; English.

The present sequence is that of a peptide fragment from the fibronectin-binding domain of human CD9 ADJ57558. The peptide, or an antibody that binds to it, is used in claimed methods for: interfering with CD9 binding to fibronectin; modifying adhesion, motility or spreading of a CD9-expressing cell on fibronectin; inhibiting proliferation or survival of CD9-expressing cells; modifying pericellular fibronectin matrix assembly; modifying invasiveness of a cell through a collagen and/or laminin matrix; and modifying cell-to-cell interaction. The methods are based on the finding that increased CD9 expression is implicated in (i) decreased adhesiveness of cells to extracellular matrix (via alpha5-beta1

CC integrin) and/or decreased cell invasiveness and/or decreased  
 CC pericellular fibronectin matrix assembly, and/or (ii) increased cell  
 CC motility, spreading, proliferation, cell survival against apoptosis,  
 CC and/or cell-to-cell contacts. Conditions or disease states involving  
 CC proliferation or survival of CD9-expressing cells can be treated, e.g.  
 CC thrombosis, atherosclerosis, vein graft failure, restenosis, transplant  
 CC arteriopathy, bleeding disorders, angiogenesis, and primary and  
 CC metastatic cancers including breast cancer, prostate cancer, colon  
 CC cancer, melanoma, ovarian cancer, neuroblastoma, glioma and glioblastoma.  
 XX Sequence 25 AA;

Query Match 100.0%; Score 132; DB 8; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-13;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQVLETFVTKSCPDAIKEVFDNK 25  
 DB 1 PKQVLETFVTKSCPDAIKEVFDNK 25

RESULT 2  
 AAR86834  
 ID AAR86834 standard; protein; 227 AA.

XX AAR86834;  
 DT 12-JUL-1996 (first entry)  
 DE Human CD9 sequence.

CC CD9 antigen; stimulated T cell; antibody; ligand; proliferation;  
 KW monoclonal antibody; ES5.2D8; 27 kD accessory protein; epitope;  
 KW immune response; cancer; infectious disease; growth factor.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 51 /note= "Potential N-linked glycosylation site"

FT Modified-site 52 /note= "Potential N-linked glycosylation site"

FT Domain 111..194 /note= "Extracellular domain"

FT Domain 135..220 /note= "Transmembrane domain"

FT Domain 221..227 /note= "Cytoplasmic domain"

PN WO9533823-A1.

PD 14-DEC-1995.

PF 01-DEC-1994; 94WO-US013782.

PR 03-JUN-1994; 94US-00253751.

PR 03-JUN-1994; 94US-00253964.

XX (USNA ) US SEC OF NAVY.

PA (UNMI ) UNIV MICHIGAN.

PA (REPK ) REPLIGEN CORP.

PA (DAND ) DANA FARBER CANCER INST INC.

PI June CH, Thompson CB, Nabel G, Gray GS, Rennert PD, Freeman GJ;

XX WPI; 1996-040230/04.

XX Selectively inducing CD8 positive T cell proliferation - by activating

PT the T cells and stimulating CD9 cell surface ligand, useful for

FT immuno:therapy of, e.g. cancer.

XX Example 10; Page 38-39; 79pp; English.

CC This sequence represents CD9 from the surface of stimulated T cells. The  
 CC antigen at residues 31-37 of human CD9 (see AAR86832) is bound by an  
 CC antibody or other ligand to stimulate the T cell population to  
 CC proliferate and expand leading to a 100- to 10000-fold increase in cell  
 CC number compared to the original population. The antigenic sequence fits  
 CC the generic sequence given in AAR86827. This epitope is recognised by the  
 CC monoclonal antibody (WAB) ES5.2D8. CD9 is a 27 kD accessory protein found  
 CC on activated T cells. The epitope was recognised by screening a phage  
 CC display library. Selective proliferation of an antigen-specific T cell  
 CC population is useful in cases where the immune response is to be up  
 CC regulated, e.g. in the treatment of cancer or infectious diseases. By  
 CC causing proliferation of the T cell population by stimulating T cell  
 CC epitope removes the need for exogenous growth factors or accessory cells  
 XX Sequence 227 AA;

Query Match 100.0%; Score 132; DB 2; Length 227;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-12;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQVLETFVTKSCPDAIKEVFDNK 25  
 DB 167 PKQVLETFVTKSCPDAIKEVFDNK 191

RESULT 3  
 ABB78366  
 ID ABB78366 standard; protein; 227 AA.

XX ABB78366;

XX 16-DEC-2002 (first entry)

XX Amino acid sequence of CD9.

XX T cell; T cell proliferation; infectious disease; cancer; immunotherapy;  
 KW immunotherapy; CD9.

XX Homo sapiens.

OS US2002115214-A1.

PN 22-AUG-2002.

PF 26-JAN-1996; 96US-00592711.

PR 23-NOV-1988; 88US-00275433.

PR 07-APR-1992; 92US-00864805.

PR 07-APR-1992; 92US-00864807.

PR 07-APR-1992; 92US-00864866.

PR 04-JUN-1993; 93US-00073223.

PR 03-JUN-1994; 94US-00253964.

PR 10-MAR-1995; 95US-00403253.

PR 04-MAY-1995; 95US-00435816.

XX (JUNE/) JUNE C H.

PA (THOM/) THOMPSON C B.

PA (NABEL/) NABEL G J.

PA (GRAY/) GRAY G S.

XX (RENN/) RENNERT P D.

PI June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;

XX WPI; 2002-712476/77.

XX Inducing a population of T cells to proliferate, by activating population  
 of T cells and stimulating an accessory molecule on the surface of the T  
 cells with a ligand which binds the accessory molecule.

XX Example 10; Page 25; 88pp; English.

XX The specification describes method for inducing a population of T cells  
 to proliferate. The method involves activating population of T cells,

stimulating an accessory molecule on T cell surface with a ligand protein) which binds the molecule, to induce proliferation of T cells, monitoring proliferation of T cells in response to continuing exposure to the ligand, and reactivating and restimulating T cells when rate of proliferation has decreased to induce further proliferation of the cells. The method is useful for inducing proliferation of T cells, for use in treatment of infectious disease, cancer and immunotherapy. The method allows for the expansion of a population of T cells in numbers sufficient to reconstitute an individual's total CD4+ or CD8+ T cell population. The resulting T cell population can be genetically transduced and used for immunotherapy or can be used in methods of in vitro analyses of infectious agents. A population of tumour-infiltrating lymphocytes can be obtained from an individual afflicted with cancer and the T cells stimulated to proliferate to sufficient numbers. The resulting T cell population can be genetically transduced to express tumour necrosis factor (TNF) or other factor and restored to the individual. CD4+ T cells expanded by this method are useful in the treatment of HIV infection in an individual. The present sequence represents CD9, an antigen present on the surface of activated T cells

Query Match 100.0%; Score 132; DB 5; Length 227;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-12;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLFTVTKSCPDAIKEVFDNK 25  
 DB 167 PKKDVLFTVTKSCPDAIKEVFDNK 191

RESULT 4  
 AAEL14636  
 ID AAEL14636 standard; protein; 227 AA.  
 XX AAEL14636;  
 AC AAEL14636;  
 DT 16-JUL-2002 (first entry)  
 DE Human CD9 antigen.  
 DE T cell; CD3; accessory molecule; CD28; cancer; infectious disease;  
 KW immunotherapy; human immunodeficiency virus; HIV infection; cytokine;  
 KW human; CD9 antigen.  
 XX Homo sapiens.  
 XX US6352694-B1.  
 XX 05-MAR-2002.  
 XX 10-MAR-1995; 95US-00403253.  
 XX 03-JUN-1994; 94US-00253964.  
 XX (GEM) GENETICS INST INC.  
 PA (UNMI) UNIV MICHIGAN.  
 XX June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;  
 PI WPI; 2002-314696/35.  
 DR Inducing T cell population to proliferate, useful in cancer therapy,  
 PT comprises activating T cells by contacting T cells in vitro with  
 PT immobilised anti-CD3 antibody and stimulating accessory molecule on T  
 PT cell surface.  
 XX Example 10; Col 42; 71pp; English.  
 PS The invention relates to a method of inducing T cell population to  
 CC proliferate for use in therapy comprising activating T cells by  
 CC contacting T cells in vitro with anti-CD3 antibody which is immobilised  
 CC on solid phase surface, and stimulating accessory molecule on T cell

surface in vitro with anti-CD28 antibody, or stimulatory form of natural ligand for CD28 such as B7-1 or B7-2. The method is useful for inducing a population of T cells to proliferate in sufficient numbers for use in therapy e.g., for treating cancer or an infectious disease. The method can be used to selectively expand the population of CD28+, CD4+, CD8+, CD28RA+ or CD28RO+ T cells for immunotherapy. The T cell population resulting by the method can be genetically transduced and used for immunotherapy or can be used for in vitro analysis of infectious agents such as human immunodeficiency virus (HIV). Proliferation of a population of CD4+ T cells obtained from an individual infected with HIV can be achieved and the cells rendered resistant to HIV infection. Following the expansion of the T cells to sufficient numbers, the expanded T cells are restored to the individual. Also CD4+ T cells expanded by the above mentioned is useful for treating HIV infection in an individual. A population of tumour-infiltrating lymphocytes can be obtained from an individual afflicted with cancer and the T cells stimulated to proliferate to sufficient numbers and restored to the individual. The supernatants from cultures of T cells expanded from above mentioned method are useful as a rich source of cytokines and can be used to sustain T cells in vivo or ex vivo. Stimulating and expanding a population of antigen specific T cells are useful in therapeutic conditions where it is desirable to upregulate an immune response. The T cell proliferation occurs in the absence of exogenous growth factors or accessory cells. The present sequence is human CD9 antigen which is expressed on surface of activated T cells

XX SQ Sequence 227 AA;

Query Match 100.0%; Score 132; DB 5; Length 227;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-12;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLFTVTKSCPDAIKEVFDNK 25  
 DB 167 PKKDVLFTVTKSCPDAIKEVFDNK 191

RESULT 5  
 ABU05057  
 ID ABU05057 standard; protein; 227 AA.  
 XX ABU05057;  
 AC ABU05057;  
 XX 29-JAN-2003 (first entry)  
 DT Human expressed protein tag (EPT) #1723.  
 DE Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
 KW protease; protease inhibitor; transporter; cytoskeletal protein;  
 KW receptor; transcription factor; cancer; MHC;  
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
 XX Homo sapiens.  
 XX WO200278524-A2.  
 XX 10-OCT-2002.  
 XX 28-MAR-2002; 2002WO-US009671.  
 XX 28-MAR-2001; 2001US-0279495P.  
 PR 21-MAY-2001; 2001US-0292544P.  
 PR 08-AUG-2001; 2001US-0310801P.  
 PR 01-OCT-2001; 2001US-0326370P.  
 PR 04-DEC-2001; 2001US-0336780P.  
 PR 20-FEB-2002; 2002US-0359885P.  
 XX (ZYCO-) ZYCOS INC.  
 PA Chicz RM, Tomlinson AJ, Urban RG;  
 PI WPI; 2003-040607/03.  
 XX DR

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XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1723; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 227 AA;
Query Match 100.0%; Score 132; DB 6; Length 227;
Best Local Similarity 100.0%; Pred. No. 2.6e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLETTFTVKSCPDPAIKEVFDNK 25
Db 167 PKKDVLETTFTVKSCPDPAIKEVFDNK 191

RESULT 6
ABU05060
ID ABU05060 standard; protein; 227 AA.
XX
AC ABU05060;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1726.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicx RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.

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XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1726; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 227 AA;
Query Match 100.0%; Score 132; DB 6; Length 227;
Best Local Similarity 100.0%; Pred. No. 2.6e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLETTFTVKSCPDPAIKEVFDNK 25
Db 167 PKKDVLETTFTVKSCPDPAIKEVFDNK 191

RESULT 7
ABW00436
ID ABW00436 standard; protein; 227 AA.
XX
AC ABW00436;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human CD9 antigenic protein.
XX
KW HIV infection; human immunodeficiency virus; therapy; antigen; human.
XX
OS Homo sapiens.
XX
PF Key Location/Qualifiers
FT Domain 111..194
FT Domain /note= "Extracellular domain"
FT Domain 195..220
FT Domain /note= "Transmembrane domain"
FT Domain 221..227
FT Domain /note= "Cytoplasmic domain"
XX
PN US2003099643-A1.
XX
PD 29-MAY-2003.
XX
PF 08-JUL-1999; 99US-00350202.
XX
PR 23-NOV-1988; 88US-00275433.
PR 22-NOV-1989; 89WO-US005304.
PR 07-APR-1992; 92US-00864805.
PR 07-APR-1992; 92US-00864807.
PR 07-APR-1992; 92US-00864866.
PR 04-JUN-1993; 93US-00073223.
PR 03-JUN-1994; 94US-00253694.
PR 10-MAR-1995; 95US-00403253.

```



XX (JUNE/) JUNE C H.  
 PA (THOM/) THOMPSON C B.  
 PA (NABEL/) NABEL G J.  
 PA (GRAY/) GRAY G S.  
 PA (RENN/) RENNERT P D.  
 XX

June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;  
 WPI; 2003-801206/75.

Treating HIV infection in individual by isolating T cells from  
 leukocytes, contacting T cells with anti-CD3 antibody for T cell  
 proliferation, separating antibody from T cells, monitoring proliferation  
 of T cells.

Example 10; Page 23; Opp; English.

The present invention relates to a novel method of treating human  
 immunodeficiency virus (HIV) infection in an individual. The method  
 involves isolating population of CD4 T cells from leukocytes, contacting  
 population of CD4+ T cells with an anti-CD3 antibody for stimulating T  
 cell proliferation, separating antibody from T cells, monitoring  
 proliferation of T cells, restimulating T cells with antibody and  
 restoring T cells to individual. The present sequence is human CD9  
 antigenic protein. This sequence is used to illustrate the method of the  
 invention

XX SQ Sequence 227 AA;  
 Query Match 100.0%; Score 132; DB 7; Length 227;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-12;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQVLETFVTKSCPDPAIKEVFDNK 25  
 DB 167 PKQVLETFVTKSCPDPAIKEVFDNK 191  
 |||||

RESULT 8  
 ADK69862  
 ID ADK69862 standard; protein; 227 AA.  
 AC ADK69862;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Human CD9 protein.  
 XX  
 CD28-associated signal; immunotherapy; infectious disease; cancer;  
 leukophoresis; human.  
 KW  
 KW  
 XX  
 OS Homo sapiens.  
 XX  
 US6534055-B1.  
 PN  
 XX  
 18-MAR-2003.  
 XX  
 PF 04-MAY-1995; 95US-00435816.  
 XX  
 07-APR-1992; 92US-00864805.  
 PR  
 07-APR-1992; 92US-00864807.  
 PR  
 07-APR-1992; 92US-00864866.  
 PR  
 04-JUN-1993; 93US-00072223.  
 PR  
 03-JUN-1994; 94US-00253964.  
 PR  
 10-MAR-1995; 95US-00403253.  
 PR  
 (GEMY ) GENETICS INST INC.  
 PA  
 XX  
 June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;  
 WPI; 2003-531074/50.

PT Expanding T cell populations, useful for preparing renewable sources of T  
 cells (e.g. CD4+) for immunotherapy or diagnostics, by stimulating a CD28  
 -associated signal on the surface of the cells with an anti-CD28  
 antibody, B7-1 or B7-2.  
 XX  
 PS Example 10; SEQ ID NO 6; 82pp; English.  
 XX

The invention relates to a method for expanding a population of T cells  
 to about 100-100000-fold over the original T cell population, or to about  
 10 log 1 0 to 12 log 1 2. The method comprises stimulating a CD28-  
 associated signal on the surface of the T cells with agent comprising an  
 anti-CD28 antibody, B7-1 or B7-2. The method is useful for inducing a  
 population of T cells (e.g. CD4+, CD28+, CD8+, CD28RA+ or CD28RO+ T  
 cells) to proliferate. The method is particularly useful for preparing a  
 renewable source of CD4+ T cells. The expanded T cell population can be  
 genetically transduced, and used for immunotherapy to treat a variety of  
 human diseases (e.g. infectious diseases or cancer), or used in  
 diagnostic protocols. T cells were obtained from leukopheresis of a  
 normal donor, and purified with FICOLL density gradient centrifugation,  
 followed by magnetic immunobead sorting. The present sequence is CD9 used  
 in the exemplification of the invention.

XX SQ Sequence 227 AA;  
 Query Match 100.0%; Score 132; DB 7; Length 227;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-12;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQVLETFVTKSCPDPAIKEVFDNK 25  
 DB 167 PKQVLETFVTKSCPDPAIKEVFDNK 191  
 |||||

RESULT 9  
 ADI19366  
 ID ADI19366 standard; protein; 227 AA.  
 XX  
 AC ADI19366;  
 XX  
 DT 15-APR-2004 (first entry)  
 XX  
 DE Human CD9 protein.  
 XX  
 T cell; immunotherapy; therapy; HIV infection; cancer;  
 infectious disease; cytostatic; antimicrobial; human.  
 KW  
 KW  
 XX  
 OS Homo sapiens.  
 XX  
 US2004001829-A1.  
 PN  
 XX  
 01-JAN-2004.  
 XX  
 PF 17-MAR-2003; 2003US-00390330.  
 XX  
 23-NOV-1988; 88US-00275433.  
 PR  
 22-NOV-1989; 89WO-US005304.  
 PR  
 07-APR-1992; 92US-00864805.  
 PR  
 07-APR-1992; 92US-00864807.  
 PR  
 07-APR-1992; 92US-00864866.  
 PR  
 04-JUN-1993; 93US-00073223.  
 PR  
 03-JUN-1994; 94US-00253964.  
 PR  
 10-MAR-1995; 95US-00403253.  
 PR  
 04-MAY-1995; 95US-00435816.  
 XX  
 (JUNE/) JUNE C H.  
 PA (THOM/) THOMPSON C B.  
 PA (NABEL/) NABEL G J.  
 PA (GRAY/) GRAY G S.  
 PA (RENN/) RENNERT P D.  
 XX  
 June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;  
 WPI; 2004-061648/06.

XX Inducing a population of T cells to proliferate, for immunotherapy or  
PT treating HIV infection, cancer or infectious disease, comprises  
PT activating a population of T cells and stimulating an accessory molecule  
PT on the surface of the T cells.  
XX  
XX Example 10; SEQ ID NO 6; 80pp; English.  
XX  
XX The invention relates to a method for inducing a population of T cells to  
CC proliferate. The method comprising activating a population of T cells,  
CC and stimulating an accessory molecule on the surface of the T cells with  
CC a ligand that binds the accessory molecule. The invention is useful for  
CC immunotherapy, for treating HIV infection, cancer or infectious disease,  
CC or in diagnostic applications. The present sequence is human CD9 protein.  
XX  
XX Sequence 227 AA;  
SQ  
Query Match 100.0%; Score 132; DB 8; Length 227;  
Best Local Similarity 100.0%; Pred. No. 2.6e-12;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 PKKDVLEFTTVKSCPDAlKEVFDNK 25  
DB 167 PKKDVLEFTTVKSCPDAlKEVFDNK 191  
|||||  
RESULT 10  
AEA89005  
ID AEA89005 standard; protein; 227 AA.  
XX  
AC AEA89005;  
XX  
DT 25-AUG-2005 (first entry)  
XX  
DE Human CD9 antigenic protein, SEQ ID NO: 6.  
XX  
XX Cell therapy; immune stimulation; immunotherapy; diagnosis;  
KW infectious disease; antimicrobial; infection; cancer; cytostatic;  
KW neoplasm; CD9; antigen.  
XX  
OS Homo sapiens.  
XX  
XX US6905681-B1.  
PN  
XX 14-JUN-2005.  
PD  
XX 08-JUL-1999; 99US-00349915.  
PF  
XX 03-JUN-1994; 94US-00253964.  
PR  
XX 10-MAR-1995; 95US-00403253.  
PR  
XX (GEMY ) GENETICS INST INC.  
PA (UNMI ) UNIV MICHIGAN.  
PA (USNA ) US SEC OF NAVY.  
XX  
XX June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;  
PI  
XX WPI; 2005-464777/47.  
XX  
XX Ex vivo proliferation of T cell population for use in therapy, involves  
PT contacting population of T cells with surface having anti-CD3 antibody  
PT and anti-CD28 antibody for activating T cells and stimulating activated T  
PT cells, respectively.  
XX  
XX Example 10; SEQ ID NO 6; 76pp; English.  
XX  
XX The present invention relates to a method of including ex vivo  
CC proliferation of a population of T cells to sufficient numbers for use in  
CC therapy. The method involves contacting population of T cells with  
CC surface having anti-CD3 antibody and anti-CD28 antibody for activating T  
CC cells and stimulating activated T cells, respectively. The invention is  
CC useful for treating cancer and infectious disease and also useful in cell  
CC therapy. The present sequence is the human CD9 antigenic protein. This

CC sequence is bound by an ES5.2D8 monoclonal antibody, which is to be used  
CC to stimulate a CD8+ T cell population.  
XX

SQ Sequence 227 AA;

Query Match 100.0%; Score 132; DB 9; Length 227;  
Best Local Similarity 100.0%; Pred. No. 2.6e-12;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PKKDVLEFTTVKSCPDAlKEVFDNK 25

DB 167 PKKDVLEFTTVKSCPDAlKEVFDNK 191  
|||||

RESULT 11

AAR27525

ID AAR27525 standard; protein; 228 AA.

XX

AC AAR27525;

XX

DT 25-MAR-2003 (revised)

DT 05-MAR-1993 (first entry)

DE Metastasis controlling peptide.

XX

KW M31-15 monoclonal antibody; cancer cell motility; prophylaxis; treatment;  
KW lung; glioblastoma.

XX

OS Homo sapiens.

XX

PN EP508417-A2.

XX

PD 14-OCT-1992.

XX

PF 09-APR-1992; 92EP-00106093.

XX

PR 12-APR-1991; 91JP-00079996.

PR 17-APR-1991; 91JP-00085396.

PR 07-FEB-1992; 92JP-00022321.

XX

XX (TAKES ) TAKEDA CHEM IND LTD.

PA (MIYA/) MIYAKE M.

XX

PI Ikeyama S, Koyama M, Senoo M, Miyake M;

XX

DR WPI; 1992-341723/42.

DR N-PSDB; AAQ29182.

XX

PT New monoclonal antibody M31-15 specific for metastasis-controlling

PT peptide - useful for treating and preventing cancer and metastasis.

XX

PS Claim 7; Fig 4; 34pp; English.

XX

CC The sequence is that of a cancer cell surface protein which is capable of  
CC suppressing the motility of cancer cells. It is specifically recognised  
CC by the monoclonal (Mab) antibody M31-15 which is useful for suppressing  
CC cancer metastasis. The polypeptide and Mab M31-15 are therefore useful in  
CC the prophylaxis and treatment of cancer, e.g. lung, glioblastoma and  
CC other metastatic cancers. (Updated on 25-MAR-2003 to correct PN field.)  
XX

SQ Sequence 228 AA;

Query Match

Best Local Similarity 100.0%; Score 132; DB 2; Length 228;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PKKDVLEFTTVKSCPDAlKEVFDNK 25

DB 168 PKKDVLEFTTVKSCPDAlKEVFDNK 192  
|||||

RESULT 12

ABB44581

AB44581 standard; protein; 228 AA.  
ABB44581;  
25-JAN-2002 (first entry)  
Human wound healing related polypeptide SEQ ID NO 38.  
Human; mouse; vulnery; dermatological; skin disorder; wound healing;  
gene therapy.  
Homo sapiens.  
CA2325226-A1.  
17-MAY-2001.  
16-NOV-2000; 2000CA-02325226.  
17-NOV-1999; 99DE-01055349.  
17-DEC-1999; 99US-0172511P.  
20-JUN-2000; 2000DE-01030149.  
(SWIT-) SWITCH BIOTECH AG.  
Regenbogen J, Wolf E, Goppelt A, Werner S, Halle J;  
WPI; 2001-433142/47.  
Use of novel polypeptide or its variant or nucleic acid encoding the  
polypeptide for diagnosing and/or preventing and/or treating skin  
disorders and/or treatment in wound healing or for identifying active  
substances.  
Disclosure; Page 193-194; 265pp; English.  
The invention relates to the use of a polypeptide (ABB44544-ABB44601,  
ABB44606-ABB44623) or its variant or encoding nucleic acid (ABA81990-  
ABA81995, ABA82016-ABA82032) with vulnerary and/or dermatological  
activity for the diagnosis, prevention and treatment of skin disorders  
and treatment in wound healing or for the identification of  
pharmacologically active substances. The nucleic acids are useful in gene  
therapy. Note: The printed sequence listing for this specification was  
incomplete, terminating part way through SEQ ID NO 106. The remaining  
data was obtained from EPO data for an equivalent patent (EP1114862)  
Sequence 228 AA;  
Query Match 100.0%; Score 132; DB 4; Length 228;  
Best Local Similarity 100.0%; Pred. No. 2.6e-12;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 PKQVLETFVTKSCPDPAIKEVFDNK 25  
DB 168 PKQVLETFVTKSCPDPAIKEVFDNK 192  
RESULT 13  
ABU05059  
ID ABU05059 standard; protein; 228 AA.  
XX  
AC ABU05059;  
XX  
DT 29-JAN-2003 (first entry)  
XX  
DE Human expressed protein tag (EPT) #1725.  
XX  
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
XX

OS Homo sapiens.  
XX  
PN WO200278524-A2.  
XX  
PD 10-OCT-2002.  
XX  
PF 28-MAR-2002; 2002WO-US009671.  
XX  
PR 28-MAR-2001; 2001US-0279495P.  
PR 21-MAY-2001; 2001US-0292544P.  
PR 08-AUG-2001; 2001US-0310801P.  
PR 01-OCT-2001; 2001US-0326370P.  
PR 04-DEC-2001; 2001US-0336780P.  
PR 20-FEB-2002; 2002US-0358985P.  
XX  
PA (ZYCO-) ZYCOS INC.  
XX  
PI Chiciz RM, Tomlinson AJ, Urban RG;  
XX  
XX WPI; 2003-040607/03.  
XX  
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.  
XX  
PS Example 2; SEQ ID NO 1725; 134pp; English.  
XX  
CC The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 228 AA;  
Query Match 100.0%; Score 132; DB 6; Length 228;  
Best Local Similarity 100.0%; Pred. No. 2.6e-12;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 PKQVLETFVTKSCPDPAIKEVFDNK 25  
DB 168 PKQVLETFVTKSCPDPAIKEVFDNK 192  
RESULT 14  
ABU05052  
ID ABU05052 standard; protein; 228 AA.  
XX  
AC ABU05052;  
XX  
DT 29-JAN-2003 (first entry)  
XX  
DE Human expressed protein tag (EPT) #1718.  
XX  
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
XX

```

OS Homo sapiens.
XX WO200278524-A2.
XX 10-OCT-2002.
XX
XX 28-MAR-2002; 2002WO-US009671.
XX
XX 28-MAR-2001; 2001US-0279495P.
XX 21-MAY-2001; 2001US-0292544P.
XX 08-AUG-2001; 2001US-0310801P.
XX 01-OCT-2001; 2001US-0326370P.
XX 04-DEC-2001; 2001US-0336780P.
XX 20-FEB-2002; 2002US-0358985P.
XX
XX (ZYCO-) ZYCOS INC.
XX
XX Chicz RM, Tomlinson AJ, Urban RG;
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.
XX
XX Example 2; SEQ ID NO 1718; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and
XX polynucleotides are particularly useful for treating or preventing
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX lymphoma or leukaemia. These are also useful for screening agents for
XX treating the above mentioned diseases. This sequence represents an
XX expressed protein tag (EPT) isolated from human tissue for translational
XX profiling. Note: This sequence does not appear in the printed
XX specification but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 228 AA;
XX
XX Query Match 100.0%; Score 132; DB 6; Length 228;
XX Best Local Similarity 100.0%; Pred. No. 2.6e-12;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 PKKDVLFTFTVKSCPDALKEVFDNK 25
XX |||||
XX Db 168 PKKDVLFTFTVKSCPDALKEVFDNK 192
XX
XX RESULT 15
XX ABU05048
XX ID ABU05048 standard; protein; 228 AA.
XX AC ABU05048;
XX
XX 29-JAN-2003 (first entry)
XX
XX Human expressed protein tag (EPT) #1714.
XX
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX protease; protease inhibitor; transporter; cytoskeletal protein;
XX receptor; transcription factor; cancer; MHC;
XX major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX

```

Query Match 100.0%; Score 132; DB 6; Length 228;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-12;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLFTFTVKSCPDALKEVFDNK 25  
 |||||  
 Db 168 PKKDVLFTFTVKSCPDALKEVFDNK 192

Search completed: January 20, 2006, 17:16:07  
 Job time : 88.963 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2006, 17:10:37 ; Search time 17.5926 Seconds  
(without alignments)  
117.486 Million cell updates/sec

Title: US-10-619-323-5

Perfect score: 132

Sequence: 1 PKKDVLFTVTKSPDAIKEVFDNK 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*  
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2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	132	100.0	29	1	US-08-254-493-6
2	132	100.0	29	1	US-08-408-222B-6
3	132	100.0	227	1	US-08-254-493-1
4	132	100.0	227	1	US-08-253-751-6
5	132	100.0	227	1	US-08-453-925-6
6	132	100.0	227	2	US-08-403-253A-6
7	132	100.0	227	2	US-08-435-816A-6
8	132	100.0	227	2	US-09-350-202-6
9	132	100.0	227	2	US-08-592-711-6
10	132	100.0	227	2	US-09-349-915B-6
11	132	100.0	228	1	US-08-408-222B-1
12	117.5	89.0	79	2	US-08-630-172-8
13	117.5	89.0	79	2	US-09-375-419-8
14	51	38.6	303	2	US-09-134-001C-5215
15	50	37.9	1905	2	US-09-964-956-44
16	47	35.6	919	2	US-09-248-796A-17485
17	47	35.6	1018	1	US-08-452-052-2
18	46	34.8	156	2	US-09-393-627B-27
19	46	34.8	456	2	US-09-492-027-2
20	46	34.8	566	2	US-09-328-352-7811
21	46	34.8	608	2	US-09-310-275-2
22	46	34.8	608	2	US-09-082-077-5
23	46	34.8	608	2	US-09-925-637-70
24	45	34.1	293	2	US-09-134-000C-4231
25	45	34.1	690	2	US-09-902-540-10349
26	44	33.3	156	2	US-09-393-627B-26
27	44	33.3	400	2	US-09-583-110-5315

28 44 33.3 411 2 US-09-248-796A-15503 Sequence 15503, A  
29 44 33.3 414 2 US-09-107-433-3551 Sequence 3551, Ap  
30 44 33.3 542 1 US-08-701-380-2 Sequence 2, Appli  
31 44 33.3 542 2 US-09-032-365A-13 Sequence 13, Appli  
32 44 33.3 643 2 US-09-949-016-10023 Sequence 10023, A  
33 44 33.3 1334 1 US-08-996-545-2 Sequence 2, Appli  
34 44 33.3 1334 2 US-09-328-320-2 Sequence 2, Appli  
35 44 33.3 1334 2 US-09-758-828-2 Sequence 2, Appli  
36 43.5 33.0 1604 2 US-09-004-838-95 Sequence 95, Appli  
37 43.5 33.0 1854 2 US-09-004-838-108 Sequence 108, App  
38 43 32.6 311 2 US-09-634-955B-5 Sequence 5, Appli  
39 43 32.6 311 2 US-09-816-760-5 Sequence 5, Appli  
40 43 32.6 311 2 US-09-838-561-5 Sequence 5, Appli  
41 43 32.6 369 2 US-09-198-452A-1048 Sequence 1048, Ap  
42 43 32.6 369 2 US-09-438-185A-977 Sequence 977, App  
43 43 32.6 511 2 US-09-134-078-21 Sequence 21, Appli  
44 43 32.6 519 1 US-08-319-387-4 Sequence 4, Appli  
45 42.5 32.2 312 2 US-09-134-001C-5583 Sequence 5583, Ap

#### ALIGNMENTS

RESULT 1  
US-08-254-493-6  
; Sequence 6, Application US/08254493  
; Patent No. 5439886  
; GENERAL INFORMATION:  
; APPLICANT: IKEYAMA, SHUICHI  
; APPLICANT: KOYAMA, MASARU  
; APPLICANT: MIYAKE, MASAYUKI  
; APPLICANT: SENO, MASAHARU  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND  
; TITLE OF INVENTION: PRODUCTION THEREOF  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
; STREET: 130 WATER STREET  
; CITY: BOSTON  
; STATE: MASSACHUSETTS  
; COUNTRY: US  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/254,493  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/865552  
; FILING DATE: 09-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 0799996-1991  
; FILING DATE: 12-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 085396-1991  
; FILING DATE: 17-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 022321-1992  
; FILING DATE: 07-FEB-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: RESNICK, DAVID S.  
; REGISTRATION NUMBER: 34235  
; REFERENCE/DOCKET NUMBER: 41777  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 523-3400  
; TELEFAX: (617) 523-6440  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:

; LENGTH: 29 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-254-493-6

Query Match 100.0%; Score 132; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 5.1e-14;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQDVLETFVTKSCPDPAIKEVFDNK 25  
|||  
DB 5 PKQDVLETFVTKSCPDPAIKEVFDNK 29

## RESULT 2

US-08-408-222B-6  
; Sequence 6, Application US/08408222B  
; Patent No. 5776727  
; GENERAL INFORMATION:  
; APPLICANT: Ikeyama, Shuichi  
; APPLICANT: Koyama, Masaru  
; APPLICANT: Miyake, Masayuki  
; APPLICANT: Senoo, Masaharu  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
; STREET: 130 WATER STREET  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/408,222B  
FILING DATE: 22-MAR-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/254,493  
FILING DATE: 06-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP-079996-1991  
FILING DATE: 12-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP-085396-1991  
FILING DATE: 14-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP-022321-1992  
FILING DATE: 07-FEB-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Resnick, David S.  
REGISTRATION NUMBER: 34,235  
REFERENCE/DOCKET NUMBER: 41777-DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-408-222B-6

Query Match 100.0%; Score 132; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 5.1e-14;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQDVLETFVTKSCPDPAIKEVFDNK 25  
|||  
DB 5 PKQDVLETFVTKSCPDPAIKEVFDNK 29

## RESULT 3

US-08-254-493-1  
; Sequence 1, Application US/08254493  
; Patent No. 5439886  
; GENERAL INFORMATION:  
; APPLICANT: IKEYAMA, SHUICHI  
; APPLICANT: KOYAMA, MASARU  
; APPLICANT: MIYAKE, MASAYUKI  
; APPLICANT: SENOO, MASAHARU  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
; STREET: 130 WATER STREET  
; CITY: BOSTON  
; STATE: MASSACHUSETTS  
; COUNTRY: US  
; ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/254,493  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/865552  
FILING DATE: 09-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 079996-1991  
FILING DATE: 12-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 085396-1991  
FILING DATE: 17-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 022321-1992  
FILING DATE: 07-FEB-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: RESNICK, DAVID S.  
REGISTRATION NUMBER: 34235  
REFERENCE/DOCKET NUMBER: 41777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 523-3400  
TELEFAX: (617) 523-6440  
TELEX: 200291 STRE UR  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 227 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-254-493-1

Query Match 100.0%; Score 132; DB 1; Length 227;  
Best Local Similarity 100.0%; Pred. No. 5.9e-13;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQDVLETFVTKSCPDPAIKEVFDNK 25  
|||  
DB 167 PKQDVLETFVTKSCPDPAIKEVFDNK 191

## RESULT 4

US-08-253-751-6  
; Sequence 6, Application US/08253751  
; Patent No. 5858358  
; GENERAL INFORMATION:  
; APPLICANT: June, Carl H.  
; APPLICANT: Thompson, Craig B.  
; APPLICANT: Nabel, Gary J.  
; APPLICANT: Gray, Gary S.  
; APPLICANT: Rennert, Paul D.  
; APPLICANT: Freeman, Gordon J.  
; TITLE OF INVENTION: METHODS FOR SELECTIVELY STIMULATING  
; TITLE OF INVENTION: PROLIFERATION OF T-CELLS  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 STATE STREET, SUITE 510  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII TEXT  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/253,751  
; FILING DATE: 3 JUNE 1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/073,223  
; FILING DATE: 4 JUNE 1993  
; APPLICATION NUMBER: US 08/200,947  
; FILING DATE: 23 FEB 1994  
; APPLICATION NUMBER: US 07/864,805  
; FILING DATE: 7 APR 1992  
; APPLICATION NUMBER: US 08/247,505  
; FILING DATE: 23 MAY 1994  
; APPLICATION NUMBER: US 07/864,866  
; FILING DATE: 7 APR 1992  
; APPLICATION NUMBER: 08/218,155  
; FILING DATE: 25 MAR 1994  
; APPLICATION NUMBER: US 07/864,807  
; FILING DATE: 7 APR 1992  
; APPLICATION NUMBER: US 07/902,467  
; FILING DATE: 16 JUNE 1992  
; APPLICATION NUMBER: US 07/275,433  
; FILING DATE: 23 NOV 1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MANDRAGOURAS, AMY E.  
; REGISTRATION NUMBER: 36,207  
; REFERENCE/DOCKET NUMBER: RPI-002CPB  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-7400  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 227 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-253-751-6

Query Match 100.0%; Score 132; DB 1; Length 227;  
Best Local Similarity 100.0%; Pred. No. 5.9e-13;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 PKQDVLETFVTKSCPDPAIKEVFDNK 25  
DB 167 PKQDVLETFVTKSCPDPAIKEVFDNK 191

RESULT 5  
US-08-453-925-6

; Sequence 6, Application US/08453925  
; Patent No. 5883223  
; GENERAL INFORMATION:  
; APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.  
; APPLICANT: Gray, Gary S., Rennert, Paul D., Freeman, Gordon J.  
; TITLE OF INVENTION: METHODS FOR SELECTIVELY STIMULATING  
; TITLE OF INVENTION: PROLIFERATION OF T-CELLS  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 STATE STREET, SUITE 510  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII TEXT  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/453,925  
; FILING DATE: 30 MAY 1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/253,751  
; FILING DATE: 3 JUNE 1994  
; APPLICATION NUMBER: US 08/073,223  
; FILING DATE: 4 JUNE 1993  
; APPLICATION NUMBER: US 08/200,947  
; FILING DATE: 23 FEB 1994  
; APPLICATION NUMBER: US 07/864,805  
; FILING DATE: 7 APR 1992  
; APPLICATION NUMBER: US 08/247,505  
; FILING DATE: 23 MAY 1994  
; APPLICATION NUMBER: US 07/864,866  
; FILING DATE: 7 APR 1992  
; APPLICATION NUMBER: 08/218,155  
; FILING DATE: 25 MAR 1994  
; APPLICATION NUMBER: US 07/864,807  
; FILING DATE: 7 APR 1992  
; APPLICATION NUMBER: US 07/902,467  
; FILING DATE: 16 JUNE 1992  
; APPLICATION NUMBER: US 07/275,433  
; FILING DATE: 23 NOV 1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MANDRAGOURAS, AMY E.  
; REGISTRATION NUMBER: 36,207  
; REFERENCE/DOCKET NUMBER: RPI-002CPB  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 227 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-453-925-6

Query Match 100.0%; Score 132; DB 1; Length 227;  
Best Local Similarity 100.0%; Pred. No. 5.9e-13;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 PKQDVLETFVTKSCPDPAIKEVFDNK 25  
DB 167 PKQDVLETFVTKSCPDPAIKEVFDNK 191

RESULT 6  
US-08-403-253A-6  
; Sequence 6, Application US/08403253A  
; Patent No. 6352694  
; GENERAL INFORMATION:

APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.  
APPLICANT: Gray, Gary S., Rennert, Paul D.  
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/403,253A  
FILING DATE: March 10, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/253,964  
FILING DATE: 3 JUNE 1994  
APPLICATION NUMBER: US 08/073,223  
FILING DATE: 4 JUNE 1993  
APPLICATION NUMBER: US 08/200,947  
FILING DATE: 23 FEB 1994  
APPLICATION NUMBER: US 07/864,805  
FILING DATE: 7 APR 1992  
APPLICATION NUMBER: US 08/247,505  
FILING DATE: 23 MAY 1994  
APPLICATION NUMBER: US 08/218,155  
FILING DATE: 25 MAR 1994  
APPLICATION NUMBER: US 07/864,807  
FILING DATE: 7 APR 1992  
APPLICATION NUMBER: US 07/902,467  
FILING DATE: 16 JUNE 1992  
APPLICATION NUMBER: US 07/275,433  
FILING DATE: 23 NOV 1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: RPI-002CP2  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 742-4214  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 227 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-403-253A-6  
Query Match 100.0%; Score 132; DB 2; Length 227;  
Best Local Similarity 100.0%; Pred. No. 5.9e-13;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 PKQDVLETFVTKSCPDAIKEVFDNK 25  
Db 167 PKQDVLETFVTKSCPDAIKEVFDNK 191  
RESULT 7  
US-08-435-816A-6  
Sequence 6, Application US/08435816A  
Patent No. 6534055  
GENERAL INFORMATION:  
APPLICANT: June, Carl H.  
APPLICANT: Thompson, Craig B.  
APPLICANT: Nabel, Gary J.

APPLICANT: Gray, Gary S.  
APPLICANT: Rennert, Paul D.  
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/435,816A  
FILING DATE: May 4, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/403,253  
FILING DATE: 10 MARCH 1995  
APPLICATION NUMBER: US 08/253,964  
FILING DATE: 3 JUNE 1994  
APPLICATION NUMBER: US 08/073,223  
FILING DATE: 4 JUNE 1993  
APPLICATION NUMBER: US 08/200,947  
FILING DATE: 23 FEB 1994  
APPLICATION NUMBER: US 07/864,805  
FILING DATE: 7 APR 1992  
APPLICATION NUMBER: US 08/247,505  
FILING DATE: 23 MAY 1994  
APPLICATION NUMBER: US 07/864,866  
FILING DATE: 7 APR 1992  
APPLICATION NUMBER: US 08/218,155  
FILING DATE: 25 MAR 1994  
APPLICATION NUMBER: US 07/864,807  
FILING DATE: 7 APR 1992  
APPLICATION NUMBER: US 07/902,467  
FILING DATE: 16 JUNE 1992  
APPLICATION NUMBER: US 07/275,433  
FILING DATE: 23 NOV 1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: RPI-002CP3  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-7400  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 227 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-435-816A-6  
Query Match 100.0%; Score 132; DB 2; Length 227;  
Best Local Similarity 100.0%; Pred. No. 5.9e-13;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 PKQDVLETFVTKSCPDAIKEVFDNK 25  
Db 167 PKQDVLETFVTKSCPDAIKEVFDNK 191  
RESULT 8  
US-09-350-202-6  
Sequence 6, Application US/09350202  
Patent No. 6887466  
GENERAL INFORMATION:  
APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.



APPLICANT: Gray, Gary S., Rennert, Paul D.  
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/350,202  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/403,253  
FILING DATE: March 10, 1995  
APPLICATION NUMBER: US 08/253,964  
FILING DATE: 3 JUNE 1994  
APPLICATION NUMBER: US 08/073,223  
FILING DATE: 4 JUNE 1993  
APPLICATION NUMBER: US 08/200,947  
FILING DATE: 23 FEB 1994  
APPLICATION NUMBER: US 07/864,805  
FILING DATE: 7 APR 1992  
APPLICATION NUMBER: US 08/218,155  
FILING DATE: 25 MAR 1994  
APPLICATION NUMBER: US 07/864,807  
FILING DATE: 7 APR 1992  
APPLICATION NUMBER: US 07/902,467  
FILING DATE: 16 JUNE 1992  
APPLICATION NUMBER: US 07/275,433  
FILING DATE: 23 NOV 1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: RPI-002CP2  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 742-4214  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 227 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-350-202-6  
Query Match 100.0%; Score 132; DB 2; Length 227;  
Best Local Similarity 100.0%; Pred. No. 5.9e-13;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 PKKDVLETFVTKSCPDAIKEVFDNK 25  
Db 167 PKKDVLETFVTKSCPDAIKEVFDNK 191  
RESULT 9  
US-08-592-711-6  
; Sequence 6, Application US/08592711  
; Patent No. 6905680  
; GENERAL INFORMATION:  
; APPLICANT: June, Carl H.  
; APPLICANT: Thompson, Craig B.

APPLICANT: Nabel, Gary J.  
APPLICANT: Gray, Gary S.  
APPLICANT: Rennert, Paul D.  
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/592,711  
FILING DATE: 26-JAN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/435,816  
FILING DATE: 4-MAY-1995  
APPLICATION NUMBER: US 08/403,253  
FILING DATE: 10-MARCH-1995  
APPLICATION NUMBER: US 08/253,964  
FILING DATE: 3-JUNE-1994  
APPLICATION NUMBER: US 08/073,223  
FILING DATE: 4-JUNE-1993  
APPLICATION NUMBER: US 08/200,947  
FILING DATE: 23-FEB-1994  
APPLICATION NUMBER: US 07/864,805  
FILING DATE: 7-APR-1992  
APPLICATION NUMBER: US 08/247,505  
FILING DATE: 23-MAY-1994  
APPLICATION NUMBER: US 07/864,866  
FILING DATE: 7-APR-1992  
APPLICATION NUMBER: US 08/218,155  
FILING DATE: 25-MAR-1994  
APPLICATION NUMBER: US 07/864,807  
FILING DATE: 7-APR-1992  
APPLICATION NUMBER: US 07/902,467  
FILING DATE: 16-JUNE-1992  
APPLICATION NUMBER: US 07/275,433  
FILING DATE: 23-NOV-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: RPI-002CP4  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 227 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-592-711-6  
Query Match 100.0%; Score 132; DB 2; Length 227;  
Best Local Similarity 100.0%; Pred. No. 5.9e-13;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 PKKDVLETFVTKSCPDAIKEVFDNK 25  
Db 167 PKKDVLETFVTKSCPDAIKEVFDNK 191  
RESULT 10  
US-09-349-915B-6  
; Sequence 6, Application US/09349915B  
; Patent No. 6905681

;; GENERAL INFORMATION:  
;; APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.  
;; Gray, Gary S., Rennert, Paul D.  
;; TITLE OF INVENTION: Methods For Selectively Stimulating  
;; Proliferation Of T-Cells  
;; NUMBER OF SEQUENCES: 14  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: HALE AND DORR LLP  
;; STREET: 60 State Street  
;; CITY: Boston  
;; STATE: Massachusetts  
;; COUNTRY: USA  
;; ZIP: 02109  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/349,915B  
;; FILING DATE: 01-Aug-2000  
;; CLASSIFICATION: <Unknown>  
;;  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/403,253  
;; FILING DATE: March 10, 1995  
;; APPLICATION NUMBER: US 08/253,964  
;; FILING DATE: 3 JUNE 1994  
;; APPLICATION NUMBER: US 08/073,223  
;; FILING DATE: 4 JUNE 1993  
;; APPLICATION NUMBER: US 08/200,947  
;; FILING DATE: 23 FEB 1994  
;; APPLICATION NUMBER: US 07/864,805  
;; FILING DATE: 7 APR 1992  
;; APPLICATION NUMBER: US 08/247,505  
;; FILING DATE: 23 MAY 1994  
;; APPLICATION NUMBER: US 07/864,866  
;; FILING DATE: 7 APR 1992  
;; APPLICATION NUMBER: US 08/218,155  
;; FILING DATE: 25 MAR 1994  
;; APPLICATION NUMBER: US 07/864,807  
;; FILING DATE: 7 APR 1992  
;; APPLICATION NUMBER: US 07/902,467  
;; FILING DATE: 16 JUNE 1992  
;; APPLICATION NUMBER: US 07/275,433  
;; FILING DATE: 23 NOV 1988  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Superko, Colleen  
;; REGISTRATION NUMBER: 39,850  
;; REFERENCE/DOCKET NUMBER: 36119-125 (US10)  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617) 526-6564  
;; TELEFAX: (617) 526-5000  
;;  
;; INFORMATION FOR SEQ ID NO: 6:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 227 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-349-915B-6

Query Match 100.0%; Score 132; DB 2; Length 227;  
Best Local Similarity 100.0%; Pred. No. 5.9e-13;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQDVLETFVTKSCPDPAIKEVFDNK 25  
DB 167 PKQDVLETFVTKSCPDPAIKEVFDNK 191

RESULT 11  
US-08-408-222B-1  
; Sequence 1, Application US/08408222B

;; Patent No. 5776727  
;; GENERAL INFORMATION:  
;; APPLICANT: Ikeyama, Shuichi  
;; APPLICANT: Koyama, Masaru  
;; APPLICANT: Miyake, Masayuki  
;; APPLICANT: Senoo, Masaharu  
;; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND  
;; NUMBER OF SEQUENCES: 7  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: DIKE, Bronstein, Roberts & Cushman  
;; STREET: 130 Water Street  
;; CITY: Boston  
;; STATE: MA  
;; COUNTRY: USA  
;; ZIP: 02109  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: DOS  
;; SOFTWARE: FastSeq Version 1.5  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/408,222B  
;; FILING DATE: 22-MAR-1995  
;; CLASSIFICATION: 536  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/254,493  
;; FILING DATE: 06-JUN-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: JP-079996-1991  
;; FILING DATE: 12-APR-1991  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: JP-085396-1991  
;; FILING DATE: 14-APR-1991  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: JP-022321-1992  
;; FILING DATE: 07-FEB-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Resnick, David S.  
;; REGISTRATION NUMBER: 34,235  
;; REFERENCE/DOCKET NUMBER: 41777-DIV  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 617-523-3400  
;; TELEFAX: 617-523-6440  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 228 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
;; FRAGMENT TYPE: internal  
;; ORIGINAL SOURCE:  
US-08-408-222B-1

Query Match 100.0%; Score 132; DB 1; Length 228;  
Best Local Similarity 100.0%; Pred. No. 5.9e-13;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQDVLETFVTKSCPDPAIKEVFDNK 25  
DB 168 PKQDVLETFVTKSCPDPAIKEVFDNK 192

RESULT 12  
US-08-630-172-8  
; Sequence 8, Application US/08630172  
; Patent No. 6060054  
; GENERAL INFORMATION:  
; APPLICANT: Staerz, Uwe  
; TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T  
; Lymphocyte Veto

NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheridan Ross & McIntosh  
STREET: 1700 Lincoln Street, 35th Floor  
CITY: Denver  
STATE: Colorado  
COUNTRY: U.S.  
ZIP: 80203  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,172  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Connell, Gary J.  
REGISTRATION NUMBER: 32,020  
REFERENCE/DOCKET NUMBER: 2879-36  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 863-9700  
TELEFAX: (303) 863-0223  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 79 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-630-172-8

Query Match 89.0%; Score 117.5; DB 2; Length 79;  
Best Local Similarity 96.0%; Pred. No. 3.3e-11;  
Matches 24; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 PKKDVLFTFTVKSPDAIKEVFDNK 25  
Db 56 PKKDVLFTFTVKSPD-IKEVFDNK 79

RESULT 13  
US-09-375-419-8  
Sequence 8, Application US/09375419  
Patent No. 6264950  
GENERAL INFORMATION:  
APPLICANT: Staerz, Uwe  
TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T  
TITLE OF INVENTION: LYMPHOCYTE VETO  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheridan Ross & McIntosh  
STREET: 1700 Lincoln Street, 35th Floor  
CITY: Denver  
STATE: Colorado  
COUNTRY: U.S.  
ZIP: 80203  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/375,419  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/630,172  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Connell, Gary J.  
REGISTRATION NUMBER: 32,020  
REFERENCE/DOCKET NUMBER: 2879-36

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 863-9700  
TELEFAX: (303) 863-0223  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 79 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-375-419-8

Query Match 89.0%; Score 117.5; DB 2; Length 79;  
Best Local Similarity 96.0%; Pred. No. 3.3e-11;  
Matches 24; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 PKKDVLFTFTVKSPDAIKEVFDNK 25  
Db 56 PKKDVLFTFTVKSPD-IKEVFDNK 79

RESULT 14  
US-09-134-001C-5215  
Sequence 5215, Application US/09134001C  
Patent No. 6380370  
GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: GTC-007  
CURRENT APPLICATION NUMBER: US/09/134,001C  
CURRENT FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/064,964  
PRIOR FILING DATE: 1997-11-08  
PRIOR APPLICATION NUMBER: US 60/055,779  
PRIOR FILING DATE: 1997-08-14  
NUMBER OF SEQ ID NOS: 5674  
SEQ ID NO 5215  
LENGTH: 303  
TYPE: PRT  
ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-5215

Query Match 38.6%; Score 51; DB 2; Length 303;  
Best Local Similarity 73.3%; Pred. No. 5.6;  
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 9 FTVKSCPDAIKEVFD 23  
Db 251 FWDKSSPDAIKEVFN 265

RESULT 15  
US-09-964-956-44  
Sequence 44, Application US/09964956  
Patent No. 6875570  
GENERAL INFORMATION:  
APPLICANT: Gerlach, Valerie L  
APPLICANT: MacDougall, John R  
APPLICANT: Smithson, Glennda  
APPLICANT: Millet, Isabelle  
APPLICANT: Stone, David  
APPLICANT: Gunther, Erik  
APPLICANT: Ellerman, Karen  
APPLICANT: Grosse, William M  
APPLICANT: Alsobrook II, John P  
APPLICANT: Lepley, Denise M  
APPLICANT: Burgess, Catherine E  
APPLICANT: Padigaru, Muralidhara  
APPLICANT: Kekuda, Ramesh  
APPLICANT: Spytek, Kimberly A  
APPLICANT: Leach, Martin D  
APPLICANT: Shimkets, Richard A  
TITLE OF INVENTION: No. 6875570el Proteins and Nucleic Acids Encoding Same

FILE REFERENCE: 21402-124  
CURRENT APPLICATION NUMBER: US/09/964,956  
CURRENT FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: 60/235,631  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: 60/235,633  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: 60/235,808  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: 60/236,064  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: 60/236,065  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: 60/236,066  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: 60/236,135  
PRIOR FILING DATE: 2000-09-28  
PRIOR APPLICATION NUMBER: 60/237,434  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/238,321  
PRIOR FILING DATE: 2000-10-05  
PRIOR APPLICATION NUMBER: 60/238,399  
PRIOR FILING DATE: 2000-10-06  
PRIOR APPLICATION NUMBER: 60/238,396  
PRIOR FILING DATE: 2000-10-06  
PRIOR APPLICATION NUMBER: 60/276,667  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/294,823  
PRIOR FILING DATE: 2001-05-31  
PRIOR APPLICATION NUMBER: 60/304,868  
PRIOR FILING DATE: 2001-07-12  
NUMBER OF SEQ ID NOS: 127  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 44  
LENGTH: 1905  
TYPE: PRT  
ORGANISM: Xenopus laevis  
US-09-964-956-44

Query Match 37.9%; Score 50; DB 2; Length 1905;  
Best Local Similarity 55.0%; Pred. No. 71;  
Matches 11; Conservative 2; Mismatches 7; Indels 0; Gaps 0;  
Qy 1 PKQVLETFVKSQDAIKE 20  
Db 343 PKESVLCLETLKKIKDKIKE 362

Search completed: January 20, 2006, 17:23:45  
Job time : 18.5926 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2006, 17:11:18 ; Search time 50.3086 Seconds  
(without alignments)  
207.633 Million cell updates/sec

Title: US-10-619-323-5

Perfect score: 132

Sequence: 1 PKDVLFTFTVKSCPDALKEVFDNK 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications\_AA\_Main:  
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2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	132	100.0	25	4	US-10-619-323-5
2	132	100.0	74	4	US-10-425-115-240878
3	132	100.0	227	3	US-08-592-711-6
4	132	100.0	227	3	US-09-183-055-6
5	132	100.0	227	3	US-09-350-202-6
6	132	100.0	227	4	US-10-390-330-6
7	132	100.0	227	5	US-10-473-127-1723
8	132	100.0	227	5	US-10-473-127-1726
9	132	100.0	228	4	US-10-156-136-39
10	132	100.0	228	4	US-10-331-496A-41
11	132	100.0	228	4	US-10-619-323-1
12	132	100.0	228	4	US-10-794-899-97
13	132	100.0	228	5	US-10-473-127-1714
14	132	100.0	228	5	US-10-473-127-1715
15	132	100.0	228	5	US-10-473-127-1716
16	132	100.0	228	5	US-10-473-127-1718
17	132	100.0	228	5	US-10-473-127-1719
18	132	100.0	228	5	US-10-473-127-1722
19	132	100.0	228	5	US-10-473-127-1725
20	132	100.0	228	5	US-10-789-378-18
21	132	100.0	228	5	US-10-482-029-144
22	132	100.0	228	5	US-10-852-335A-187
23	132	100.0	228	6	US-11-041-419-39
24	132	100.0	275	3	US-09-925-301-1381
25	132	100.0	275	4	US-10-106-698-5930
26	132	100.0	275	5	US-10-473-127-1720
27	132	100.0	275	5	US-10-473-127-1721

28 132 100.0 454 5 US-10-450-763-44426 Sequence 44426, A  
29 117.5 89.0 79 5 US-10-473-127-1724 Sequence 1724, Ap  
30 98 74.2 226 4 US-10-205-194-162 Sequence 162, App  
31 95 72.0 18 4 US-10-619-323-6 Sequence 6, Appli  
32 61 46.2 30 5 US-10-473-127-1717 Sequence 1717, Ap  
33 52 39.4 452 4 US-10-408-765A-2385 Sequence 2385, Ap  
34 51 38.6 303 4 US-10-724-972A-4282 Sequence 4282, Ap  
35 51 38.6 336 4 US-10-424-599-256255 Sequence 256255,  
36 50 37.9 1336 4 US-10-369-493-3672 Sequence 3672, Ap  
37 50 37.9 1305 3 US-09-964-956-44 Sequence 44, Appl  
38 49.5 37.5 258 4 US-10-437-963-169601 Sequence 169601,  
39 49 37.1 10 5 US-10-473-127-165 Sequence 165, App  
40 49 37.1 89 4 US-10-424-599-235139 Sequence 235139,  
41 48.5 36.7 468 4 US-10-335-977-9438 Sequence 9438, Ap  
42 48.5 36.7 500 4 US-10-335-977-9439 Sequence 9439, Ap  
43 48 36.4 518 4 US-10-163-198-35 Sequence 35, Appl  
44 47.5 36.0 662 4 US-10-437-963-179488 Sequence 179488,  
45 47 35.6 217 4 US-10-298-638-15 Sequence 15, Appl

#### ALIGNMENTS

RESULT 1  
US-10-619-323-5  
; Sequence 5, Application US/10619323  
; Publication No. US20040136985A1  
; GENERAL INFORMATION:  
; APPLICANT: Jennings, Lisa K.  
; APPLICANT: Longhurst, Celia M.  
; APPLICANT: Cook, George A.  
; APPLICANT: Bao, Jianxiong  
; APPLICANT: Zhang, Chunxiang  
; APPLICANT: White, Melanie M.  
; APPLICANT: Crossno, Jr., Joseph T.  
; APPLICANT: Lu, Yi  
; TITLE OF INVENTION: METHODS OF MODIFYING BEHAVIOR OF CD9-EXPRESSING CELLS  
; FILE REFERENCE: 20609/241  
; CURRENT APPLICATION NUMBER: US/10/619,323  
; CURRENT FILING DATE: 2003-07-14  
; PRIOR APPLICATION NUMBER: 60/395,864  
; PRIOR FILING DATE: 2002-07-12  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: CD9 peptide  
US-10-619-323-5

Query Match 100.0%; Score 132; DB 4; Length 25;  
Best Local Similarity 100.0%; Pred. No. 8.4e-13;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PKDVLFTFTVKSCPDALKEVFDNK 25

Db 1 PKDVLFTFTVKSCPDALKEVFDNK 25

#### RESULT 2

US-10-425-115-240878  
; Sequence 240878, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B

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; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 240878
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(74)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_15125C.1.pep
; US-10-425-115-240878

Query Match          100.0%; Score 132; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 3e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQDVLETFVKSCPDPAIKEVFDNK 25
Db 20 PKQDVLETFVKSCPDPAIKEVFDNK 44

RESULT 3
US-08-592-711-6
; Sequence 6, Application US/08592711
; Publication No. US20020115214A1
; GENERAL INFORMATION:
; APPLICANT: June, Carl H.
; APPLICANT: Thompson, Craig B.
; APPLICANT: Nabel, Gary J.
; APPLICANT: Gray, Gary S.
; APPLICANT: Rennert, Paul D.
; TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,711
; FILING DATE: 26-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/435,816
; FILING DATE: 4-MAY-1995
; APPLICATION NUMBER: US 08/403,253
; FILING DATE: 10-MARCH-1995
; APPLICATION NUMBER: US 08/253,964
; FILING DATE: 3-JUNE-1994
; APPLICATION NUMBER: US 08/073,223
; FILING DATE: 4-JUNE-1993
; APPLICATION NUMBER: US 08/200,947
; FILING DATE: 23-FEB-1994
; APPLICATION NUMBER: US 07/864,805
; FILING DATE: 7-APR-1992
; APPLICATION NUMBER: US 08/247,505
; FILING DATE: 23-MAY-1994
; APPLICATION NUMBER: US 07/864,866
; FILING DATE: 7-APR-1992
; APPLICATION NUMBER: US 08/218,155
; FILING DATE: 25-MAR-1994
; APPLICATION NUMBER: US 07/864,807
; FILING DATE: 7-APR-1992
; APPLICATION NUMBER: US 07/902,467
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; FILING DATE: 16-JUNE-1992
; APPLICATION NUMBER: US 07/275,433
; FILING DATE: 23-NOV-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-002CP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-592-711-6

Query Match          100.0%; Score 132; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQDVLETFVKSCPDPAIKEVFDNK 25
Db 167 PKQDVLETFVKSCPDPAIKEVFDNK 191

RESULT 4
US-09-183-055-6
; Sequence 6, Application US/09183055
; Publication No. US20020076407A1
; GENERAL INFORMATION:
; APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.
; APPLICANT: Gray, Gary S., Rennert, Paul D.
; TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALE AND DORR LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/183,055
; FILING DATE: 30-Oct-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/403,253
; FILING DATE: March 10, 1995
; APPLICATION NUMBER: US 08/253,964
; FILING DATE: 3 JUNE 1994
; APPLICATION NUMBER: US 08/073,223
; FILING DATE: 4 JUNE 1993
; APPLICATION NUMBER: US 08/200,947
; FILING DATE: 23 FEB 1994
; APPLICATION NUMBER: US 07/864,805
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/247,505
; FILING DATE: 23 MAY 1994
; APPLICATION NUMBER: US 07/864,866
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/218,155
; FILING DATE: 25 MAR 1994
; APPLICATION NUMBER: US 07/864,807
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 07/902,467
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FILING DATE: 16 JUNE 1992  
APPLICATION NUMBER: US 07/275,433  
FILING DATE: 23 NOV 1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Superko, Colleen  
REGISTRATION NUMBER: 39,850  
REFERENCE/DOCKET NUMBER: 36119-125US8  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6564  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 227 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-183-055-6

Query Match 100.0%; Score 132; DB 3; Length 227;  
Best Local Similarity 100.0%; Pred. No. 1.1e-11;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKDVLFTFTVKSCPDPAIKEVFDNK 25  
|||  
DB 167 PKDVLFTFTVKSCPDPAIKEVFDNK 191

RESULT 5  
US-09-350-202-6  
; Sequence 6, Application US/09350202  
; Publication NO. US2003009643A1  
; GENERAL INFORMATION:  
; APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.  
; APPLICANT: Gray, Gary S., Rennert, Paul D.  
; TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/350,202  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/403,253  
; FILING DATE: March 10, 1995  
; APPLICATION NUMBER: US 08/253,964  
; FILING DATE: 3 JUNE 1994  
; APPLICATION NUMBER: US 08/073,223  
; FILING DATE: 4 JUNE 1993  
; APPLICATION NUMBER: US 08/200,947  
; FILING DATE: 23 FEB 1994  
; APPLICATION NUMBER: US 07/864,805  
; FILING DATE: 7 APR 1992  
; APPLICATION NUMBER: US 08/247,505  
; FILING DATE: 23 MAY 1994  
; APPLICATION NUMBER: US 07/864,866  
; FILING DATE: 7 APR 1992  
; APPLICATION NUMBER: US 08/218,155  
; FILING DATE: 25 MAR 1994  
; APPLICATION NUMBER: US 07/864,807  
; FILING DATE: 7 APR 1992  
; APPLICATION NUMBER: US 07/902,467

FILING DATE: 16 JUNE 1992  
APPLICATION NUMBER: US 07/275,433  
FILING DATE: 23 NOV 1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: RPI-002CP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 742-4214  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 227 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-350-202-6

Query Match 100.0%; Score 132; DB 3; Length 227;  
Best Local Similarity 100.0%; Pred. No. 1.1e-11;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKDVLFTFTVKSCPDPAIKEVFDNK 25  
|||  
DB 167 PKDVLFTFTVKSCPDPAIKEVFDNK 191

RESULT 6  
US-10-390-330-6  
; Sequence 6, Application US/10390330  
; Publication NO. US20040001829A1  
; GENERAL INFORMATION:  
; APPLICANT: June, Carl H.  
; APPLICANT: Thompson, Craig B.  
; APPLICANT: Nabel, Gary J.  
; APPLICANT: Gray, Gary S.  
; APPLICANT: Rennert, Paul D.  
; TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street, Suite 510  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/390,330  
; FILING DATE: March 17, 2003  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/435,816A  
; FILING DATE: May 4, 1995  
; CLASSIFICATION:  
; APPLICATION NUMBER: US 08/403,253  
; FILING DATE: 10 MARCH 1995  
; APPLICATION NUMBER: US 08/253,964  
; FILING DATE: 3 JUNE 1994  
; APPLICATION NUMBER: US 08/073,223  
; FILING DATE: 4 JUNE 1993  
; APPLICATION NUMBER: US 08/200,947  
; FILING DATE: 23 FEB 1994  
; APPLICATION NUMBER: US 07/864,805  
; FILING DATE: 7 APR 1992  
; APPLICATION NUMBER: US 08/247,505  
; FILING DATE: 23 MAY 1994  
; APPLICATION NUMBER: US 07/864,866

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; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/218,155
; FILING DATE: 25 MAR 1994
; APPLICATION NUMBER: US 07/864,807
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 07/902,467
; FILING DATE: 16 JUNE 1992
; APPLICATION NUMBER: US 07/275,433
; FILING DATE: 23 NOV 1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-390-330-6

Query Match 100.0%; Score 132; DB 4; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 PKKDVLETFVTKSCPDAlKEVFNK 25
Db 167 PKKDVLETFVTKSCPDAlKEVFNK 191
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RESULT 7
US-10-473-127-1723
; Sequence 1723, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/292,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1723
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1723
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Query Match 100.0%; Score 132; DB 5; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 PKKDVLETFVTKSCPDAlKEVFNK 25
Db 167 PKKDVLETFVTKSCPDAlKEVFNK 191
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RESULT 8

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US-10-473-127-1726
; Sequence 1726, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1726
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1726

Query Match 100.0%; Score 132; DB 5; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 PKKDVLETFVTKSCPDAlKEVFNK 25
Db 167 PKKDVLETFVTKSCPDAlKEVFNK 191
```

```
RESULT 9
US-10-156-136-39
; Sequence 39, Application US/10156136
; Publication No. US20030129696A1
; GENERAL INFORMATION:
; APPLICANT: NI, et al.
; TITLE OF INVENTION: Polynucleotides and Polypeptides Encoding Receptors
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Ave
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/156,136
; FILING DATE: 29-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,146
; FILING DATE: <Unknown>
; APPLICATION NUMBER: WO US98/00959
; FILING DATE: 21-JAN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: A. Anders Brookes
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF354PCT
; TELECOMMUNICATION INFORMATION:
```



TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8439  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 228 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
US-10-156-136-39

Query Match 100.0%; Score 132; DB 4; Length 228;  
Best Local Similarity 100.0%; Pred. No. 1.1e-11;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQDVLETFVTKSCPDPAIKEVFDNK 25  
DB 168 PKQDVLETFVTKSCPDPAIKEVFDNK 192

## RESULT 10

US-10-331-496A-41  
Sequence 41, Application US/10331496A  
Publication No. US20030228305A1  
GENERAL INFORMATION:  
APPLICANT: FRANTZ, GRETCHEN  
APPLICANT: HILLAN, KENNETH J.  
APPLICANT: PHILLIPS, HEIDI S.  
APPLICANT: POLAKIS, PAUL  
APPLICANT: SMITH, VICTORIA  
APPLICANT: SPENCER, SUSAN D.  
APPLICANT: WILLIAMS, P. MICKEY  
APPLICANT: WU, THOMAS D.  
APPLICANT: ZHANG, ZEMIN

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND  
TREATMENT OF TUMOR

FILE REFERENCE: P5014R1-PCT  
CURRENT APPLICATION NUMBER: US/10/331,496A  
CURRENT FILING DATE: 2002-12-30  
PRIOR APPLICATION NUMBER: US 60/345,444  
PRIOR FILING DATE: 2002-01-02  
PRIOR APPLICATION NUMBER: US 60/351,885  
PRIOR FILING DATE: 2002-01-25  
PRIOR APPLICATION NUMBER: US 60/360,066  
PRIOR FILING DATE: 2002-02-25  
PRIOR APPLICATION NUMBER: US 60/362,004  
PRIOR FILING DATE: 2002-03-05  
PRIOR APPLICATION NUMBER: US 60/366,869  
PRIOR FILING DATE: 2002-03-20  
PRIOR APPLICATION NUMBER: US 60/366,284  
PRIOR FILING DATE: 2002-03-21  
PRIOR APPLICATION NUMBER: US 60/368,679  
PRIOR FILING DATE: 2002-03-28  
PRIOR APPLICATION NUMBER: US 60/404,809  
PRIOR FILING DATE: 2002-08-19  
PRIOR APPLICATION NUMBER: US 60/405,645  
PRIOR FILING DATE: 2002-08-21  
NUMBER OF SEQ ID NOS: 95

SEQ ID NO 41  
LENGTH: 228  
TYPE: PRT

ORGANISM: Homo sapien  
US-10-331-496A-41

Query Match 100.0%; Score 132; DB 4; Length 228;  
Best Local Similarity 100.0%; Pred. No. 1.1e-11;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQDVLETFVTKSCPDPAIKEVFDNK 25  
DB 168 PKQDVLETFVTKSCPDPAIKEVFDNK 192

## RESULT 11

US-10-619-323-1  
Sequence 1, Application US/10619323  
Publication No. US20040136985A1  
GENERAL INFORMATION:  
APPLICANT: Jennings, Lisa K.  
APPLICANT: Longhurst, Celia M.  
APPLICANT: Cook, George A.  
APPLICANT: Bao, Jianxiong  
APPLICANT: Zhang, Chunxiang  
APPLICANT: White, Melanie M.  
APPLICANT: Cossano, Jr., Joseph T.  
APPLICANT: Lu, Yi

TITLE OF INVENTION: METHODS OF MODIFYING BEHAVIOR OF CD9-EXPRESSING CELLS  
FILE REFERENCE: 20609/241  
CURRENT APPLICATION NUMBER: US/10/619,323  
CURRENT FILING DATE: 2003-07-14  
PRIOR APPLICATION NUMBER: 60/395,864  
PRIOR FILING DATE: 2002-07-12  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1

LENGTH: 228  
TYPE: PRT

ORGANISM: Homo sapien  
US-10-619-323-1

Query Match 100.0%; Score 132; DB 4; Length 228;  
Best Local Similarity 100.0%; Pred. No. 1.1e-11;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQDVLETFVTKSCPDPAIKEVFDNK 25  
DB 168 PKQDVLETFVTKSCPDPAIKEVFDNK 192

## RESULT 12

US-10-794-899-97  
Sequence 97, Application US/10794899  
Publication No. US20040146516A1  
GENERAL INFORMATION:

APPLICANT: Utah Ventures  
TITLE OF INVENTION: Lumen-Exposed Molecules and Methods Targeted Delivery  
FILE REFERENCE: 27110-715  
CURRENT APPLICATION NUMBER: US/10/794,899  
CURRENT FILING DATE: 2004-03-05  
NUMBER OF SEQ ID NOS: 121  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 97

LENGTH: 228  
TYPE: PRT

ORGANISM: Homo sapiens  
US-10-794-899-97

Query Match 100.0%; Score 132; DB 4; Length 228;  
Best Local Similarity 100.0%; Pred. No. 1.1e-11;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQDVLETFVTKSCPDPAIKEVFDNK 25  
DB 168 PKQDVLETFVTKSCPDPAIKEVFDNK 192

## RESULT 13

US-10-473-127-1714  
Sequence 1714, Application US/10473127  
Publication No. US20040236091A1  
GENERAL INFORMATION:  
APPLICANT: Zycos Inc.  
TITLE OF INVENTION: TRANSLATIONAL PROFILING  
FILE REFERENCE: 08191-026W01  
CURRENT APPLICATION NUMBER: US/10/473,127

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; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1714
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1714

Query Match      100.0%; Score 132; DB 5; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PKKDVLETTTVKSCPDPAIKEVFDNK 25
DB      168 PKKDVLETTTVKSCPDPAIKEVFDNK 192

RESULT 14
US-10-473-127-1715
; Sequence 1715, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026WO1
; CURRENT APPLICATION NUMBER: US/10/473,127
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1715
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1715

Query Match      100.0%; Score 132; DB 5; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PKKDVLETTTVKSCPDPAIKEVFDNK 25
DB      168 PKKDVLETTTVKSCPDPAIKEVFDNK 192

RESULT 15
US-10-473-127-1716
; Sequence 1716, Application US/10473127
; Publication No. US20040236091A1
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2006, 17:16:18 ; Search time 4.32099 Seconds  
(without alignments)  
58.632 Million cell updates/sec

Title: US-10-619-323-5  
Perfect score: 132  
Sequence: 1 PKKDVLETFVKSCPDPAKEVFDNK 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 70606 seqs, 10133881 residues

Total number of hits satisfying chosen parameters: 70606

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA\_New.\*  
1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pap.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pap.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pap.\*  
4: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pap.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pap.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pap.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pap.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	132	100.0	228	6	US-10-821-234-1266
2	43	32.6	364	6	US-10-510-947-2
3	42.5	32.2	130	7	US-11-055-822-690
4	42.5	32.2	130	7	US-11-055-822-768
5	41	31.1	274	6	US-10-454-437-354
6	41	31.1	409	6	US-10-978-927-1
7	41	31.1	528	6	US-10-978-927-6
8	41	31.1	529	6	US-10-821-234-1520
9	41	31.1	529	6	US-10-978-927-9
10	41	31.1	529	6	US-10-978-927-13
11	41	31.1	645	6	US-10-763-712A-17
12	41	31.1	645	6	US-10-763-712A-105
13	41	31.1	662	7	US-11-137-131-2
14	41	31.1	662	7	US-11-137-131-4
15	41	31.1	870	7	US-11-165-211-48
16	41	31.1	870	7	US-11-165-226-58
17	40.5	30.7	924	6	US-10-467-657-4290
18	40	30.3	174	7	US-11-149-349-10
19	40	30.3	367	6	US-10-467-657-1440
20	40	30.3	898	7	US-11-145-631-11
21	40	30.3	1218	7	US-11-052-554A-123
22	39.5	29.9	959	6	US-10-467-962B-4
23	39.5	29.9	2197	7	US-11-075-185-8
24	39	29.5	219	7	US-11-074-176-106
25	39	29.5	351	6	US-10-981-873-27

Sequence 9, Appli  
Sequence 17, Appl  
Sequence 18, Appl  
Sequence 29, Appl  
Sequence 47, Appl  
Sequence 6, Appli  
Sequence 8, Appli  
Sequence 10, Appl  
Sequence 12, Appl  
Sequence 15, Appl  
Sequence 5, Appli  
Sequence 6, Appli  
Sequence 4, Appli  
Sequence 12, Appl  
Sequence 1178, Ap  
Sequence 185, App  
Sequence 501, App  
Sequence 60, Appl  
Sequence 5004, Ap  
Sequence 8, Appli

440 6 US-10-606-302-9  
932 7 US-11-188-743-17  
932 7 US-11-188-743-18  
397 6 US-10-858-730-29  
975 7 US-11-103-957-47  
176 7 US-11-134-703-6  
176 7 US-11-134-703-8  
246 7 US-11-134-703-10  
246 7 US-11-134-703-12  
257 6 US-10-642-272A-5  
257 6 US-10-642-272A-6  
268 7 US-11-134-703-4  
268 7 US-11-134-703-18  
468 7 US-11-054-385-12  
741 6 US-10-793-626-1178  
306 6 US-10-485-517-185  
587 6 US-10-623-155-501  
724 6 US-10-131-826A-60  
852 6 US-10-467-657-5004  
2204 6 US-10-495-083-8

ALIGNMENTS

RESULT 1  
US-10-821-234-1266  
; Sequence 1266, Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Andarmani, Susan  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
; FILE REFERENCE: 821A  
; CURRENT APPLICATION NUMBER: US/10/821,234  
; CURRENT FILING DATE: 2004-04-07  
; PRIOR APPLICATION NUMBER: US 60/462,047  
; PRIOR FILING DATE: 2003-04-07  
; NUMBER OF SEQ ID NOS: 1704  
; SOFTWARE: pt SEQ\_genes Version 1.0  
; SEQ ID NO 1266  
; LENGTH: 228  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-821-234-1266

Query Match 100.0%; Score 132; DB 6; Length 228;  
Best Local Similarity 100.0%; Pred. No. 2.1e-13;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLETFVKSCPDPAKEVFDNK 25  
DB 168 PKKDVLETFVKSCPDPAKEVFDNK 192

RESULT 2

US-10-510-947-2  
; Sequence 2, Application US/10510947  
; Publication No. US20050255123A1  
; GENERAL INFORMATION:  
; APPLICANT: The Trustees of the University of Pennsylvania  
; APPLICANT: Wilson, James M.  
; APPLICANT: Medina, Maria Fe C.  
; APPLICANT: Kobinger, Gary  
; TITLE OF INVENTION: Chimeric Ebola Virus Envelopes and Uses Therefor  
; FILE REFERENCE: UPN-02811PCT  
; CURRENT APPLICATION NUMBER: US/10/510,947  
; CURRENT FILING DATE: 2004-10-28  
; PRIOR APPLICATION NUMBER: US 60/376,480  
; PRIOR FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/385,704









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OM protein - protein search, using sw model

Run on: January 20, 2006, 17:06:32 ; Search time 17.5926 Seconds  
(without alignments)  
136.729 Million cell updates/sec

Title: US-10-619-323-5  
Perfect score: 132  
Sequence: 1 PKKDVLETFVKSCPDARKEVFDNK 25  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	132	100.0	228	1 A40402	CD9 antigen [valid
2	131	99.2	228	1 A42929	CD9 antigen - gree
3	98	74.2	226	1 S39262	CD9 antigen - rat
4	94	71.2	226	2 I49589	antigen - mouse
5	61	46.2	226	1 JX0221	CD9 antigen - bovi
6	54	40.9	64	2 H91000	hypothetical prote
7	54	40.9	64	2 B90779	hypothetical prote
8	52	39.4	439	2 T29587	hypothetical prote
9	52	39.4	435	2 S16559	cellulase (EC 3.2.
10	50	37.9	1905	2 I51553	Plexin - African c
11	49	37.1	159	2 AE2547	hypothetical prote
12	48.5	36.7	500	2 F71978	hypothetical prote
13	48	36.4	1057	2 T15720	hypothetical prote
14	47.5	36.0	439	2 T16414	hypothetical prote
15	47	35.6	68	1 Q1B50L	hypothetical prote
16	47	35.6	300	2 G89915	conserved hypotet
17	47	35.6	480	2 C97121	p-loop ATPase doma
18	47	35.6	1020	2 S05944	neutroal cell surf
19	47	35.6	1021	2 A57112	contactin precurs
20	46	34.8	294	2 G87166	enoyl-CoA hydrat
21	46	34.8	336	2 JC4102	hypothetical 36.9k
22	46	34.8	387	1 BRADN1	41k fiber protein
23	46	34.8	423	2 E90569	conserved hypotet
24	46	34.8	502	2 T22045	hypothetical prote
25	46	34.8	608	2 C89760	two-component sens
26	46	34.8	820	2 T27909	hypothetical prote
27	46	34.8	828	2 C71951	probable flagellar
28	46	34.8	1048	1 YGVCAR	anGR protein - Vib
29	46	34.8	1139	2 S44800	F1089.8 protein -

30	46	34.8	1405	2 T04426	hypothetical prote
31	46	34.8	1980	2 S54307	myosin heavy chain
32	45.5	34.5	192	2 A85534	hypothetical prote
33	45.5	34.5	192	2 E90683	hypothetical prote
34	45.5	34.5	192	2 C64767	yail protein - Esc
35	45.5	34.5	1335	2 JQ1258	RNA-directed RNA p
36	45	34.1	25	2 PC4445	L-ascorbate peroxi
37	45	34.1	134	2 T30024	hypothetical prote
38	45	34.1	195	2 T03086	probable thymidine
39	45	34.1	372	1 VVVPK1	coat protein vpi -
40	45	34.1	483	2 D86486	protein F2899.5 [i
41	45	34.1	867	2 D75091	large helicase-rel
42	45	34.1	1217	2 T13996	pol protein - friu
43	44.5	33.7	231	2 E82652	phage-related repr
44	44.5	33.7	545	2 T02578	hypothetical prote
45	44.5	33.7	586	2 S66697	probable membrane

ALIGNMENTS

RESULT 1  
A40402

CD9 antigen [validated] - human

N;Alternate names: motility-related protein-1

C;Species: Homo sapiens (man)

C;Date: 06-Dec-1991 #sequence revision 07-Jul-1995 #text\_change 09-Jul-2004

C;Accession: A46123; A40402; JH0555; A39029; S10564

R;Rubinstein, B.; Benoist, P.; Billard, M.; Plaisance, S.; Prenant, M.; Uzan, G.; Bouche

Genomics 16, 132-138, 1993

A;Title: Organization of the human CD9 gene.

A;Reference number: A46123; MUID:93252369; PMID:8486348

A;Accession: A46123

A;Molecule type: DNA

A;Residues: 1-228 <RUB>

A;Cross-references: UNIPROT:P21926; UNIPARC:UPI000003B45A; GB:S60489; NID:g300112; PIDN

A;Experimental source: leukocyte

R;Lanza, P.; Wolf, D.; Fox, C.P.; Kieffer, N.; Seyer, J.M.; Fried, V.A.; Coughlin, S.R.

J. Biol. Chem. 266, 10638-10645, 1991

A;Title: CDNA cloning and expression of platelet p24/CD9. Evidence for a new family of

A;Reference number: A40402; MUID:91244846; PMID:2037603

A;Accession: A40402

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-228 <LAN>

A;Cross-references: UNIPARC:UPI000003B45A; GB:I34068; GB:M61880; NID:G508495; PIDN:AAA5

A;Note: parts of this sequence, including the amino end of the mature protein, were con

R;Miyake, M.; Koyama, M.; Seno, M.; Ikeyama, S.

J. Exp. Med. 174, 1347-1354, 1991

A;Title: Identification of the motility-related protein (MRP-1), recognized by monoclon

A;Reference number: JH0555; MUID:92078843; PMID:1720807

A;Accession: JH0555

A;Molecule type: mRNA

A;Residues: 1-228 <MIY>

A;Cross-references: UNIPARC:UPI000003B45A; GB:X60111; NID:g34768; PIDN:CAA42708.1; PID:

A;Experimental source: breast carcinoma

A;Note: this protein has the epitope defined by cell motility-inhibiting monoclonal ant

R;Bouchet, C.; Benoist, P.; Frachet, P.; Billard, M.; Worthington, R.E.; Gagnon, J.; Uz

J. Biol. Chem. 266, 117-122, 1991

A;Title: Molecular cloning of the CD9 antigen. A new family of cell surface proteins.

A;Reference number: A39029; MUID:91093112; PMID:1840589

A;Accession: A39029

A;Molecule type: mRNA

A;Residues: 1-8, 'S', '10-66, 'A', '68-193, 195-228 <BOU>

A;Cross-references: UNIPARC:UPI0000174148; GB:M38690

A;Note: parts of this sequence, including the amino end of the mature protein, were con

R;Higashihara, M.; Takahata, K.; Yotomi, Y.; Nakahara, K.; Kurokawa, K.

FEBS Lett. 264, 270-274, 1990

A;Title: Purification and partial characterization of CD9 antigen of human platelets.

A;Reference number: S10564; MUID:90292223; PMID:2358073

A;Accession: S10564

A;Molecule type: protein

A;Residues: 2-8,'X',10-21 <HIG>  
C;Cross-references: UNIPARC:UPI000017414C  
C;Genetics:  
A;Gene: GDB:CD9; MIC3  
A;Cross-references: GDB:120582; OMIM:143030  
A;Map position: 12p13-12p13  
C;Superfamily: CD9 antigen  
C;Keywords: glycoprotein; transmembrane protein  
F;2-228/Product: CD9 antigen #status experimental <MAT>  
F;2-11/Domain: intracellular #status predicted <CY1>  
F;12-35/Domain: transmembrane #status predicted <TM1>  
F;36-55/Domain: extracellular #status predicted <EX1>  
F;56-82/Domain: transmembrane #status predicted <TM2>  
F;83-86/Domain: intracellular #status predicted <CY2>  
F;87-111/Domain: transmembrane #status predicted <TM3>  
F;112-194/Domain: extracellular #status predicted <EX2>  
F;195-221/Domain: transmembrane #status predicted <TM4>  
F;222-228/Domain: intracellular #status predicted <CY3>  
F;53/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 132; DB 1; Length 228;  
Best Local Similarity 100.0%; Pred. No. 6.9e-12;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKQVLETFVKSCPDPAIKEVFNDK 25  
|||||:|||||:|||||:|||||:|||||:  
Db 168 PKKQVLETFVKSCPDPAIKEVFNDK 192

RESULT 2  
CD9 antigen - green monkey  
N;Alternate names: 27K diphtheria toxin receptor-associated protein DRAP27  
C;Species: Carcophthecus aethiops (green monkey, grivet)  
C;Date: 01-Oct-1992 #sequence\_revision 09-Aug-1996 #text\_change 09-Jul-2004  
A;Accession: A42929  
R;Mitsumura, T.; Iwamoto, R.; Umata, T.; Yomo, T.; Urabe, I.; Tsuneoka, M.; Mekada, E.  
J. Cell Biol. 118, 1389-1399, 1992  
A;Title: The 27-kD diphtheria toxin receptor-associated protein (DRAP27) from vero cells  
epitops on toxin-sensitive cells.  
A;Reference number: A42929; MUID:92394967; PMID:1522113  
A;Accession: A42929  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-228 <MIT>  
C;Cross-references: UNIPROT:P30409; UNIPARC:UPI000016C3B8; GB:D10726; NID:g218565; PIDN:  
C;Superfamily: CD9 antigen  
C;Keywords: glycoprotein; transmembrane protein  
F;2-228/Product: CD9 antigen #status predicted <MAT>  
F;2-11/Domain: intracellular #status predicted <CY1>  
F;12-35/Domain: transmembrane #status predicted <TM1>  
F;36-55/Domain: extracellular #status predicted <EX1>  
F;56-82/Domain: transmembrane #status predicted <TM2>  
F;83-86/Domain: intracellular #status predicted <CY2>  
F;87-111/Domain: transmembrane #status predicted <TM3>  
F;112-194/Domain: extracellular #status predicted <EX2>  
F;195-221/Domain: transmembrane #status predicted <TM4>  
F;222-228/Domain: intracellular #status predicted <CY3>  
F;52-53/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 99.2%; Score 131; DB 1; Length 228;  
Best Local Similarity 96.0%; Pred. No. 9.7e-12;  
Matches 24; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKQVLETFVKSCPDPAIKEVFNDK 25  
|||||:|||||:|||||:|||||:|||||:  
Db 168 PKKQVLETFVKSCPDPAIKEVFNDK 192

RESULT 3  
CD9 antigen - rat  
N;Alternate names: platelet cell surface glycoprotein

A;Residues: 2-8,'X',10-21 <HIG>  
C;Cross-references: UNIPARC:UPI000017414C  
C;Genetics:  
A;Gene: GDB:CD9; MIC3  
A;Cross-references: GDB:120582; OMIM:143030  
A;Map position: 12p13-12p13  
C;Superfamily: CD9 antigen  
C;Keywords: glycoprotein; transmembrane protein  
F;2-228/Product: CD9 antigen #status experimental <MAT>  
F;2-11/Domain: intracellular #status predicted <CY1>  
F;12-35/Domain: transmembrane #status predicted <TM1>  
F;36-55/Domain: extracellular #status predicted <EX1>  
F;56-82/Domain: transmembrane #status predicted <TM2>  
F;83-86/Domain: intracellular #status predicted <CY2>  
F;87-111/Domain: transmembrane #status predicted <TM3>  
F;112-194/Domain: extracellular #status predicted <EX2>  
F;195-221/Domain: transmembrane #status predicted <TM4>  
F;222-228/Domain: intracellular #status predicted <CY3>  
F;53/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 132; DB 1; Length 228;  
Best Local Similarity 100.0%; Pred. No. 6.9e-12;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKQVLETFVKSCPDPAIKEVFNDK 25  
|||||:|||||:|||||:|||||:|||||:  
Db 168 PKKQVLETFVKSCPDPAIKEVFNDK 192

RESULT 2  
CD9 antigen - green monkey  
N;Alternate names: 27K diphtheria toxin receptor-associated protein DRAP27  
C;Species: Carcophthecus aethiops (green monkey, grivet)  
C;Date: 01-Oct-1992 #sequence\_revision 09-Aug-1996 #text\_change 09-Jul-2004  
A;Accession: A42929  
R;Mitsumura, T.; Iwamoto, R.; Umata, T.; Yomo, T.; Urabe, I.; Tsuneoka, M.; Mekada, E.  
J. Cell Biol. 118, 1389-1399, 1992  
A;Title: The 27-kD diphtheria toxin receptor-associated protein (DRAP27) from vero cells  
epitops on toxin-sensitive cells.  
A;Reference number: A42929; MUID:92394967; PMID:1522113  
A;Accession: A42929  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-228 <MIT>  
C;Cross-references: UNIPROT:P30409; UNIPARC:UPI000016C3B8; GB:D10726; NID:g218565; PIDN:  
C;Superfamily: CD9 antigen  
C;Keywords: glycoprotein; transmembrane protein  
F;2-228/Product: CD9 antigen #status predicted <MAT>  
F;2-11/Domain: intracellular #status predicted <CY1>  
F;12-35/Domain: transmembrane #status predicted <TM1>  
F;36-55/Domain: extracellular #status predicted <EX1>  
F;56-82/Domain: transmembrane #status predicted <TM2>  
F;83-86/Domain: intracellular #status predicted <CY2>  
F;87-111/Domain: transmembrane #status predicted <TM3>  
F;112-194/Domain: extracellular #status predicted <EX2>  
F;195-221/Domain: transmembrane #status predicted <TM4>  
F;222-228/Domain: intracellular #status predicted <CY3>  
F;52-53/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 99.2%; Score 131; DB 1; Length 228;  
Best Local Similarity 96.0%; Pred. No. 9.7e-12;  
Matches 24; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKQVLETFVKSCPDPAIKEVFNDK 25  
|||||:|||||:|||||:|||||:|||||:  
Db 168 PKKQVLETFVKSCPDPAIKEVFNDK 192

RESULT 3  
CD9 antigen - rat  
N;Alternate names: platelet cell surface glycoprotein

C;Species: Rattus norvegicus (Norway rat)  
C;Date: 06-Jan-1995 #sequence\_revision 09-Aug-1996 #text\_change 09-Jul-2004  
C;Accession: I56562; S39262  
R;Kaprielian, Z.; Cho, K.O.; Hadjiargyrou, M.; Patterson, P.H.  
J. Neurosci. 15, 562-573, 1995  
A;Title: CD9, a major platelet cell surface glycoprotein, is a ROCA antigen and is expressed in the developing rat brain.  
A;Reference number: I56562; MUID:95123481; PMID:7823164  
A;Accession: I56562  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-226 <RES>  
A;Cross-references: UNIPROT:P40241; UNIPARC:UPI00001708C6; EMBL:X76489; NID:g434314; P1  
C;Genetics:  
A;Gene: CD9  
C;Superfamily: CD9 antigen  
C;Keywords: glycoprotein; transmembrane protein  
F;2-11/Domain: intracellular #status predicted <CY1>  
F;12-35/Domain: transmembrane #status predicted <TM1>  
F;36-53/Domain: extracellular #status predicted <EX1>  
F;54-80/Domain: transmembrane #status predicted <TM2>  
F;81-84/Domain: intracellular #status predicted <CY2>  
F;85-109/Domain: transmembrane #status predicted <TM3>  
F;110-192/Domain: extracellular #status predicted <EX2>  
F;193-219/Domain: transmembrane #status predicted <TM4>  
F;220-226/Domain: intracellular #status predicted <CY3>  
F;50/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 74.2%; Score 98; DB 1; Length 226;  
Best Local Similarity 76.0%; Pred. No. 7.1e-07;  
Matches 19; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 PKKQVLETFVKSCPDPAIKEVFNDK 25  
|||||:|||||:|||||:|||||:|||||:  
Db 166 PKKQVLETFVKSCPDPAIDEVFHSK 190

RESULT 4  
I49589  
antigen - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I49589  
R;Rubinstein, E.; Billard, M.; Plaisance, S.; Prenant, M.; Boucheix, C.  
Thromb. Res. 71, 377-383, 1993  
A;Title: Molecular cloning of the mouse equivalent of CD9 antigen.  
A;Reference number: I49589; MUID:94054345; PMID:8236164  
A;Accession: I49589  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-226 <RES>  
A;Cross-references: UNIPROT:P40240; UNIPARC:UPI0000003E37; GB:L08115; NID:g388911; PIDN:  
C;Superfamily: CD9 antigen

Query Match 71.2%; Score 94; DB 2; Length 226;  
Best Local Similarity 68.0%; Pred. No. 2.8e-06;  
Matches 17; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 PKKQVLETFVKSCPDPAIKEVFNDK 25  
|||||:|||||:|||||:|||||:|||||:  
Db 166 PKKQVLETFVKSCPDPAISEVFNNK 190

RESULT 5  
JX0221  
CD9 antigen - bovine  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 09-Oct-1992 #sequence\_revision 09-Aug-1996 #text\_change 09-Jul-2004  
C;Accession: JX0221  
R;Martin-Alonso, J.M.; Hernando, N.; Ghosh, S.; Coca-Prados, M.  
J. Biochem. 112, 63-67, 1992  
A;Title: Molecular cloning of the bovine CD9 antigen from ocular ciliary epithelial cells.  
A;Reference number: JX0221; MUID:93054422; PMID:1339429  
A;Accession: JX0221

A;Molecule type: mRNA  
A;Residues: 1-226 <MAR>  
A;Cross-references: UNIPROT:P30932; UNIPARC:UPI0000167C21; GB:W81720; NID:g162820; PIDN:  
A;Experimental source: ocular ciliary epithelial cell  
C;Superfamily: CD9 antigen  
C;Keywords: glycoprotein; transmembrane protein  
F;2-226/Product: CD9 antigen #status predicted <MAT>  
F;2-11/Domain: intracellular #status predicted <CY1>  
F;12-35/Domain: transmembrane #status predicted <TM1>  
F;36-53/Domain: extracellular #status predicted <EX1>  
F;54-76/Domain: transmembrane #status predicted <TM2>  
F;77-80/Domain: intracellular #status predicted <CY2>  
F;81-109/Domain: transmembrane #status predicted <TM3>  
F;110-192/Domain: extracellular #status predicted <EX2>  
F;193-219/Domain: transmembrane #status predicted <TM4>  
F;220-226/Domain: intracellular #status predicted <CY3>  
F;50/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 46.2%; Score 61; DB 1; Length 226;  
Best Local Similarity 36.0%; Pred. No. 0.2;  
Matches 9; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Qy 1 PKQDVLETFVTKSCPDAIKEVFNK 25  
Db 166 PPKNLDSLKTRCPPEAIDEIFRSK 190

RESULT 6  
H91000  
hypothetical protein ECs2976 [imported] - Escherichia coli (strain O157:H7, substrain R1  
C;Species: Escherichia coli  
C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004  
C;Accession: H91000  
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
gaawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene  
A;Reference number: A99629; MUID:21156231; PMID:11258796  
A;Accession: H91000  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-64 <HAY>  
A;Cross-references: UNIPROT:Q8X5B8; UNIPARC:UPI000005FCE7; GB:BA000007; PIDN:BA036399.1;  
A;Experimental source: strain O157:H7, substrain R1MD 0509952  
C;Genetics:  
A;Gene: ECs2976  
C;Superfamily: phage lambda hypothetical 7.9K protein (nin region)

Query Match 40.9%; Score 54; DB 2; Length 64;  
Best Local Similarity 50.0%; Pred. No. 0.64;  
Matches 9; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 8 TFTVKSQDAIKEVFNK 25  
Db 2 TFTVKTIPDMLVEAYENQ 19

RESULT 7  
B90779  
hypothetical protein ECs1202 [imported] - Escherichia coli (strain O157:H7, substrain R1  
C;Species: Escherichia coli  
C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004  
C;Accession: B90779  
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
gaawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene  
A;Reference number: A99629; MUID:21156231; PMID:11258796  
A;Accession: B90779  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-64 <HAY>  
A;Cross-references: UNIPROT:Q8X5B8; UNIPARC:UPI000005FCE7; GB:BA000007; PIDN:BA036425.1;

A;Experimental source: strain O157:H7, substrain R1MD 0509952  
C;Genetics:  
A;Gene: ECs1202  
C;Superfamily: phage lambda hypothetical 7.9K protein (nin region)

Query Match 40.9%; Score 54; DB 2; Length 64;  
Best Local Similarity 50.0%; Pred. No. 0.64;  
Matches 9; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 8 TFTVKSQDAIKEVFNK 25  
Db 2 TFTVKTIPDMLVEAYENQ 19

RESULT 8  
T29587  
hypothetical protein F55F8.5 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 05-Oct-2004  
C;Accession: T29587  
R;Gattung, S.; Scheet, P.; Kemp, K.  
submitted to the EMBL Data Library, November 1996  
A;Description: The sequence of C. elegans cosmid F55F8.  
A;Reference number: Z20647  
A;Accession: T29587  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-439 <GAT>  
A;Cross-references: UNIPROT:P91343; UNIPARC:UPI000013B8F3; EMBL:U80447; PIDN:AAB37809.1  
A;Experimental source: strain Bristol N2; clone F55F8  
C;Genetics:  
A;Gene: CESP:F55F8.5  
A;Map position: 1  
A;Introns: 31/2; 64/1; 95/3; 131/2; 173/1; 204/3; 312/1; 354/1; 398/2

Query Match 39.4%; Score 52; DB 2; Length 439;  
Best Local Similarity 44.0%; Pred. No. 8.4;  
Matches 11; Conservative 4; Mismatches 6; Indels 4; Gaps 1;

Qy 1 PKQDVLETFVTKSCPDAIKEVFNK 25  
Db 331 PKSDLL-----ISSCTDAIPRLYDPK 351

RESULT 9  
S16559  
cellulase (EC 3.2.1.4) - Ruminococcus flavefaciens  
C;Species: Ruminococcus flavefaciens  
C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
C;Accession: S16559  
R;Cunningham, C.; McPherson, C.A.; Martin, J.; Harris, W.J.; Flint, H.J.  
Mol. Gen. Genet. 228, 320-323, 1991  
A;Title: Sequence of a cellulase gene from the rumen anaerobe Ruminococcus flavefaciens  
A;Reference number: S16559; MUID:91360084; PMID:1886616  
A;Accession: S16559  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-455 <CUN>  
A;Cross-references: UNIPROT:Q53302; UNIPARC:UPI00000836E7; GB:S55178; NID:g234871; PIDN:  
C;Superfamily: cellulase CCA; Clostridium cellulase repeat homology  
C;Keywords: glycosidase; hydrolase

Query Match 39.4%; Score 52; DB 2; Length 455;  
Best Local Similarity 41.4%; Pred. No. 8.7;  
Matches 12; Conservative 4; Mismatches 7; Indels 6; Gaps 1;

Qy 1 PKQDV-----LETFTVKSQDAIKEVFNK 23  
Db 68 PSKPIPLDSAGLETETTCWCPASQELFD 96

RESULT 10  
I51553



C;Species: phage lambda  
C;Date: 13-Jun-1983 #sequence revision 13-Jun-1983 #text\_change 10-Sep-1999  
C;Accession: F43011; B43017; A04396  
R;Daniels, D.  
submitted to the Nucleic Acid Sequence Database, September 1982  
A;Reference number: A94614  
A;Accession: F43011  
A;Molecule type: DNA  
A;Residues: 1-68 <DNA>  
A;Cross-references: UNIPARC:UPI0000174BCA  
R;Sanger, F.; Coulson, A.R.; Hong, G.F.; Hill, D.F.; Petersen, G.B.  
J. Mol. Biol. 162, 729-773, 1982  
A;Title: Nucleotide sequence of bacteriophage lambda DNA.  
A;Reference number: A92891; MUID:83189071; PMID:6221115  
A;Accession: B43017  
A;Molecule type: DNA  
A;Residues: 1-68 <SAN>  
A;Cross-references: UNIPARC:UPI0000174BCA; GB:J02459; GB:M17233; GB:M24325; GB:V00636; G  
C;Genetics:  
A;Map position: 88.74-89.16  
C;Superfamily: phage lambda hypothetical 7.9K protein (nin region)  
  
Query Match 35.6%; Score 47; DB 1; Length 68;  
Best Local Similarity 44.4%; Pred. No. 7.3;  
Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
  
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Db 2 TFSVKTIPTDMLVETGNG 19  
  
Search completed: January 20, 2006, 17:22:37  
Job time : 18.5926 secs

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GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2006, 17:05:21 ; Search time 95.0617 Seconds  
(without alignments)  
185.545 Million cell updates/sec

Title: US-10-619-323-5  
Perfect score: 132  
Sequence: 1 PKKDVLETFVKSCPAIKEVFDNK 25

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 70528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	132	100.0	227	1	CD9_HUMAN
2	132	100.0	228	2	Q5J7W6_HUMAN
3	131	99.2	227	1	CD9_CERAE
4	98	74.2	225	1	CD9_FELCA
5	96	72.7	225	1	CD9_FELCA
6	94	71.2	225	1	CD9_MOUSE
7	89	67.4	226	2	Q8MJ48_PIG
8	87	65.9	227	2	Q4REW0_TETNG
9	86	65.2	225	1	CD9_PIG
10	84	63.6	227	2	Q6NKG7_BRARE
11	70	53.0	224	2	Q9IBC9_CHICK
12	62	47.0	228	2	Q6Q8E5_XENLA
13	61	46.2	225	1	CD9_BOVIN
14	58	43.9	246	2	Q6P0W1_BRARE
15	55.5	42.0	236	2	Q7ZTR5_XENLA
16	55	41.7	230	2	Q8AJU1_ONCMY
17	54	40.9	64	1	NINH_BFP33
18	54	40.9	64	1	NINH_BFVT2
19	54	40.9	64	2	Q8X5E8_9VIRU
20	54	40.9	64	2	Q7AK37_ECO57
21	53.5	40.5	398	2	Q60KA7_CAERB
22	53.5	40.5	896	2	Q8IBB9_PLAF7
23	53	40.2	642	2	Q6CQB0_KJULA
24	52	39.4	439	1	YIM3M_CABEL
25	52	39.4	448	2	Q9NET3_HUMAN
26	52	39.4	452	2	Q96PV4_HUMAN
27	52	39.4	455	2	Q53302_RUMFL
28	52	39.4	759	2	Q05143_RUMFL
29	52	39.4	994	2	Q6CEH0_YARLI
30	51.5	39.0	1235	2	Q517S3_ENTHI
31	51	38.6	64	1	NINH_BPH19

RESULT 1

ID	CD9_HUMAN	STANDARD;	PRT;	227 AA.
AC	F21926; Q96ES4;			
DT	01-MAY-1991 (Rel. 18, Created)			
DT	01-APR-1993 (Rel. 25, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	CD9 antigen (p24) (Leukocyte antigen MIC3) (Motility-related protein) (MRP-1) (Tetraspanin-29) (TSPAN-29).			
GN	Name=CD9; Synonyms=MIC3, TSPAN29;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 1-4.			
RX	MEDLINE=91093112; PubMed=1840589;			
RA	Boucheix C., Benoit P., Frachet P., Billard M., Worthington R.E.,			
RA	Gagnon J., Uzan G.;			
RT	"Molecular cloning of the CD9 antigen. A new family of cell surface proteins.";			
RL	J. Biol. Chem. 266:117-122(1991).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE [MRNA], AND PARTIAL PROTEIN SEQUENCE.			
RX	MEDLINE=91244846; PubMed=2037603;			
RA	Lanza F., Wolf D., Fox C.F., Kieffer N., Seyer J.M., Fried V.A.,			
RA	Coughlin S.R., Phillips D.R., Jennings L.K.;			
RT	"cDNA cloning and expression of platelet p24/CD9. Evidence for a new family of multiple membrane-spanning proteins.";			
RL	J. Biol. Chem. 266:10638-10645(1991).			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=9207843; PubMed=1720807; DOI=10.1084/jem.174.6.1347;			
RA	Miyake M., Koyama M., Seno M., Ikegama S.;			
RT	"Identification of the motility-related protein (MRP-1), recognized by monoclonal antibody M31-15, which inhibits cell motility.";			
RL	J. Exp. Med. 174:1347-1354(1991).			
RN	[4]			
RP	NUCLEOTIDE SEQUENCE [GENOMIC DNA].			
RC	TISSUE=Leukocyte;			
RX	MEDLINE=93252369; PubMed=8486348;			
RA	Rubinstein E., Benoit P., Billard M., Plaisance S., Prenant M.,			
RA	Uzan G., Boucheix C.;			
RT	"Organization of the human CD9 gene.";			
RL	Genomics 16:132-138(1993).			
RN	[5]			
RP	NUCLEOTIDE SEQUENCE [GENOMIC DNA].			
RA	Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O.,			
RA	Rajkumar N., Yi Q., Nickerson D.A.;			
RT	"SeattleSNPs, NHLBI HL6682 program for genomic applications, UW-FHRC, Seattle, WA (URL: http://pga.gs.washington.edu).";			
RL	Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.			
RN	[6]			

Q777W6 bacterioph  
Q7Y277 phage phi 4  
Q6DKM9 xenopus lae  
Q8CSN0 staphylococ  
Q5HPF1 staphylococ  
Q5Y296 nocardia fa  
Q4XUR1 plasmodium  
Q52F04 magnaporthe  
Q9C499 neurospora  
Q7RVZ9 neurospora  
Q5USA2 xenopus lae  
Q51823 xenopus lae  
Q51954 bacteroides  
Q851Q5 oryza sativ

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RC TISSUE=Ovary;  
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zerborg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshitsuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [7]  
RP PROTEIN SEQUENCE OF 1-20.  
RC TISSUE=Platelet;  
RX MEDLINE=90292223; PubMed=2358073; DOI=10.1016/0014-5793(90)80265-K;  
RA Higashihara M., Takahata K., Yatomi Y., Nakahara K., Kurokawa K.;  
RT "Purification and partial characterization of CD9 antigen of human  
RT platelets.";  
RL FEBS Lett. 264:270-274 (1990).  
RN [8]  
RP ROLE IN CELL MOTILITY AND METASTASIS.  
RX PubMed=8478605; DOI=10.1084/jem.177.5.1231;  
RA Ikevama S., Koyama M., Yamaoka M., Sasada R., Miyake M.;  
RT "Suppression of cell motility and metastasis by transfection with  
RT human motility-related protein (MRP-1/CD9) DNA.";  
RL J. Exp. Med. 177:1231-1237 (1993).  
RN [9]  
RP ROLE IN CELL ADHESION.  
RX PubMed=7511626;  
RA Masellis-Smith A., Shaw A.R.;  
RT "CD9-regulated adhesion. Anti-CD9 monoclonal antibody induce pre-B  
RT cell adhesion to bone marrow fibroblasts through de novo recognition  
RT of fibronectin.";  
RL J. Immunol. 152:2768-2777 (1994).  
RN [10]  
RP ROLE IN GAMETE FUSION.  
RX PubMed=14575715; DOI=10.1016/j.bbrc.2003.09.196;  
RA Higginbottom A., Takahashi Y., Bolling L., Coonrod S.A., White J.M.,  
RA Partridge L.J., Monk P.N.;  
RT "Structural requirements for the inhibitory action of the CD9 large  
RT extracellular domain in sperm/oocyte binding and fusion.";  
RL Biochem. Biophys. Res. Commun. 311:208-214 (2003).  
RN [11]  
RP SUBUNIT.  
RX PubMed=14556650; DOI=10.1042/BJ20031037;  
RA Kovalev O.V., Yang X., Kolesnikova T.V., Hemler M.E.;  
RT "Evidence for specific tetraspanin homodimers: inhibition of  
RT palmitoylation makes cysteine residues available for cross-linking.";  
RL Biochem. J. 377:407-417 (2004).  
RN [12]  
RP PHOSPHORYLATION.  
RX MEDLINE=93327758; PubMed=7687539;  
RA Chalupny M.J., Kanner S.B., Schieven G.L., Wee S., Gilliland L.K.,  
RA Aruffo A., Ledbetter J.A.;  
RT "Tyrosine phosphorylation of CD19 in pre-B and mature B cells.";  
RL EMBO J. 12:2691-2696 (1993).  
RN [13]  
RP PALMITOYLATION, AND MUTAGENESIS OF CYS-8; CYS-77; CYS-78; CYS-86;  
RX CYS-217 AND CYS-218.  
RX PubMed=11959120; DOI=10.1016/S0014-5793(02)02522-X;  
RA Charrin S., Manie S., Oualid M., Billard M., Boucheix C.,  
RA Rubinstein E.;  
RT "Differential stability of tetraspanin/tetraspanin interactions: role  
RT of palmitoylation.";  
RL FEBS Lett. 516:139-144 (2002).  
RN [14]  
RP INTERACTION WITH PTGFRN.  
RX MEDLINE=21216740; PubMed=11278880; DOI=10.1074/jbc.M011297200;  
RA Charrin S., Le Nacur F., Oualid M., Billard M., Faure G., Hanash S.M.,  
RA Boucheix C., Rubinstein E.;  
RT "The major CD9 and CD81 molecular partner. Identification and  
RT characterization of the complexes.";  
RL J. Biol. Chem. 276:14329-14337 (2001).  
CC -!- FUNCTION: Involved in platelet activation and aggregation.  
CC Regulates paranodal junction formation. Required for gamete  
CC fusion. Involved in cell adhesion, cell motility and tumor  
CC metastasis.  
CC -!- SUBUNIT: Forms both disulfide-linked homodimers and higher  
CC homooligomers as well as heterooligomers with other members of the  
CC tetraspanin family. Associates with CR2/CD21 and with  
CC PTGFRN/CD9P1.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: Expressed by a variety of hematopoietic and  
CC epithelial cells.  
CC -!- PTM: Protein exists in three forms with molecular masses between  
CC 22 and 27 kDa, and is known to carry covalently linked fatty  
CC acids.  
CC -!- PTM: Phosphorylated on tyrosine following B-cell activation.  
CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.  
CC  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC  
CC EMBL; S60489; AAC60586.1; -; Genomic DNA.  
CC EMBL; S60462; AAC60586.1; JOINED; Genomic DNA.  
CC EMBL; S60463; AAC60586.1; JOINED; Genomic DNA.  
CC EMBL; S60464; AAC60586.1; JOINED; Genomic DNA.  
CC EMBL; S60700; AAC60586.1; JOINED; Genomic DNA.  
CC EMBL; S60699; AAC60586.1; JOINED; Genomic DNA.  
CC EMBL; S60465; AAC60586.1; JOINED; Genomic DNA.  
CC EMBL; S60472; AAC60586.1; JOINED; Genomic DNA.  
CC EMBL; M38690; AAA80320.1; -; mRNA.  
CC EMBL; L34068; AAA59982.1; -; mRNA.  
CC EMBL; X60111; CAA42708.1; -; mRNA.  
CC EMBL; L08118; -; NOT ANNOTATED CDS; Genomic DNA.  
CC EMBL; L08119; AAA51954.1; ALT SEQ; Genomic DNA.  
CC EMBL; L08120; AAA51955.1; ALT SEQ; Genomic DNA.  
CC EMBL; L08121; AAA51956.1; -; Genomic DNA.  
CC EMBL; L08122; AAA51957.1; -; Genomic DNA.  
CC EMBL; L08123; AAA51958.1; -; Genomic DNA.  
CC EMBL; L08124; AAA51959.1; -; Genomic DNA.  
CC EMBL; L08125; -; NOT ANNOTATED CDS; Genomic DNA.  
CC EMBL; AY422198; AAQ87878.1; -; Genomic DNA.  
CC EMBL; BC011988; AAH11988.1; -; mRNA.  
CC PIR; A46123; A40402.  
CC ENSEMBL; ENSG0000010278; Homo sapiens.  
CC HGNC; HGNC:1709; CD9.  
CC H-InvDB; HTX0010357; --  
CC Reactome; P21926; --  
CC MIM; 143030; --  
CC GO; GO:0005887; C:integral to plasma membrane; NAS.  
CC GO; GO:0005886; C:plasma membrane; NAS.  
CC GO; GO:0005515; F:protein binding; IPI.  
CC GO; GO:0007155; P:cell adhesion; IDA.  
CC GO; GO:0006928; P:cell motility; IDA.  
CC GO; GO:0007342; P:fusion of sperm to egg plasma membrane; IDA.  
CC GO; GO:0030913; P:paranodal junction formation; ISS.  
CC GO; GO:0030169; P:platelet activation; NAS.  
CC InterPro; IPR000301; Transmem 4.  
CC Pfam; PF00335; Tetraspanin; I.  
CC PRINTS; PR00259; TMFOUR.



DR PROSITE; PS00421; TM4\_1; 1.  
 KW Antigen; Cell adhesion; Direct protein sequencing; Fertilization;  
 Query Match 100.0%; Score 132; DB 1; Length 227;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-11; Indels 0; Gaps 0;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 PKKDVLETFVKSCPDPAIKEVFNK 25  
 DB 167 PKKDVLETFVKSCPDPAIKEVFNK 191  
 RESULT 2  
 ID Q5J7W6 HUMAN PRELIMINARY; PRT; 228 AA.  
 AC Q5J7W6;  
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
 DE Growth-inhibiting gene 2 protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Kim J.W.;  
 RT "Identification of a human growth inhibition gene 2 (GIG2).";  
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY423720; AAS00483.1; -, mRNA.  
 SQ SEQUENCE 228 AA; 25416 MW; F68333E0C20611D8 CRC64;  
 Query Match 100.0%; Score 132; DB 2; Length 228;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-11; Indels 0; Gaps 0;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 PKKDVLETFVKSCPDPAIKEVFNK 25  
 DB 168 PKKDVLETFVKSCPDPAIKEVFNK 192  
 RESULT 3  
 ID CD9 CERAE STANDARD; PRT; 227 AA.  
 AC P30409;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE CD9 antigen (27 kDa diphtheria toxin receptor-associated protein) (DRAP27).  
 GN Name=CD9;  
 OS Cercopithecus aethiops (Green monkey) (Grivet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini;  
 OC Cercopithecidae; Cercopithecinae; Cercopithecus.  
 OX NCBI\_TaxID=9534;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE (MRNA).  
 RX MEDLINE=92394967; PubMed=1522113; DOI=10.1083/jcb.118.6.1389;  
 RA Mitamura T., Iwamoto R., Umata T., Yomo T., Urabe I., Tsuneoka M.,  
 RA Mekada E.;  
 RT "The 27-kD diphtheria toxin receptor-associated protein (DRAP27) from  
 RT vero cells is the monkey homologue of human CD9 antigen: expression of  
 RT DRAP27 elevates the number of diphtheria toxin receptors on toxin-  
 RT sensitive cells.";  
 RL J. Cell Biol. 118:1389-1399(1992).  
 CC -1- FUNCTION: Involved in platelet activation and aggregation.  
 CC Regulates paranodal junction formation. Required for gamete  
 CC fusion. Involved in cell adhesion, cell motility and tumor  
 CC metastasis (By similarity).  
 CC -1- FUNCTION: Expression of DRAP27 elevates the number of diphtheria  
 CC toxin receptors on toxin-sensitive cells.

CC -1- SUBUNIT: Forms both disulfide-linked homodimers and higher  
 CC homooligomers as well as heterooligomers with other members of the  
 CC tetraspanin family. Associates with CR2/CD21 and with PTGFRN/CD9P1  
 CC (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- PTM: Phosphorylated on tyrosine following B-cell activation (By  
 CC similarity).  
 CC -1- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL; D10726; BAA01569.1; -, mRNA.  
 DR PIR; A42929; A42929.  
 DR GO; GO:0005887; C:integral to plasma membrane; ISS.  
 DR GO; GO:0005515; P:protein binding; ISS.  
 DR GO; GO:0007155; P:cell adhesion; ISS.  
 DR GO; GO:0006928; P:cell motility; ISS.  
 DR GO; GO:0007342; P:fusion of sperm to egg plasma membrane; ISS.  
 DR GO; GO:0030913; P:paranodal junction formation; ISS.  
 DR GO; GO:0030168; P:platelet activation; ISS.  
 DR InterPro; IPR000301; Transmem\_4.  
 DR Pfam; PF00335; Tetraspanin; 1.  
 DR PRINTS; PR0259; TMPOUR.  
 DR PROSITE; PS00421; TM4\_1; 1.  
 KW Antigen; Cell adhesion; Fertilization; Glycoprotein; Lipoprotein;  
 KW Palmitate; Phosphorylation; Transmembrane.  
 FT INIT MET 0  
 FT TOPO DOM 1 11 Cytoplasmic (Potential).  
 FT TRANSMEM 12 32 Potential.  
 FT TOPO DOM 33 54 Extracellular (Potential).  
 FT TRANSMEM 55 75 Potential.  
 FT TOPO DOM 76 86 Cytoplasmic (Potential).  
 FT TRANSMEM 87 110 Potential.  
 FT TOPO DOM 111 194 Extracellular (Potential).  
 FT TRANSMEM 195 220 Potential.  
 FT TOPO DOM 221 227 Cytoplasmic (Potential).  
 FT LIPID 8 8 S-palmitoyl cysteine (By similarity).  
 FT LIPID 77 77 S-palmitoyl cysteine (By similarity).  
 FT LIPID 78 78 S-palmitoyl cysteine (By similarity).  
 FT LIPID 86 86 S-palmitoyl cysteine (By similarity).  
 FT LIPID 217 217 S-palmitoyl cysteine (By similarity).  
 FT LIPID 218 218 S-palmitoyl cysteine (By similarity).  
 FT CARBOHYD 51 51 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 52 52 N-linked (GlcNAc...) (Potential).  
 SQ SEQUENCE 227 AA; 25300 MW; 8E3474E7A590374A CRC64;  
 Query Match 99.2%; Score 131; DB 1; Length 227;  
 Best Local Similarity 96.0%; Pred. No. 9.6e-11; Indels 0; Gaps 0;  
 Matches 24; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 PKKDVLETFVKSCPDPAIKEVFNK 25  
 DB 167 PKKDVLETFVKSCPDPAIKEVFNK 191  
 RESULT 4  
 ID CD9 RAT STANDARD; PRT; 225 AA.  
 AC P40241;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE CD9 antigen.  
 GN Name=CD9;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;

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RN  [1] NUCLEOTIDE SEQUENCE [MRNA].
RP  STRAIN=Sprague-Dawley; TISSUE=Sciatic nerve;
RC  MEDLINE=95123481; PubMed=7823164;
RX  Kaprielian Z., Cho K.O., Hadjiargyrou M., Patterson P.H.;
RT  "CD9, a major platelet cell surface glycoprotein, is a ROCA antigen
RT  and is expressed in the nervous system.";
RL  J. Neurosci. 15:562-573 (1995).
CC  -!- FUNCTION: Involved in platelet activation and aggregation.
CC  Regulates paranodal junction formation. Required for gamete
CC  fusion. Involved in cell adhesion, cell motility and tumor
CC  metastasis (By similarity).
CC  -!- SUBUNIT: Forms both disulfide-linked homodimers and higher
CC  homooligomers as well as heterooligomers with other members of the
CC  tetraspanin family. Associates with CR2/CD21 and with PTGFRN/CD9P1
CC  (By similarity).
CC  -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC  -!- TISSUE SPECIFICITY: Expressed in the peripheral nervous system.
CC  -!- PTM: Phosphorylated on tyrosine following B-cell activation (By
CC  similarity).
CC  -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC  -----
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CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use as long as its content is in no way modified and this statement is not
CC  removed.
CC  -----
DR  EMBL; X76489; CAA54027.1; -; mRNA.
DR  PIR; I56562; S39262.
DR  Ensembl; ENSRNOG0000019556; Rattus norvegicus.
DR  RGD; 2318; Cd9.
DR  GO; GO:0009986; C:cell surface; IDA.
DR  GO; GO:0005887; C:integral to plasma membrane; ISS.
DR  GO; GO:0005515; F:protein binding; IPI.
DR  GO; GO:0007155; P:cell adhesion; ISS.
DR  GO; GO:0006928; P:cell motility; ISS.
DR  GO; GO:0007342; P:fusion of sperm to egg plasma membrane; ISS.
DR  GO; GO:0030913; P:paranodal junction formation; ISS.
DR  GO; GO:0030168; P:platelet activation; ISS.
DR  InterPro; IPR000301; Transmem 4.
DR  Pfam; PF00335; Tetraspannin; I.
DR  PRINTS; PR00259; TMFOUR.
DR  PROSITE; PS00421; TM4_1; 1.
KW  Antigen; Cell adhesion; Fertilization; Glycoprotein; Lipoprotein;
KW  Palmitate; Phosphorylation; Transmembrane.
FT  INIT MET 0 0
FT  TOPO_DOM 1 11 Cytoplasmic (Potential).
FT  TRANSMEM 12 32 Potential.
FT  TOPO_DOM 33 52 Extracellular (Potential).
FT  TRANSMEM 53 73 Potential.
FT  TOPO_DOM 74 84 Cytoplasmic (Potential).
FT  TRANSMEM 85 108 Extracellular (Potential).
FT  TOPO_DOM 109 192 Potential.
FT  TRANSMEM 193 218 Potential.
FT  TOPO_DOM 219 225 Cytoplasmic (Potential).
FT  LIPID 8 8 S-palmitoyl cysteine (By similarity).
FT  LIPID 75 75 S-palmitoyl cysteine (By similarity).
FT  LIPID 76 76 S-palmitoyl cysteine (By similarity).
FT  LIPID 84 84 S-palmitoyl cysteine (By similarity).
FT  LIPID 215 215 S-palmitoyl cysteine (By similarity).
FT  LIPID 216 216 S-palmitoyl cysteine (By similarity).
FT  CARBOHYD 49 49 N-linked (GlcNAc...) (Potential).
SQ  SEQUENCE 225 AA; 25084 MW; 7889619f99A59C9D CRC64;

Query Match 74.2%; Score 98; DB 1; Length 225;
Best Local Similarity 76.0%; Pred. No. 6.5e-06;
Matches 19; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 PKQVLETFVTKSPDAIKEVFDNK 25
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Db 165 PKQVLESFQVKSCPDAIDVFHSK 189

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RESULT 5
CD9_FELCA STANDARD; PRT; 225 AA.
ID CD9_FELCA
AC P40239;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE CD9 antigen.
GN Name=CD9;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Pissipedia; Felidae;
OC Felinae; Felis.
OC NCBI_TaxID=9685;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX PubMed=7753050; DOI=10.1016/0161-5890(95)00008-3;
RA Willett B.J., Neil J.C.;
RT "cDNA cloning and eukaryotic expression of feline CD9.";
RL Mol. Immunol. 32:417-423 (1995).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA].
RA Morikawa S.;
RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Involved in platelet activation and aggregation.
CC Regulates paranodal junction formation. Required for gamete
CC fusion. Involved in cell adhesion, cell motility and tumor
CC metastasis (By similarity).
CC -!- SUBUNIT: Forms both disulfide-linked homodimers and higher
CC homooligomers as well as heterooligomers with other members of the
CC tetraspanin family. Associates with CR2/CD21 and with PTGFRN/CD9P1
CC (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- PTM: Phosphorylated on tyrosine following B-cell activation (By
CC similarity).
CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC  -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC  -----
DR  EMBL; I35275; AAA92867.1; -; mRNA.
DR  EMBL; D30786; BAA06452.1; -; mRNA.
DR  GO; GO:0005887; C:integral to plasma membrane; ISS.
DR  GO; GO:0005515; F:protein binding; ISS.
DR  GO; GO:0007155; P:cell adhesion; ISS.
DR  GO; GO:0006928; P:cell motility; ISS.
DR  GO; GO:0007342; P:fusion of sperm to egg plasma membrane; ISS.
DR  GO; GO:0030913; P:paranodal junction formation; ISS.
DR  GO; GO:0030168; P:platelet activation; ISS.
DR  InterPro; IPR000301; Transmem 4.
DR  Pfam; PF00335; Tetraspannin; I.
DR  PRINTS; PR00259; TMFOUR.
DR  PROSITE; PS00421; TM4_1; 1.
KW  Antigen; Cell adhesion; Fertilization; Lipoprotein; Palmitate;
KW  Phosphorylation; Transmembrane.
FT  INIT MET 0 0
FT  TOPO_DOM 1 11 Cytoplasmic (Potential).
FT  TRANSMEM 12 32 Potential.
FT  TOPO_DOM 33 52 Extracellular (Potential).
FT  TRANSMEM 53 73 Potential.
FT  TOPO_DOM 74 84 Cytoplasmic (Potential).
FT  TRANSMEM 85 108 Extracellular (Potential).
FT  TOPO_DOM 109 192 Potential.
FT  TRANSMEM 193 218 Potential.
FT  TOPO_DOM 219 225 Cytoplasmic (Potential).
FT  LIPID 8 8 S-palmitoyl cysteine (By similarity).
FT  LIPID 75 75 S-palmitoyl cysteine (By similarity).
FT  LIPID 76 76 S-palmitoyl cysteine (By similarity).
FT  LIPID 84 84 S-palmitoyl cysteine (By similarity).

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FT LIPID 215 215 S-palmitoyl cysteine (By similarity).  
 FT LIPID 216 216 S-palmitoyl cysteine (By similarity).  
 FT CONFLICT 82 S -> Y (in Ref. 2).  
 SQ SEQUENCE 225 AA; 24927 MW; 5A049774501B03B3 CRC64;

Query Match 72.7%; Score 96; DB 1; Length 225;  
 Best Local Similarity 68.0%; Pred. No. 1.3e-05;  
 Matches 17; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 PKKDVLETFVKSPDAIKVEFDNK 25  
 |||||:|||||:|||||:|||||:|||||:  
 DB 165 PQKDILSSITVKPCPEAIKEVFNK 189

RESULT 6

CD9\_MOUSE  
 ID\_CD9\_MOUSE STANDARD; PRT; 225 AA.  
 AC P40240;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE CD9 antigen.  
 GN Name=CD9;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]

NUCLEOTIDE SEQUENCE [MRNA].  
 RC STRAIN=BALB/c; TISSUE=Kidney;  
 RX MEDLINE=94054345; PubMed=8236164; DOI=10.1016/0049-3848(93)90162-H;  
 RA Rubinstein E., Billard M., Plaisance S., Prenant M., Bouchaix C.;  
 RT "Molecular cloning of the mouse equivalent of CD9 antigen."  
 RL Thromb. Res. 71:377-383(1993).  
 RN [2]

NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RC STRAIN=C57BL/6J; TISSUE=Kidney;  
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
 RA Gaasterland T., Gariboldi M., Glasi C., Godzik A., Gough J.,  
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Wiki H.,  
 RA Nagashima T., Nunata K., Okido T., Pavan W.J., Perlea G., Pesole G.,  
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sadelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Walestedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazaki N., Sato K.,  
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
 RA Hara A., Haehizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Saeki D., Shibata K., Shinagawa A.,  
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs."  
 RL Nature 420:563-573(2002).  
 RN [3]

NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [4]

ROLE IN GAMETE FUSION.  
 RP PubMed=10700183; DOI=10.1038/73502;  
 RX Kaji K., Oda S., Shikano T., Ohnuki T., Uemateu Y., Sakagami J.,  
 RT Tada N., Miyazaki S., Kudo A.;  
 RT "The gamete fusion process is defective in eggs of Cd9-deficient  
 RT mice."  
 RL Nat. Genet. 24:279-282(2000).  
 RN [5]

ROLE IN PARANODAL FORMATION, AND TISSUE SPECIFICITY.  
 RP PubMed=14715942; DOI=10.1523/JNEUROSCI.1484-03.2004;  
 RX Ishibashi T., Ding L., Ikenaka K., Inoue Y., Miyado K., Mekada E.,  
 RA Baba H.;  
 RT "Tetraspanin protein CD9 is a novel paranodal component regulating  
 RT paranodal junctional formation."  
 RL J. Neurosci. 24:96-102(2004).  
 RN [6]

FUNCTION AS RECEPTOR FOR PSG17.  
 RP PubMed=11805154; DOI=10.1084/jem.20011741;  
 RX Waterhouse R., Ha C., Dveksler G.S.;  
 RT "Murine CD9 is the receptor for pregnancy-specific glycoprotein 17."  
 RL J. Exp. Med. 195:277-282(2002).

-1- FUNCTION: Involved in platelet activation and aggregation.  
 CC Regulates paranodal junction formation. Required for gamete  
 CC fusion. Involved in cell adhesion, cell motility and tumor  
 CC metastasis. Acts as a receptor for PSG17.  
 CC -1- SUBUNIT: Forms both disulfide-linked homodimers and higher  
 CC homooligomers as well as heterooligomers with other members of the  
 CC tetraspanin family. Associates with CR2/CD21 and with PTGFRN/CD9P1  
 CC (By similarity).

-1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- TISSUE SPECIFICITY: Expressed predominantly in the peripheral  
 CC nervous system.  
 CC -1- PTM: Phosphorylated on tyrosine following B-cell activation (By  
 CC similarity).

-1- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.  
 CC  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.

ENBL; L08115; AAA37405.1; -; mRNA.  
 DR ENBL; AK002251; BAB21965.1; -; mRNA.  
 DR ENBL; AK012793; BAB28473.1; -; mRNA.  
 DR ENBL; BC070474; AAH70474.1; -; mRNA.  
 DR PIR; I49589; I49589.  
 DR Ensembl; ENSMUSG0000030342; Mus musculus.  
 DR MGI; MGI:89348; CD9.  
 DR GO; GO:0005887; C:integral to plasma membrane; ISS.  
 DR GO; GO:0005886; C:plasma membrane; TAS.  
 DR GO; GO:0005515; F:protein binding; IPI.  
 DR GO; GO:0007155; P:cell adhesion; ISS.



RNA NUCLEOTIDE SEQUENCE [MRNA].  
RC TISSUE=Smooth muscle;  
RA PubMed=14610355; DOI=10.1159/000074170;  
RX Yubero N., Jimenez-Marín A., Yelie M., Morera L., Barbancho M.J.,  
RA Llanes D., Garrido J.J.;  
RT "Molecular cloning, expression pattern and chromosomal mapping of pig  
CD9 antigen.";  
RL Cytogenet. Genome Res. 101:143-146(2003).  
CC -1- FUNCTION: Involved in platelet activation and aggregation.  
CC Regulates paranodal junction formation. Required for gamete  
CC fusion. Involved in cell adhesion, cell motility and tumor  
CC metastasis (By similarity).  
CC  
CC -1- SUBUNIT: Forms both disulfide-linked homodimers and higher  
CC homooligomers as well as heterooligomers with other members of the  
CC tetraspanin family. Associates with CR2/CD21 and with PTGFRN/CD9p1  
CC (By similarity).  
CC  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC  
CC -1- PTM: Phosphorylated on tyrosine following B-cell activation (By  
CC similarity).  
CC  
CC -1- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.  
CC  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC  
CC EMBL, AY072785; AAL68966.1; -, mRNA.  
DR GO: GO:0005887; C: integral to plasma membrane; ISS.  
DR GO: GO:0005515; P: protein binding; ISS.  
DR GO: GO:0007155; P: cell adhesion; ISS.  
DR GO: GO:0006928; P: cell motility; ISS.  
DR GO: GO:0007342; P: fusion of sperm to egg plasma membrane; ISS.  
DR GO: GO:003013; P: paranodal junction formation; ISS.  
DR GO: GO:0030168; P: platelet activation; ISS.  
DR InterPro: IPR000301; Transmem\_4.  
DR Pfam: PF00335; Tetraspanin; 1.  
DR PRINTS: PR00259; TMFOUR.  
DR PROSITE: PS00421; TM4\_1; 1.  
KW Antigen; Cell adhesion; Fertilization; Glycoprotein; Lipoprotein;  
KW Palmitate; Phosphorylation; Transmembrane.  
FT INIT MET 0 0 By similarity.  
FT TOPO\_DOM 1 11 Cytoplasmic (Potential).  
FT TRANSMEM 12 32 Potential.  
FT TOPO\_DOM 33 52 Extracellular (Potential).  
FT TRANSMEM 53 73 Potential.  
FT TOPO\_DOM 74 84 Cytoplasmic (Potential).  
FT TRANSMEM 85 108 Potential.  
FT TOPO\_DOM 109 192 Extracellular (Potential).  
FT TRANSMEM 193 218 Potential.  
FT TOPO\_DOM 219 225 Cytoplasmic (Potential).  
FT LIPID 8 8 S-palmitoyl cysteine (By similarity).  
FT LIPID 75 75 S-palmitoyl cysteine (By similarity).  
FT LIPID 76 76 S-palmitoyl cysteine (By similarity).  
FT LIPID 84 84 S-palmitoyl cysteine (By similarity).  
FT LIPID 215 215 S-palmitoyl cysteine (By similarity).  
FT LIPID 216 216 S-palmitoyl cysteine (By similarity).  
FT CARBOHYD 49 49 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 50 50 N-linked (GlcNAc...) (Potential).  
SQ SEQUENCE 225 AA; 25070 MW; FF280FE39BC11545 CRC64;

Query Match 65.2%; Score 86; DB 1; Length 225;  
Best Local Similarity 60.0%; Pred. No. 0.00037;  
Matches 15; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 PKKDVLTFTVKSCPDIAKEVFDNK 25  
Q91BC9\_CHICK  
ID Q91BC9\_CHICK PRELIMINARY; PRT; 224 AA.  
AC Q91BC9;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

RESULT 10  
Q6NWG7\_BRARE

Q6NWG7\_BRARE PRELIMINARY; PRT; 227 AA.  
Q6NWG7;  
AC Q6NWG7;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Hypothetical protein cd9.  
DE Names:cd9;  
GN Brachydanio rerio (Zebrafish) (Danio rerio).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OC NCBI\_TaxID=7955;  
RN [1]  
RC NUCLEOTIDE SEQUENCE.  
RP STRAIN=Wild-type; TISSUE=Eye, and Kidney;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Brownstein M.J., Ustin T.S., Toshiyuki S., Carninci P., Frange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Maman A., Rodriguez S., Sanchez A.,  
RA Whiting M., Maman A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RC NUCLEOTIDE SEQUENCE.  
RP TISSUE=Kidney;  
RC Director MGC Project;  
RA Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RC NUCLEOTIDE SEQUENCE.  
RP STRAIN=Wild-type; TISSUE=Eye;  
RA Director MGC Project;  
RA Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC067597; AAH67597.1; -, mRNA.  
DR EMBL; BC059691; AAH59691.1; -, mRNA.  
DR ZFIN; ZDB-GENE-030131-1175; cd9.  
DR GO: GO:0016021; C: integral to membrane; IEA.  
DR InterPro: IPR000301; Transmem\_4.  
DR Pfam: PF00335; Tetraspanin; 1.  
DR PRINTS: PR00259; TMFOUR.  
DR PROSITE: PS00421; TM4\_1; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 227 AA; 25116 MW; 26E5BC25F4E638B8 CRC64;

Query Match 63.6%; Score 84; DB 2; Length 227;  
Best Local Similarity 60.0%; Pred. No. 0.00073;  
Matches 15; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 PKKDVLTFTVKSCPDIAKEVFDNK 25  
Q91BC9\_CHICK  
ID Q91BC9\_CHICK PRELIMINARY; PRT; 224 AA.  
AC Q91BC9;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)





DR	GO; GO:0006928; P:cell motility; ISS.
DR	GO; GO:0007342; P:fusion of sperm to egg plasma membrane; ISS.
DR	GO; GO:0030913; P:paranodal junction formation; ISS.
DR	GO; GO:0030168; P:platelet activation; ISS.
DR	InterPro; IPR000301; Transmem 4.
DR	Pfam; PF00335; Tetraspannin; 1.
DR	PRINTS; PR00259; TMFOUR.
DR	PROSITE; PS00421; TW4_1; 1.
KW	Antigen; Cell adhesion; Fertilization; Glycoprotein; Lipoprotein;
KW	Palmitate; Phosphorylation; Transmembrane.
FT	INIT MET            0       0 By similarity.
FT	TOPO_DOM          1      11 Cytoplasmic (Potential).
FT	TRANSMEM         12     32 Potential.
FT	TOPO_DOM         33     52 Extracellular (Potential).
FT	TRANSMEM         53     73 Potential.
FT	TOPO_DOM         74     84 Cytoplasmic (Potential).
FT	TRANSMEM         85    108 Potential.
FT	TOPO_DOM        109    192 Extracellular (Potential).
FT	TRANSMEM        193    218 Potential.
FT	TOPO_DOM        219    225 Cytoplasmic (Potential).
FT	LIPID             8      8 S-palmitoyl cysteine (By similarity).
FT	LIPID            75     75 S-palmitoyl cysteine (By similarity).
FT	LIPID            76     76 S-palmitoyl cysteine (By similarity).
FT	LIPID            84     84 S-palmitoyl cysteine (By similarity).
FT	LIPID            215    215 S-palmitoyl cysteine (By similarity).
FT	LIPID            216    216 S-palmitoyl cysteine (By similarity).
FT	CARBOHYD        49     49 N-linked (GlcNAc..) (potential).
SQ	SEQUENCE 225 AA; 25127 MW; ECE67DB91A0858E7 CRC64;
Query Match                    46.2%; Score 61; DB 1; Length 225;	
Best Local Similarity        36.0%; Pred. No. 1.7;	
Matches    9; Conservative    9; Mismatches    7; Indels    0; Gaps    0;	
Qy	1 PKKDVLETFVTKSCPDAIKEVFNDK 25     : : : : :     :           :   165 PPKNLIDLKTRPCPEAIDEIFRSK 189
RESULT 14	
ID	Q6P0W1 BRARE PRELIMINARY; PRT; 246 AA.
AC	Q6P0W1
DC	05-JUN-2004 (TrEMBLrel. 27, Created)
DT	05-JUN-2004 (TrEMBLrel. 27, Last sequence update)
DT	10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE	Hypothetical protein zgc:65811.
GN	ORFNames=zgc:65811;
OS	Brachydanio rerio (Zebrafish) (Danio rerio).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Acyrotoperygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC	Cyprinidae; Danio.
RX	NCBI_TaxID=7955;
ON	[1]
RP	NUCLEOTIDE SEQUENCE.
TX	TISSUE=Kidney, and Whole;
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haie F.,
RA	Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Ustin T.B., Toshlyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA	Boak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Vallalon D.K., Muszy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahey J., Helton E., Kettawan M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA	Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;





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OM protein - protein search, using sw model

Run on: January 20, 2006, 17:03:51 ; Search time 63.3333 Seconds  
(without alignments)  
124.876 Million cell updates/sec

Title: US-10-619-323-6

Perfect score: 95  
Sequence: 1 PKQVLETFVKSCPDAI 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21.\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*  
9: Geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	100.0	18	ADJ57563	Adj57563 Human CD9
2	95	100.0	25	ADJ57562	Adj57562 Human CD9
3	95	100.0	227	AAR86834	Aar86834 Human CD9
4	95	100.0	227	ABB78366	Abb78366 Amino aci
5	95	100.0	227	AAE14636	Aae14636 Human CD9
6	95	100.0	227	ABU05057	Abu05057 Human exp
7	95	100.0	227	ABU05060	Abu05060 Human exp
8	95	100.0	227	ABW00436	Abw00436 Human CD9
9	95	100.0	227	ADK69862	Adk69862 Human CD9
10	95	100.0	227	ADI19366	Adi19366 Human CD9
11	95	100.0	227	AEA89005	Aea89005 Human CD9
12	95	100.0	228	AAR27525	Aar27525 Metaastai
13	95	100.0	228	ABBA4581	Abba4581 Human wou
14	95	100.0	228	ABU05059	Abu05059 Human exp
15	95	100.0	228	ABU05052	Abu05052 Human exp
16	95	100.0	228	ABU05048	Abu05048 Human exp
17	95	100.0	228	ABU05056	Abu05056 Human exp
18	95	100.0	228	ABU05049	Abu05049 Human exp
19	95	100.0	228	ABU05050	Abu05050 Human exp
20	95	100.0	228	ABU05053	Abu05053 Human exp
21	95	100.0	228	ABW01519	Abw01519 Protein #
22	95	100.0	228	ADD89037	Add89037 TR1278. 1
23	95	100.0	228	ADG32002	Adg32002 Human hom
24	95	100.0	228	ADJ57558	Adj57558 Human CD9

25	95	100.0	228	8	ADL26782	Adl26782 Human CD9
26	95	100.0	228	8	ADL82853	Adl82853 Human PRO
27	95	100.0	228	8	ADP23088	Adp23088 PRO polyp
28	95	100.0	228	8	ADR73450	Adr73450 Human CD9
29	95	100.0	228	9	ADV70263	Adv70263 Tumor-ass
30	95	100.0	228	9	ADY97163	Ady97163 Human CD9
31	95	100.0	228	9	ADY19604	Ady19604 PRO polyp
32	95	100.0	228	9	ADY14362	Ady14362 PRO polyp
33	95	100.0	228	9	AE98450	Aeb98450 Human CD9
34	95	100.0	228	3	AB43936	Aeb43936 Human can
35	95	100.0	275	4	AG75156	Aag75156 Human col
36	95	100.0	275	6	ABU05055	Abu05055 Human exp
37	95	100.0	275	6	ABU05054	Abu05054 Human exp
38	95	100.0	454	4	ABG14067	Abg14067 Novel hum
39	87	91.6	79	2	AAW35851	Aaw35851 Human CD9
40	87	91.6	79	6	ABU05058	Abu05058 Human exp
41	79	83.2	226	7	ADB85281	Adb85281 Rat G9 eu
42	67	70.5	226	4	ABB44580	Abb44580 Mouse wou
43	67	70.5	226	5	ABB57234	Abb57234 Mouse isc
44	67	70.5	226	9	ADV25799	Adv25799 Mouse CD9
45	67	70.5	226	9	AEA55045	Aea55045 Mouse CD9

ALIGNMENTS

RESULT 1  
ADJ57563  
ID ADJ57563 standard; peptide; 18 AA.  
XX  
AC ADJ57563;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Human CD9 fibronectin-binding domain peptide fragment.  
XX  
KW Human; CD9; antithrombotic; antiarteriosclerotic; vasotropic;  
KW haemostatic; antiangiogenic; cytostatic.  
XX  
OS Homo sapiens.  
XX  
PN WO2004007685-A2.  
XX  
PD 22-JAN-2004.  
XX  
PF 14-JUL-2003; 2003WO-US022050.  
XX  
PR 12-JUL-2002; 2002US-0395864P.  
XX (UYTE-) UNIV TENNESSEE RES FOUND.  
XX Jennings LK, Longhurst CM, Cook GA, Bao J, Zhang C, White MM;  
XX Crosseno JT, Lu Y;  
XX WPI; 2004-122924/12.  
XX Interfering with CD9 binding to fibronectin by binding a fibronectin-binding domain of the CD9 protein or polypeptide, useful in treating thrombosis, atherosclerosis, restenosis, bleeding disorders, angiogenesis and cancers.  
XX Claim 7; SEQ ID NO 6; 126pp; English.  
XX The present sequence is that of a peptide fragment from the fibronectin-binding domain of human CD9 ADJ57558. The peptide, or an antibody that binds to it, is used in claimed methods for: interfering with CD9 binding to fibronectin; modifying adhesion, motility or spreading of a CD9-expressing cell on fibronectin; inhibiting proliferation or survival of CD9-expressing cells; modifying pericellular fibronectin matrix assembly; modifying invasiveness of a cell through a collagen and/or laminin matrix; and modifying cell-to-cell interaction. The methods are based on the finding that increased CD9 expression is implicated in (i) decreased adhesiveness of cells to extracellular matrix (via alpha5-beta-1

CC integrin) and/or decreased cell invasiveness and/or decreased  
CC pericellular fibronectin matrix assembly, and/or (ii) increased cell  
CC motility, spreading, proliferation, cell survival against apoptosis,  
CC and/or cell-to-cell contacts. Conditions or disease states involving  
CC proliferation or survival of CD9-expressing cells can be treated, e.g.  
CC thrombosis, atherosclerosis, vein graft failure, restenosis, transplant  
CC arteriopathy, bleeding disorders, angiogenesis, and primary and  
CC metastatic cancers including breast cancer, prostate cancer, colon  
CC cancer, melanoma, ovarian cancer, neuroblastoma, glioma and glioblastoma.  
XX  
SQ Sequence 18 AA;

Query Match 100.0%; Score 95; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.9e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLETFVVKSCPDAI 18  
|||  
Db 1 PKKDVLETFVVKSCPDAI 18

RESULT 2  
ADJ57562  
ID ADJ57562 standard; peptide; 25 AA.  
XX  
AC ADJ57562;

XX 06-MAY-2004 (first entry)

XX Human CD9 fibronectin-binding domain peptide fragment.

XX Human; CD9; antithrombotic; antiarteriosclerotic; vasotropic;  
KW haemostatic; antiangiogenic; cytostatic.

XX Homo sapiens.

XX WO2004007685-A2.

XX 22-JAN-2004.

XX 14-JUL-2003; 2003WO-US022050.

XX 12-JUL-2002; 2002US-039864P.

XX (UYTE-) UNIV TENNESSEE RES FOUND.

XX Jennings LK, Longhurst CM, Cook GA, Bao J, Zhang C, White MW;  
PI Crossano JT, Lu Y;

XX WPI; 2004-122924/12.

XX Interfering with CD9 binding to fibronectin by binding a fibronectin-  
PT binding domain of the CD9 protein or polypeptide, useful in treating  
PT thrombosis, atherosclerosis, restenosis, bleeding disorders, angiogenesis  
PT and cancers.

XX Claim 7; SEQ ID NO 5; 126pp; English.

XX The present sequence is that of a peptide fragment from the fibronectin-  
CC binding domain of human CD9 ADJ57558. The peptide, or an antibody that  
CC binds to it, is used in claimed methods for: interfering with CD9 binding  
CC to fibronectin; modifying adhesion, motility or spreading of a CD9-  
CC expressing cell on fibronectin; inhibiting proliferation or survival of  
CC CD9-expressing cells; modifying pericellular fibronectin matrix assembly;  
CC modifying invasiveness of a cell through a collagen and/or laminin matrix  
CC ; and modifying cell-to-cell interaction. The methods are based on the  
CC finding that increased CD9 expression is implicated in (i) decreased  
CC adhesiveness of cells to extracellular matrix (via alpha5-beta1  
CC integrin) and/or decreased cell invasiveness and/or decreased  
CC pericellular fibronectin matrix assembly, and/or (ii) increased cell  
CC motility, spreading, proliferation, cell survival against apoptosis,  
CC and/or cell-to-cell contacts. Conditions or disease states involving  
CC proliferation or survival of CD9-expressing cells can be treated, e.g.

CC thrombosis, atherosclerosis, vein graft failure, restenosis, transplant  
CC arteriopathy, bleeding disorders, angiogenesis, and primary and  
CC metastatic cancers including breast cancer, prostate cancer, colon  
CC cancer, melanoma, ovarian cancer, neuroblastoma, glioma and glioblastoma.  
XX  
SQ Sequence 25 AA;

Query Match 100.0%; Score 95; DB 8; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.7e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLETFVVKSCPDAI 18  
|||  
Db 1 PKKDVLETFVVKSCPDAI 18

RESULT 3  
AAR86834  
ID AAR86834 standard; protein; 227 AA.

XX AAR86834;

XX 12-JUL-1996 (first entry)

XX Human CD9 sequence.

XX CD9 antigen; stimulated T cell; antibody; ligand; proliferation;  
KW monoclonal antibody; ES5.2D8; 27 kD accessory protein; epitope;  
KW immune response; cancer; infectious disease; growth factor.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 51 /note= "Potential N-linked glycosylation site"

FT Modified-site 52 /note= "Potential N-linked glycosylation site"

FT Domain 111..194 /note= "Extracellular domain"

FT Domain 195..220 /note= "Transmembrane domain"

FT Domain 221..227 /note= "Cytoplasmic domain"

XX WO9533823-A1.

XX 14-DEC-1995.

XX 01-DEC-1994; 94WO-US013782.

XX 03-JUN-1994; 94US-00253751.

XX 03-JUN-1994; 94US-00253964.

XX (USNA ) US SEC OF NAVY.

XX (UNMI ) UNIV MICHIGAN.

XX (REPK ) REPLIGEN CORP.

XX (DAND ) DANA FARBER CANCER INST INC.

XX June CH, Thompson CB, Nabel G, Gray GS, Rennert PD, Freeman GJ;

XX WPI; 1996-040230/04.

XX Selectively inducing CD8 positive T cell proliferation - by activating

XX the T cells and stimulating CD9 cell surface ligand, useful for

XX immuno:therapy of, e.g. cancer.

XX Example 10; Page 38-39; 79pp; English.

XX This sequence represents CD9 from the surface of stimulated T cells. The  
CC antigen at residues 31-37 of human CD9 (see AAR86832) is bound by an  
CC antibody or other ligand to stimulate the T cell population to  
CC proliferate and expand leading to a 100- to 10000-fold increase in cell  
CC number compared to the original population. The antigenic sequence fits

CC the generic sequence given in AAR86827. This epitope is recognised by the  
 CC monoclonal antibody (MAB) B55.2D8. CD9 is a 27 kD accessory protein found  
 CC on activated T cells. The epitope was recognised by screening a phage  
 CC display library. Selective proliferation of an antigen-specific T cell  
 CC population is useful in cases where the immune response is to be up  
 CC regulated, e.g. in the treatment of cancer or infectious diseases. By  
 CC causing proliferation of the T cell population by stimulating T cell  
 CC epitope removes the need for exogenous growth factors or accessory cells  
 XX  
 XX Sequence 227 AA;

Query Match 100.0%; Score 95; DB 2; Length 227;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLETFVTKSCPDAl 18  
 |||||  
 DB 167 PKKDVLETFVTKSCPDAl 184

RESULT 4  
 ID ABB78366 standard; protein; 227 AA.  
 XX  
 AC ABB78366;

XX 16-DEC-2002 (first entry)

XX Amino acid sequence of CD9.

XX T cell; T cell proliferation; infectious disease; cancer; immunotherapy;  
 KW immunotherapy; CD9.

XX Homo sapiens.

XX US2002115214-A1.

XX 22-AUG-2002.

XX 26-JAN-1996; 96US-00592711.

XX 23-NOV-1988; 88US-00275433.

XX 07-APR-1992; 92US-00864805.

XX 07-APR-1992; 92US-00864807.

XX 07-APR-1992; 92US-00864866.

XX 04-JUN-1993; 93US-00073223.

XX 03-JUN-1994; 94US-00253964.

XX 10-MAR-1995; 95US-00403253.

XX 04-MAY-1995; 95US-00435816.

XX (JUNE/) JUNE C H.

XX (THOM/) THOMPSON C B.

XX (NABE/) NABEL G J.

XX (GRAY/) GRAY G S.

XX (RENN/) RENNERT P D.

XX June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;

XX WPI; 2002-712476/77.

XX Inducing a population of T cells to proliferate, by activating population  
 of T cells and stimulating an accessory molecule on the surface of the T  
 cells with a ligand which binds the accessory molecule.  
 XX  
 XX Example 10; Page 25; 88pp; English.

XX The specification describes method for inducing a population of T cells  
 CC to proliferate. The method involves activating population of T cells,  
 CC stimulating an accessory molecule on T cell surface with a ligand  
 CC (protein) which binds the molecule, to induce proliferation of T cells,  
 CC monitoring proliferation of T cells in response to continuing exposure to  
 CC the ligand, and reactivating and restimulating T cells when rate of  
 CC proliferation has decreased to induce further proliferation of the cells.

CC The method is useful for inducing proliferation of T cells, for use in  
 CC treatment of infectious disease, cancer and immunotherapy. The method  
 CC allows for the expansion of a population of T cells in numbers sufficient  
 CC to reconstitute an individual's total CD4+ or CD8+ T cell population.  
 CC The resulting T cell population can be genetically transduced and used  
 CC for immunotherapy or can be used in methods of in vitro analyses of  
 CC infectious agents. A population of tumour-infiltrating lymphocytes can be  
 CC obtained from an individual afflicted with cancer and the T cells  
 CC stimulated to proliferate to sufficient numbers. The resulting T cell  
 CC population can be genetically transduced to express tumour necrosis  
 CC factor (TNF) or other factor and restored to the individual. CD4+ T cells  
 CC expanded by this method are useful in the treatment of HIV infection in  
 CC an individual. The present sequence represents CD9, an antigen present on  
 CC the surface of activated T cells  
 XX  
 XX Sequence 227 AA;

Query Match 100.0%; Score 95; DB 5; Length 227;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLETFVTKSCPDAl 18  
 |||||  
 DB 167 PKKDVLETFVTKSCPDAl 184

RESULT 5  
 AAE14636 standard; protein; 227 AA.  
 XX  
 AC AAE14636;

XX 16-JUL-2002 (first entry)

XX Human CD9 antigen.

XX T cell; CD3; accessory molecule; CD28; cancer; infectious disease;  
 KW immunotherapy; human immunodeficiency virus; HIV infection; cytokine;  
 KW human; CD9 antigen.

XX Homo sapiens.

XX US6352694-B1.

XX 05-MAR-2002.

XX 10-MAR-1995; 95US-00403253.

XX 03-JUN-1994; 94US-00253964.

XX (GEWY ) GENETICS INST INC.

XX (UNMI ) UNIV MICHIGAN.

XX June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;

XX WPI; 2002-314696/35.

XX Inducing T cell population to proliferate, useful in cancer therapy,  
 PT comprises activating T cells by contacting T cells in vitro with  
 PT immobilized anti-CD3 antibody and stimulating accessory molecule on T  
 PT cell surface.  
 XX  
 XX Example 10; Col 42; 71pp; English.

XX The invention relates to a method of inducing T cell population to

CC proliferate for use in therapy comprising activating T cells by  
 CC contacting T cells in vitro with anti-CD3 antibody which is immobilised  
 CC on solid phase surface, and stimulating accessory molecule on T cell  
 CC surface in vitro with anti-CD28 antibody, or stimulatory form of natural  
 CC ligand for CD28 such as B7-1 or B7-2. The method is useful for inducing a  
 CC population of T cells to proliferate in sufficient numbers for use in  
 CC therapy e.g., for treating cancer or an infectious disease. The method  
 CC can be used to selectively expand the population of CD28<sup>+</sup>, CD4<sup>+</sup>, CD8<sup>+</sup>,

CC CD28RA<sup>+</sup> or CD28RO<sup>+</sup> T cells for immunotherapy. The T cell population  
 CC resulting by the method can be genetically transduced and used for  
 CC immunotherapy or can be used for in vitro analysis of infectious agents  
 CC such as human immunodeficiency virus (HIV). Proliferation of a population  
 CC of CD4<sup>+</sup> T cells obtained from an individual infected with HIV can be  
 CC achieved and the cells rendered resistant to HIV infection. Following the  
 CC expansion of the T cells to sufficient numbers, the expanded T cells are  
 CC restored to the individual. Also CD4<sup>+</sup> T cells expanded by the above  
 CC mentioned is useful for treating HIV infection in an individual. A  
 CC population of tumour-infiltrating lymphocytes can be obtained from an  
 CC individual afflicted with cancer and the T cells stimulated to  
 CC proliferate to sufficient numbers and restored to the individual. The  
 CC supernatants from cultures of T cells expanded from above mentioned  
 CC method are useful as a rich source of cytokines and can be used to  
 CC sustain T cells in vivo or ex vivo. Stimulating and expanding a  
 CC population of antigen specific T cells are useful in therapeutic  
 CC conditions where it is desirable to upregulate an immune response. The T  
 CC cell proliferation occurs in the absence of exogenous growth factors or  
 CC accessory cells. The present sequence is human CD9 antigen which is  
 CC expressed on surface of activated T cells  
 XX  
 SQ Sequence 227 AA;

Query Match 100.0%; Score 95; DB 5; Length 227;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQDVLETFVKSCPDAI 18  
 |||||  
 Db 167 PKQDVLETFVKSCPDAI 184

RESULT 6  
 ABU05057  
 ID ABU05057 standard; protein; 227 AA.

XX AC ABU05057;

XX DT 29-JAN-2003 (first entry)

XX DE Human expressed protein tag (EPT) #1723.

XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
 KW protease; protease inhibitor; transporter; cytoskeletal protein;  
 KW receptor; transcription factor; cancer; MHC;  
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX OS Homo sapiens.

XX PN WO200278524-A2.

XX PD 10-OCT-2002.

XX PF 28-MAR-2002; 2002WO-US009671.

XX PR 28-MAR-2001; 2001US-0279495P.

XX PR 21-MAY-2001; 2001US-0292544P.

XX PR 08-AUG-2001; 2001US-0310801P.

XX PR 01-OCT-2001; 2001US-0326370P.

XX PR 04-DEC-2001; 2001US-0336780P.

XX PR 20-FEB-2002; 2002US-0358985P.

XX PA (ZYCO-) ZYCOS INC.

XX PI Chicx RM, Tomlinson AJ, Urban RG;

XX DR WPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
 PT cytoskeletal proteins, receptors or transcription factors), useful for  
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
 PT leukemia.

XX PS Example 2; SEQ ID NO 1723; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a  
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
 CC transporter, cytoskeletal protein, receptor or transcription factor. The  
 CC polypeptide is useful as an immunogenic composition for eliciting in a  
 CC mammal an immunogenic response directed against any of the purified  
 CC polypeptide. The purified polypeptide, or the antibody that binds to this  
 CC polypeptide, is useful for treating cancer. The polypeptide is also  
 CC useful for identifying compounds that binds to a naturally processed  
 CC class I or class II MHC-binding polypeptide. The polypeptides and  
 CC polynucleotides are particularly useful for treating or preventing  
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
 CC lymphoma or leukaemia. These are also useful for screening agents for  
 CC treating the above mentioned diseases. This sequence represents an  
 CC expressed protein tag (EPT) isolated from human tissue for translational  
 CC profiling. Note: This sequence does not appear in the printed  
 CC specification but was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 227 AA;

Query Match 100.0%; Score 95; DB 6; Length 227;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQDVLETFVKSCPDAI 18  
 |||||  
 Db 167 PKQDVLETFVKSCPDAI 184

RESULT 7  
 ABU05060

ID ABU05060 standard; protein; 227 AA.

XX AC ABU05060;

XX DT 29-JAN-2003 (first entry)

XX DE Human expressed protein tag (EPT) #1726.

XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
 KW protease; protease inhibitor; transporter; cytoskeletal protein;  
 KW receptor; transcription factor; cancer; MHC;  
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX OS Homo sapiens.

XX PN WO200278524-A2.

XX PD 10-OCT-2002.

XX PF 28-MAR-2002; 2002WO-US009671.

XX PR 28-MAR-2001; 2001US-0279495P.

XX PR 21-MAY-2001; 2001US-0292544P.

XX PR 08-AUG-2001; 2001US-0310801P.

XX PR 01-OCT-2001; 2001US-0326370P.

XX PR 04-DEC-2001; 2001US-0336780P.

XX PR 20-FEB-2002; 2002US-0358985P.

XX PA (ZYCO-) ZYCOS INC.

XX PI Chicx RM, Tomlinson AJ, Urban RG;

XX DR WPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
 PT cytoskeletal proteins, receptors or transcription factors), useful for  
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
 PT leukemia.

XX PS Example 2; SEQ ID NO 1726; 134pp; English.  
 XX CC The invention describes a purified polypeptide, which comprises a  
 CC fragment of a kinase, phosphatase, protease, or transcription inhibitor,  
 CC transporter, cytoskeletal protein, receptor or transcription factor. The  
 CC polypeptide is useful as an immunogenic composition for eliciting in a  
 CC mammal an immunogenic response directed against any of the purified  
 CC polypeptide. The purified polypeptide, or the antibody that binds to this  
 CC polypeptide, is useful for treating cancer. The polypeptide is also  
 CC useful for identifying compounds that binds to a naturally processed  
 CC class I or class II MHC-binding polypeptide. The polypeptides and  
 CC polynucleotides are particularly useful for treating or preventing  
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
 CC lymphoma or leukaemia. These are also useful for screening agents for  
 CC treating the above mentioned diseases. This sequence represents an  
 CC expressed protein tag (EPT) isolated from human tissue for translational  
 CC profiling. Note: This sequence does not appear in the printed  
 CC specification but was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 227 AA;

Query Match 100.0%; Score 95; DB 6; Length 227;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLETFVKSCPDAI 18  
 |||||  
 DB 167 PKKDVLETFVKSCPDAI 184

RESULT 8  
 AEW00436  
 ID AEW00436 standard; protein; 227 AA.

XX AC AEW00436;  
 XX DT 15-JAN-2004 (first entry)  
 XX DE Human CD9 antigenic protein.  
 XX KW HIV infection; human immunodeficiency virus; therapy; antigen; human.

XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 FT Domain 111..194  
 FT /note= "Extracellular domain"  
 FT Domain 195..220  
 FT /note= "Transmembrane domain"  
 FT Domain 221..227  
 FT /note= "Cytoplasmic domain"

XX US2003099643-A1.  
 XX PN 29-MAY-2003.  
 XX PD 08-JUL-1999; 99US-00350202.  
 XX PR 23-NOV-1988; 88US-00275433.  
 XX PR 22-NOV-1989; 89WO-US005304.  
 XX PR 07-APR-1992; 92US-00864805.  
 XX PR 07-APR-1992; 92US-00864807.  
 XX PR 07-APR-1992; 92US-00864866.  
 XX PR 04-JUN-1993; 93US-00073223.  
 XX PR 03-JUN-1994; 94US-00253694.  
 XX PR 10-MAR-1995; 95US-00403253.

XX (JUNE/) JUNE C H.  
 XX (THOM/) THOMPSON C B.  
 XX (NABEL/) NABEL G J.  
 XX (GRAY/) GRAY G S.

PA (RENN/) RENNERT P D.  
 XX PI June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;  
 XX WIPI; 2003-801206/75.  
 XX DR Treating HIV infection in individual by isolating T cells from  
 FT leukocytes, contacting T cells with anti-CD3 antibody for T cell  
 PT proliferation, separating antibody from T cells, monitoring proliferation  
 PT of T cells.  
 XX Example 10; Page 23; Opp; English.  
 XX The present invention relates to a novel method of treating human  
 CC immunodeficiency virus (HIV) infection in an individual. The method  
 CC involves isolating population of CD4 T cells from leukocytes, contacting  
 CC population of CD4+ T cells with an anti-CD3 antibody for stimulating T  
 CC cell proliferation, separating antibody from T cells, monitoring  
 CC proliferation of T cells, restimulating T cells with antibody and  
 CC restoring T cells to individual. The present sequence is human CD9  
 CC antigenic protein. This sequence is used to illustrate the method of the  
 CC invention  
 XX SQ Sequence 227 AA;

Query Match 100.0%; Score 95; DB 7; Length 227;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLETFVKSCPDAI 18  
 |||||  
 DB 167 PKKDVLETFVKSCPDAI 184

RESULT 9  
 ADK69862  
 ID ADK69862 standard; protein; 227 AA.

XX AC ADK69862;  
 XX DT 06-MAY-2004 (first entry)  
 XX DE Human CD9 protein.  
 XX KW CD28-associated signal; immunotherapy; infectious disease; cancer;  
 XX leukopheresis; human.

XX OS Homo sapiens.  
 XX PN US6534055-B1.  
 XX PD 18-MAR-2003.  
 XX PF 04-MAY-1995; 95US-00435816.  
 XX PR 07-APR-1992; 92US-00864805.  
 XX PR 07-APR-1992; 92US-00864807.  
 XX PR 07-APR-1992; 92US-00864866.  
 XX PR 04-JUN-1993; 93US-00073223.  
 XX PR 03-JUN-1994; 94US-00253964.  
 XX PR 10-MAR-1995; 95US-00403253.

XX (GEMY ) GENETICS INST INC.  
 XX PI June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;  
 XX WIPI; 2003-531074/50.

XX PT Expanding T cell populations, useful for preparing renewable sources of T  
 PT cells (e.g. CD4+) for immunotherapy or diagnostics, by stimulating a CD28  
 PT -associated signal on the surface of the cells with an anti-CD28  
 PT antibody, B7-1 or B7-2.  
 XX

PS Example 10; SEQ ID NO 6; 82pp; English.

XX The invention relates to a method for expanding a population of T cells

CC to about 100-10000-fold over the original T cell population, or to about

CC 10 log 1 0 to 12 log 1 2. The method comprises stimulating a CD28-

CC associated signal on the surface of the T cells with agent comprising an

CC anti-CD28 antibody, B7-1 or B7-2. The method is useful for inducing a

CC population of T cells (e.g. CD4+, CD28+, CD8+, CD28RA+ or CD28RO+ T

CC cells) to proliferate. The method is particularly useful for preparing a

CC renewable source of CD4+ T cells. The expanded T cell population can be

CC genetically transduced, and used for immunotherapy to treat a variety of

CC human diseases (e.g. infectious diseases or cancer), or used in

CC diagnostic protocols. T cells were obtained from leukopheresis of a

CC normal donor, and purified with FICOLL density gradient centrifugation,

CC followed by magnetic immunobead sorting. The present sequence is CD9 used

CC in the exemplification of the invention.

XX Sequence 227 AA;

SQ

Query Match 100.0%; Score 95; DB 7; Length 227;

Best Local Similarity 100.0%; Pred. No. 3.3e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLETFVKSCPDAl 18

Db |||||

167 PKKDVLETFVKSCPDAl 184

RESULT 10

AD119366

ID AD119366 standard; protein; 227 AA.

XX

AC AD119366;

XX

DT 15-APR-2004 (first entry)

XX

DE Human CD9 protein.

XX

XX T cell; immunotherapy; therapy; HIV infection; cancer;

KW infectious disease; cytostatic; antimicrobial; human.

XX

OS Homo sapiens.

XX

PN US2004001829-A1.

XX

PD 01-JAN-2004.

XX

PF 17-MAR-2003; 2003US-00390330.

XX

PR 23-NOV-1988; 88US-00275433.

PR 22-NOV-1989; 89WO-US005304.

PR 07-APR-1992; 92US-00864805.

PR 07-APR-1992; 92US-00864807.

PR 07-APR-1992; 92US-00864866.

PR 04-JUN-1993; 93US-00073223.

PR 03-JUN-1994; 94US-00253964.

PR 10-MAR-1995; 95US-00403253.

PR 04-MAY-1995; 95US-00435816.

XX

PA (JUNE/) JUNE C H.

PA (THOM/) THOMPSON C B.

PA (NABE/) NABEL G J.

PA (GRAY/) GRAY G S.

PA (RENN/) RENNERT P D.

XX

PI June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;

XX WPI; 2004-061648/06.

DR

XX Inducing a population of T cells to proliferate, for immunotherapy or

PT treating HIV infection, cancer or infectious disease, comprises

PT activating a population of T cells and stimulating an accessory molecule

PT on the surface of the T cells.

XX Example 10; SEQ ID NO 6; 80pp; English.

XX The invention relates to a method for inducing a population of T cells to

CC proliferate. The method comprising activating a population of T cells,

CC and stimulating an accessory molecule on the surface of the T cells with

CC a ligand that binds the accessory molecule. The invention is useful for

CC immunotherapy, for treating HIV infection, cancer or infectious disease,

CC or in diagnostic applications. The present sequence is human CD9 protein.

XX Sequence 227 AA;

SQ

Query Match 100.0%; Score 95; DB 8; Length 227;

Best Local Similarity 100.0%; Pred. No. 3.3e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLETFVKSCPDAl 18

Db |||||

167 PKKDVLETFVKSCPDAl 184

RESULT 11

AEA89005

ID AEA89005 standard; protein; 227 AA.

XX

AC AEA89005;

XX

DT 25-AUG-2005 (first entry)

XX

DE Human CD9 antigenic protein, SEQ ID NO: 6.

XX

KW Cell therapy; immune stimulation; immunotherapy; diagnosis;

KW infectious disease; antimicrobial; infection; cancer; cytostatic;

XX neoplasm; CD9; antigen.

XX

OS Homo sapiens.

XX

PN US6905681-B1.

XX

PD 14-JUN-2005.

XX

PF 08-JUL-1999; 99US-00349915.

XX

PR 03-JUN-1994; 94US-00253964.

PR 10-MAR-1995; 95US-00403253.

XX

PA (GEMV ) GENETICS INST INC.

PA (UNMI ) UNIV MICHIGAN.

PA (USNA ) US SEC OF NAVY.

XX

PI June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;

XX WPI; 2005-464777/47.

DR

XX Ex vivo proliferation of T cell population for use in therapy, involves

PT contacting population of T cells with surface having anti-CD3 antibody

PT and anti-CD28 antibody for activating T cells and stimulating activated T

PT cells, respectively.

XX

XX Example 10; SEQ ID NO 6; 76pp; English.

XX The present invention relates to a method of including ex vivo

CC proliferation of a population of T cells to sufficient numbers for use in

CC therapy. The method involves contacting population of T cells with

CC surface having anti-CD3 antibody and anti-CD28 antibody for activating T

CC cells and stimulating activated T cells, respectively. The invention is

CC useful for treating cancer and infectious disease and also useful in cell

CC therapy. The present sequence is the human CD9 antigenic protein. This

CC sequence is bound by an ES5.2D8 monoclonal antibody, which is to be used

CC to stimulate a CD8+ T cell population.

XX

SQ Sequence 227 AA;

Query Match 100.0%; Score 95; DB 9; Length 227;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLETFVKSCPDAl 18  
 Db 167 PKKDVLETFVKSCPDAl 184

RESULT 12  
 AAR27525  
 ID AAR27525 standard; protein; 228 AA.  
 XX AC  
 XX AAR27525;  
 XX AC  
 XX 25-MAR-2003 (revised)  
 DT 05-MAR-1993 (first entry)  
 XX XX  
 XX Metastasis controlling peptide.  
 XX XX  
 XX M31-15 monoclonal antibody; cancer cell motility; prophylaxis; treatment;  
 KW lung; glioblastoma.  
 XX Homo sapiens.  
 XX OS  
 XX EP508417-A2.  
 XX PN  
 XX 14-OCT-1992.  
 XX PD  
 XX 09-APR-1992; 92EP-00106093.  
 XX PF  
 XX 12-APR-1991; 91JP-00079996.  
 XX PR  
 XX 17-APR-1991; 91JP-00085396.  
 XX PR  
 XX 07-FEB-1992; 92JP-00023221.  
 XX XX  
 XX (TAKE ) TAKEDA CHEM IND LTD.  
 XX PA  
 XX (MIYA/) MIYAKE M.  
 XX XX  
 XX Ikeyama S, Koyama M, Senoo M, Miyake M;  
 XX PI  
 XX WPI; 1992-341723/42.  
 XX DR  
 XX N-PSDB; AAQ29182.  
 XX DR  
 XX New monoclonal antibody M31-15 specific for metastasis-controlling  
 PT peptide - useful for treating and preventing cancer and metastasis.  
 XX PT  
 XX Claim 7; Fig 4; 34pp; English.  
 XX PS  
 XX The sequence is that of a cancer cell surface protein which is capable of  
 CC suppressing the motility of cancer cells. It is specifically recognised  
 CC by the monoclonal (Mab) antibody M13-15 which is useful for suppressing  
 CC cancer metastasis. The polypeptide and Mab M31-15 are therefore useful in  
 CC the prophylaxis and treatment of cancer, e.g. lung, glioblastoma and  
 CC other metastatic cancers. (Updated on 25-MAR-2003 to correct PN field.)  
 XX CC  
 XX SQ Sequence 228 AA;

Query Match 100.0%; Score 95; DB 2; Length 228;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLETFVKSCPDAl 18  
 Db 168 PKKDVLETFVKSCPDAl 185

RESULT 13  
 ABB44581  
 ID ABB44581 standard; protein; 228 AA.  
 XX AC  
 XX ABB44581;  
 XX AC  
 XX 25-JAN-2002 (first entry)  
 DT

XX XX Human wound healing related polypeptide SEQ ID NO 38.  
 DE XX  
 XX Human; mouse; vulnery; dermatological; skin disorder; wound healing;  
 KW gene therapy.  
 XX KW  
 XX Homo sapiens.  
 OS OS  
 XX CA2325226-A1.  
 PN PN  
 XX 17-MAY-2001.  
 PD PD  
 XX 16-NOV-2000; 2000CA-02325226.  
 PF PF  
 XX 17-NOV-1999; 99DS-01055349.  
 PR PR  
 XX 17-DEC-1999; 99US-0172511P.  
 PR PR  
 XX 20-JUN-2000; 2000DE-01030149.  
 XX XX  
 XX (SWIT-) SWITCH BIOTECH AG.  
 PA PA  
 XX Regenbogen J, Wolf E, Goppelt A, Werner S, Halle J;  
 XX PI  
 XX WPI; 2001-433142/47.  
 XX DR  
 XX Use of novel polypeptide or its variant or nucleic acid encoding the  
 PT polypeptide for diagnosing and/or preventing and/or treating skin  
 PT disorders and/or treatment in wound healing or for identifying active  
 PT substances.  
 XX PT  
 XX Disclosure; Page 193-194; 265pp; English.  
 PS PS  
 XX The invention relates to the use of a polypeptide (ABB44544-ABB44601,  
 CC ABB44606-ABB44623) or its variant or encoding nucleic acid (ABA81990-  
 CC ABA81995, ABA82016-ABA82032) with vulnery and/or dermatological  
 CC activity for the diagnosis, prevention and treatment of skin disorders  
 CC and treatment in wound healing or for the identification of  
 CC pharmacologically active substances. The nucleic acids are useful in gene  
 CC therapy. Note: The printed sequence listing for this specification was  
 CC incomplete, terminating part way through SEQ ID NO 106. The remaining  
 CC data was obtained from EPO data for an equivalent patent (EP1114862)  
 XX CC  
 XX SQ Sequence 228 AA;

Query Match 100.0%; Score 95; DB 4; Length 228;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLETFVKSCPDAl 18  
 Db 168 PKKDVLETFVKSCPDAl 185

RESULT 14  
 ABU05059  
 ID ABU05059 standard; protein; 228 AA.  
 XX XX  
 XX AC ABU05059;  
 XX XX  
 XX 29-JAN-2003 (first entry)  
 DT DT  
 XX Human expressed protein tag (EPT) #1725.  
 XX DE  
 XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
 KW protease; protease inhibitor; transporter; cytoskeletal protein;  
 KW receptor; transcription factor; cancer; MHC;  
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
 XX KW  
 XX Homo sapiens.  
 OS OS  
 XX WO200278524-A2.  
 PN PN  
 XX 10-OCT-2002.  
 DT DT

```

XX PF 28-MAR-2002; 2002WO-US009671.
XX XX
XX PR 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX PR 01-OCT-2001; 2001US-0326370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002US-0358985P.
XX PA (ZYCO-) ZYCOS INC.
XX XX
XX PI Chiciz RM, Tomlinson AJ, Urban RG;
XX XX
XX DR WPI; 2003-040607/03.
XX XX
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX PT cytoskeletal proteins, receptors or transcription factors), useful for
XX PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX PT leukemia.
XX XX
XX PS Example 2; SEQ ID NO 1725; 134pp; English.
XX XX
XX CC The invention describes a purified polypeptide, which comprises a
XX CC fragment of a kinase, phosphatase, protease, protease inhibitor,
XX CC transporter, cytoskeletal protein, receptor or transcription factor. The
XX CC polypeptide is useful as an immunogenic composition for eliciting in a
XX CC mammal an immunogenic response directed against any of the purified
XX CC polypeptide. The purified polypeptide, or the antibody that binds to this
XX CC polypeptide, is useful for treating cancer. The polypeptide is also
XX CC useful for identifying compounds that binds to a naturally processed
XX CC class I or class II MHC-binding polypeptide. The polypeptides and
XX CC polynucleotides are particularly useful for treating or preventing
XX CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX CC lymphoma or leukaemia. These are also useful for screening agents for
XX CC treating the above mentioned diseases. This sequence represents an
XX CC expressed protein tag (EPT) isolated from human tissue for translational
XX CC profiling. Note: This sequence does not appear in the printed
XX CC specification but was obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 228 AA;

Query Match 100.0%; Score 95; DB 6; Length 228;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLFTTVKSCPDAI 18
DB 168 PKKDVLFTTVKSCPDAI 185

RESULT 15
ABU05052
ID ABU05052 standard; protein; 228 AA.
XX AC ABU05052;
XX XX
XX DT 29-JAN-2003 (first entry)
XX XX
XX DE Human expressed protein tag (EPT) #1718.
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX KW protease; protease inhibitor; transporter; cytoskeletal protein;
XX KW receptor; transcription factor; cancer; MHC;
XX KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX OS Homo sapiens.
XX XX
XX PN WO200278524-A2.
XX XX
XX PD 10-OCT-2002.

```

```

XX PF 28-MAR-2002; 2002WO-US009671.
XX XX
XX PR 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX PR 01-OCT-2001; 2001US-0326370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002US-0358985P.
XX PA (ZYCO-) ZYCOS INC.
XX XX
XX PI Chiciz RM, Tomlinson AJ, Urban RG;
XX XX
XX DR WPI; 2003-040607/03.
XX XX
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX PT cytoskeletal proteins, receptors or transcription factors), useful for
XX PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX PT leukemia.
XX XX
XX PS Example 2; SEQ ID NO 1718; 134pp; English.
XX XX
XX CC The invention describes a purified polypeptide, which comprises a
XX CC fragment of a kinase, phosphatase, protease, protease inhibitor,
XX CC transporter, cytoskeletal protein, receptor or transcription factor. The
XX CC polypeptide is useful as an immunogenic composition for eliciting in a
XX CC mammal an immunogenic response directed against any of the purified
XX CC polypeptide. The purified polypeptide, or the antibody that binds to this
XX CC polypeptide, is useful for treating cancer. The polypeptide is also
XX CC useful for identifying compounds that binds to a naturally processed
XX CC class I or class II MHC-binding polypeptide. The polypeptides and
XX CC polynucleotides are particularly useful for treating or preventing
XX CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX CC lymphoma or leukaemia. These are also useful for screening agents for
XX CC treating the above mentioned diseases. This sequence represents an
XX CC expressed protein tag (EPT) isolated from human tissue for translational
XX CC profiling. Note: This sequence does not appear in the printed
XX CC specification but was obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 228 AA;

Query Match 100.0%; Score 95; DB 6; Length 228;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLFTTVKSCPDAI 18
DB 168 PKKDVLFTTVKSCPDAI 185

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Search completed: January 20, 2006, 17:16:07  
Job time : 63.3333 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2006, 17:10:37 ; Search time 12.6667 Seconds  
(without alignments)  
117.486 Million cell updates/sec

Title: US-10-619-323-6

Perfect score: 95  
Sequence: 1 PKKDVLETFVKSCPDAl 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	100.0	29	1	US-08-254-493-6
2	95	100.0	29	1	US-08-408-222B-6
3	95	100.0	227	1	US-08-254-493-1
4	95	100.0	227	1	US-08-253-751-6
5	95	100.0	227	1	US-08-453-925-6
6	95	100.0	227	2	US-08-403-253A-6
7	95	100.0	227	2	US-08-435-816A-6
8	95	100.0	227	2	US-09-350-202-6
9	95	100.0	227	2	US-08-592-711-6
10	95	100.0	227	2	US-09-349-915B-6
11	95	100.0	228	1	US-08-408-222B-1
12	87	91.6	79	2	US-08-630-172-8
13	87	91.6	79	2	US-09-375-419-8
14	47	49.5	1018	1	US-08-452-052-2
15	43	45.3	542	1	US-08-701-380-2
16	43	45.3	542	2	US-09-032-365A-13
17	43	45.3	1334	1	US-08-996-545-2
18	43	45.3	1334	2	US-09-328-320-2
19	43	45.3	1334	2	US-09-758-828-2
20	42	44.2	68	2	US-09-583-110-3271
21	42	44.2	97	2	US-10-039-836A-2
22	42	44.2	100	2	US-09-107-433-4841
23	42	44.2	643	2	US-09-949-016-10023
24	41	43.2	180	2	US-09-270-767-48380
25	41	43.2	520	2	US-10-104-047-2424
26	41	43.2	520	2	US-10-104-047-2730
27	40	42.1	103	2	US-09-603-208A-194

28	40	42.1	276	2	US-09-328-352-5682	Sequence 5682, Ap
29	40	42.1	411	2	US-09-248-796A-15503	Sequence 15503, A
30	40	42.1	456	2	US-09-492-027-2	Sequence 2, Appli
31	40	42.1	690	2	US-09-902-540-10349	Sequence 10349, A
32	40	42.1	1905	2	US-09-964-956-44	Sequence 44, Appl
33	39.5	41.6	65	2	US-09-149-476-645	Sequence 645, App
34	39	41.1	159	2	US-09-107-532A-3789	Sequence 3789, Ap
35	39	41.1	194	2	US-09-873-075A-1	Sequence 1, Appli
36	39	41.1	229	1	US-08-817-997A-2	Sequence 2, Appli
37	39	41.1	327	2	US-09-252-991A-25546	Sequence 25546, A
38	39	41.1	1018	1	US-08-408-093-6	Sequence 6, Appli
39	39	41.1	1018	1	US-08-408-420A-6	Sequence 6, Appli
40	39	41.1	1018	1	US-08-714-901-6	Sequence 6, Appli
41	39	41.1	1018	2	US-08-040-741-6	Sequence 6, Appli
42	39	41.1	1044	2	US-09-949-016-10321	Sequence 10321, A
43	38.5	40.5	426	2	US-09-134-000C-6758	Sequence 6758, Ap
44	38	40.0	129	2	US-09-250-124A-29	Sequence 29, Appl
45	38	40.0	166	2	US-09-621-976-5267	Sequence 5267, Ap

## ALIGNMENTS

## RESULT 1

US-08-254-493-6  
; Sequence 6, Application US/08254493  
; Patent No. 5439886

## GENERAL INFORMATION:

APPLICANT: IKEYAMA, SHUICHI  
APPLICANT: KOYAMA, MASARU  
APPLICANT: MIYAKE, MASAYUKI  
APPLICANT: SENOO, MASAHARU  
TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND  
PRODUCTION THEREOF  
TITLE OF INVENTION:  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
STREET: 130 WATER STREET  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: US  
ZIP: 02109

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/254,493  
FILING DATE:

## CLASSIFICATION:

435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/865552  
FILING DATE: 09-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 0799996-1991  
FILING DATE: 12-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 085396-1991  
FILING DATE: 17-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 022321-1992  
FILING DATE: 07-FEB-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: RESNICK, DAVID S.  
REGISTRATION NUMBER: 34235  
REFERENCE/DOCKET NUMBER: 41777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 523-3400  
TELEFAX: (617) 523-6440  
TELEX: 200291 STRE UR  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:

;  
; LENGTH: 29 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-254-493-6

Query Match 100.0%; Score 95; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 2.4e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQVLETFVTKSCPDAl 18  
Db 5 PKQVLETFVTKSCPDAl 22

## RESULT 2

US-08-408-222B-6  
; Sequence 6, Application US/08408222B  
; Patent No. 5776727  
; GENERAL INFORMATION:  
; APPLICANT: Ikeyama, Shuichi  
; APPLICANT: Koyama, Masaru  
; APPLICANT: Miyake, Masayuki  
; APPLICANT: Senoo, Masaharu  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
; STREET: 130 WATER STREET  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/408,222B  
; FILING DATE: 22-MAR-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/254,493  
; FILING DATE: 06-JUN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP-079996-1991  
; FILING DATE: 12-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP-085396-1991  
; FILING DATE: 14-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP-022321-1992  
; FILING DATE: 07-FEB-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: RESNICK, DAVID S.  
; REGISTRATION NUMBER: 34,235  
; REFERENCE/DOCKET NUMBER: 41777-DIV  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-523-3400  
; TELEFAX: 617-523-6440  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 29 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-408-222B-6

Query Match 100.0%; Score 95; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 2.4e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQVLETFVTKSCPDAl 18  
Db 5 PKQVLETFVTKSCPDAl 22

## RESULT 3

US-08-254-493-1  
; Sequence 1, Application US/08254493  
; Patent No. 5439886  
; GENERAL INFORMATION:  
; APPLICANT: IKEYAMA, SHUICHI  
; APPLICANT: KOYAMA, MASARU  
; APPLICANT: MIYAKE, MASAYUKI  
; APPLICANT: SENOO, MASAHARU  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
; STREET: 130 WATER STREET  
; CITY: BOSTON  
; STATE: MASSACHUSETTS  
; COUNTRY: US  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/254,493  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/865552  
; FILING DATE: 09-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 079996-1991  
; FILING DATE: 12-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 085396-1991  
; FILING DATE: 17-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 022321-1992  
; FILING DATE: 07-FEB-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: RESNICK, DAVID S.  
; REGISTRATION NUMBER: 34235  
; REFERENCE/DOCKET NUMBER: 41777  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 523-3400  
; TELEFAX: (617) 523-6440  
; TELEX: 200291 STRE UR  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 227 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-254-493-1

Query Match 100.0%; Score 95; DB 1; Length 227;  
Best Local Similarity 100.0%; Pred. No. 2.5e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQVLETFVTKSCPDAl 18  
Db 167 PKQVLETFVTKSCPDAl 184

## RESULT 4

US-08-253-751-6  
; Sequence 6, Application US/08253751  
; Patent No. 5858358

GENERAL INFORMATION:  
; APPLICANT: June, Carl H.  
; APPLICANT: Thompson, Craig B.  
; APPLICANT: Nabel, Gary J.  
; APPLICANT: Gray, Gary S.  
; APPLICANT: Rennert, Paul D.  
; APPLICANT: Freeman, Gordon J.  
; TITLE OF INVENTION: METHODS FOR SELECTIVELY STIMULATING  
; TITLE OF INVENTION: PROLIFERATION OF T-CELLS  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 STATE STREET, SUITE 510  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII TEXT  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/253,751  
; FILING DATE: 3 JUNE 1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/073,223  
; FILING DATE: 4 JUNE 1993  
; APPLICATION NUMBER: US 08/200,947  
; FILING DATE: 23 FEB 1994  
; APPLICATION NUMBER: US 07/864,805  
; FILING DATE: 7 APR 1992  
; APPLICATION NUMBER: US 08/247,505  
; FILING DATE: 23 MAY 1994  
; APPLICATION NUMBER: US 07/864,866  
; FILING DATE: 7 APR 1992  
; APPLICATION NUMBER: 08/218,155  
; FILING DATE: 25 MAR 1994  
; APPLICATION NUMBER: US 07/864,807  
; FILING DATE: 7 APR 1992  
; APPLICATION NUMBER: US 07/902,467  
; FILING DATE: 16 JUNE 1992  
; APPLICATION NUMBER: US 07/275,433  
; FILING DATE: 23 NOV 1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MANDRAGOURAS, AMY E.  
; REGISTRATION NUMBER: 36,207  
; REFERENCE/DOCKET NUMBER: RPI-002CPB  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-7400  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 227 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-253-751-6

Query Match 100.0%; Score 95; DB 1; Length 227;  
Best Local Similarity 100.0%; Pred. No. 2.5e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQVLETFVTKSCPDAI 18  
Db 167 PKQVLETFVTKSCPDAI 184

RESULT 5  
US-08-453-925-6

; Sequence 6, Application US/08453925  
; Patent No. 5883223

GENERAL INFORMATION:  
; APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.  
; APPLICANT: Gray, Gary S., Rennert, Paul D., Freeman, Gordon J.  
; TITLE OF INVENTION: METHODS FOR SELECTIVELY STIMULATING  
; TITLE OF INVENTION: PROLIFERATION OF T-CELLS  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 STATE STREET, SUITE 510  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII TEXT  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/453,925  
; FILING DATE: 30 MAY 1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/253,751  
; FILING DATE: 3 JUNE 1994  
; APPLICATION NUMBER: US 08/073,223  
; FILING DATE: 4 JUNE 1993  
; APPLICATION NUMBER: US 08/200,947  
; FILING DATE: 23 FEB 1994  
; APPLICATION NUMBER: US 07/864,805  
; FILING DATE: 7 APR 1992  
; APPLICATION NUMBER: US 08/247,505  
; FILING DATE: 23 MAY 1994  
; APPLICATION NUMBER: US 07/864,866  
; FILING DATE: 7 APR 1992  
; APPLICATION NUMBER: 08/218,155  
; FILING DATE: 25 MAR 1994  
; APPLICATION NUMBER: US 07/864,807  
; FILING DATE: 7 APR 1992  
; APPLICATION NUMBER: US 07/902,467  
; FILING DATE: 16 JUNE 1992  
; APPLICATION NUMBER: US 07/275,433  
; FILING DATE: 23 NOV 1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MANDRAGOURAS, AMY E.  
; REGISTRATION NUMBER: 36,207  
; REFERENCE/DOCKET NUMBER: RPI-002CPB  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 227 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-453-925-6

Query Match 100.0%; Score 95; DB 1; Length 227;  
Best Local Similarity 100.0%; Pred. No. 2.5e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQVLETFVTKSCPDAI 18  
Db 167 PKQVLETFVTKSCPDAI 184

RESULT 6  
US-08-403-253A-6  
; Sequence 6, Application US/08403253A  
; Patent No. 6352694  
; GENERAL INFORMATION:

APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.  
APPLICANT: Gray, Gary S., Rennert, Paul D.  
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSER: LAHIVE & COCKFIELD  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/403,253A  
FILING DATE: March 10, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/253,964  
FILING DATE: 3 JUNE 1994  
APPLICATION NUMBER: US 08/073,223  
FILING DATE: 4 JUNE 1993  
APPLICATION NUMBER: US 08/200,947  
FILING DATE: 23 FEB 1994  
APPLICATION NUMBER: US 07/864,805  
FILING DATE: 7 APR 1992  
APPLICATION NUMBER: US 08/247,505  
FILING DATE: 23 MAY 1994  
APPLICATION NUMBER: US 07/864,866  
FILING DATE: 7 APR 1992  
APPLICATION NUMBER: US 08/218,155  
FILING DATE: 25 MAR 1994  
APPLICATION NUMBER: US 07/864,807  
FILING DATE: 7 APR 1992  
APPLICATION NUMBER: US 07/902,467  
FILING DATE: 16 JUNE 1992  
APPLICATION NUMBER: US 07/275,433  
FILING DATE: 23 NOV 1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: RPT-002CP2  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 742-4214  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 227 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-403-253A-6

Query Match 100.0%; Score 95; DB 2; Length 227;  
Best Local Similarity 100.0%; Pred. No. 2.5e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLFTFTVKSCPDAl 18  
Db 167 PKKDVLFTFTVKSCPDAl 184

## RESULT 7

US-08-435-816A-6  
Sequence 6, Application US/08435816A  
Patent No. 6534055  
GENERAL INFORMATION:  
APPLICANT: June, Carl H.  
APPLICANT: Thompson, Craig B.  
APPLICANT: Nabel, Gary J.

APPLICANT: Gray, Gary S.  
APPLICANT: Rennert, Paul D.  
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSER: LAHIVE & COCKFIELD  
STREET: 60 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/435,816A  
FILING DATE: May 4, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/403,253  
FILING DATE: 10 MARCH 1995  
APPLICATION NUMBER: US 08/253,964  
FILING DATE: 3 JUNE 1994  
APPLICATION NUMBER: US 08/073,223  
FILING DATE: 4 JUNE 1993  
APPLICATION NUMBER: US 08/200,947  
FILING DATE: 23 FEB 1994  
APPLICATION NUMBER: US 07/864,805  
FILING DATE: 7 APR 1992  
APPLICATION NUMBER: US 08/247,505  
FILING DATE: 23 MAY 1994  
APPLICATION NUMBER: US 07/864,866  
FILING DATE: 7 APR 1992  
APPLICATION NUMBER: US 08/218,155  
FILING DATE: 25 MAR 1994  
APPLICATION NUMBER: US 07/864,807  
FILING DATE: 7 APR 1992  
APPLICATION NUMBER: US 07/902,467  
FILING DATE: 16 JUNE 1992  
APPLICATION NUMBER: US 07/275,433  
FILING DATE: 23 NOV 1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: RPT-002CP3  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 227 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-435-816A-6

Query Match 100.0%; Score 95; DB 2; Length 227;  
Best Local Similarity 100.0%; Pred. No. 2.5e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLFTFTVKSCPDAl 18  
Db 167 PKKDVLFTFTVKSCPDAl 184

## RESULT 8

US-09-350-202-6  
Sequence 6, Application US/09350202  
Patent No. 6887466  
GENERAL INFORMATION:  
APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.

APPLICANT: Gray, Gary S., Rennert, Paul D.  
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/350,202  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/403,253  
FILING DATE: March 10, 1995  
APPLICATION NUMBER: US 08/253,964  
FILING DATE: 3 JUNE 1994  
APPLICATION NUMBER: US 08/073,223  
FILING DATE: 4 JUNE 1993  
APPLICATION NUMBER: US 08/200,947  
FILING DATE: 23 FEB 1994  
APPLICATION NUMBER: US 07/864,805  
FILING DATE: 7 APR 1992  
APPLICATION NUMBER: US 08/247,505  
FILING DATE: 23 MAY 1994  
APPLICATION NUMBER: US 07/864,866  
FILING DATE: 7 APR 1992  
APPLICATION NUMBER: US 08/218,155  
FILING DATE: 25 MAR 1994  
APPLICATION NUMBER: US 07/864,807  
FILING DATE: 7 APR 1992  
APPLICATION NUMBER: US 07/902,467  
FILING DATE: 16 JUNE 1992  
APPLICATION NUMBER: US 07/275,433  
FILING DATE: 23 NOV 1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: RPI-002CP2  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 742-4214  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 227 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-350-202-6

Query Match 100.0%; Score 95; DB 2; Length 227;  
Best Local Similarity 100.0%; Pred. No. 2.5e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQDVLETFVTKSCPDAI 18  
Db 167 PKQDVLETFVTKSCPDAI 184

RESULT 9  
US-08-592-711-6  
; Sequence 6, Application US/08592711  
; Patent No. 6905680  
; GENERAL INFORMATION:  
; APPLICANT: June, Carl H.  
; APPLICANT: Thompson, Craig B.

APPLICANT: Nabel, Gary J.  
APPLICANT: Gray, Gary S.  
APPLICANT: Rennert, Paul D.  
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/592,711  
FILING DATE: 26-JAN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/435,816  
FILING DATE: 4-MAY-1995  
APPLICATION NUMBER: US 08/403,253  
FILING DATE: 10-MARCH-1995  
APPLICATION NUMBER: US 08/253,964  
FILING DATE: 3-JUNE-1994  
APPLICATION NUMBER: US 08/073,223  
FILING DATE: 4-JUNE-1993  
APPLICATION NUMBER: US 08/200,947  
FILING DATE: 23-FEB-1994  
APPLICATION NUMBER: US 07/864,805  
FILING DATE: 7-APR-1992  
APPLICATION NUMBER: US 08/247,505  
FILING DATE: 23-MAY-1994  
APPLICATION NUMBER: US 07/864,866  
FILING DATE: 7-APR-1992  
APPLICATION NUMBER: US 08/218,155  
FILING DATE: 25-MAR-1994  
APPLICATION NUMBER: US 07/864,807  
FILING DATE: 7-APR-1992  
APPLICATION NUMBER: US 07/902,467  
FILING DATE: 16-JUNE-1992  
APPLICATION NUMBER: US 07/275,433  
FILING DATE: 23-NOV-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: RPI-002CP4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 227 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-592-711-6

Query Match 100.0%; Score 95; DB 2; Length 227;  
Best Local Similarity 100.0%; Pred. No. 2.5e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQDVLETFVTKSCPDAI 18  
Db 167 PKQDVLETFVTKSCPDAI 184

RESULT 10  
US-09-349-915B-6  
; Sequence 6, Application US/09349915B  
; Patent No. 6905681

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; GENERAL INFORMATION:
; APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.
; TITLE OF INVENTION: Methods For Selectively Stimulating
; Proliferation Of T-Cells
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALE AND DORR LLP
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/349,915B
; FILING DATE: 01-AUG-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/403,253
; FILING DATE: March 10, 1995
; APPLICATION NUMBER: US 08/253,964
; FILING DATE: 3 JUNE 1994
; APPLICATION NUMBER: US 08/073,223
; FILING DATE: 4 JUNE 1993
; APPLICATION NUMBER: US 08/200,947
; FILING DATE: 23 FEB 1994
; APPLICATION NUMBER: US 07/864,805
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/247,505
; FILING DATE: 23 MAY 1994
; APPLICATION NUMBER: US 07/864,866
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/218,155
; FILING DATE: 25 MAR 1994
; APPLICATION NUMBER: US 07/864,807
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 07/902,467
; FILING DATE: 16 JUNE 1992
; APPLICATION NUMBER: US 07/275,433
; FILING DATE: 23 NOV 1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Superko, Colleen
; REGISTRATION NUMBER: 39,850
; REFERENCE/DOCKET NUMBER: 36119-125 (US10)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 526-6564
; TELEFAX: (617) 526-5000
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
; LENGTH: 227 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ANTI-SENSE: NO
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-09-349-915B-6
;
; Query Match 100.0%; Score 95; DB 2; Length 227;
; Best Local Similarity 100.0%; Pred. No. 2.5e-08;
; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; US-09-349-915B-6
;
; QY 1 PKQDVLETFVTKSCPDAI 18
; |||||
; DB 167 PKQDVLETFVTKSCPDAI 184
;
; RESULT 11
; US-08-408-222B-1
; Sequence 1, Application US/08408222B
;
; Patent No. 5776727
; GENERAL INFORMATION:
; APPLICANT: Ikeyama, Shuichi
; APPLICANT: Koyama, Masaru
; APPLICANT: Miyake, Masauyuki
; APPLICANT: Senoo, Masaharu
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dike, Bronstein, Roberts & Cushman
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/408,222B
; FILING DATE: 22-MAR-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/254,493
; FILING DATE: 06-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP-079996-1991
; FILING DATE: 12-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP-085396-1991
; FILING DATE: 14-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP-022321-1992
; FILING DATE: 07-FEB-1994
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 41777-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-08-408-222B-1
;
; Query Match 100.0%; Score 95; DB 1; Length 228;
; Best Local Similarity 100.0%; Pred. No. 2.6e-08;
; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 PKQDVLETFVTKSCPDAI 18
; |||||
; DB 168 PKQDVLETFVTKSCPDAI 185
;
; RESULT 12
; US-08-630-172-8
; Sequence 8, Application US/08630172
; Patent No. 6060054
; GENERAL INFORMATION:
; APPLICANT: Staerz, Uwe
; TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T
; LYMPHOCYTE VETO
;

```

NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheridan Ross & McIntosh  
STREET: 1700 Lincoln Street, 35th Floor  
CITY: Denver  
STATE: Colorado  
COUNTRY: U.S.  
ZIP: 80203  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,172  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Connell, Gary J.  
REGISTRATION NUMBER: 32,020  
REFERENCE/DOCKET NUMBER: 2879-36  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 863-9700  
TELEFAX: (303) 863-0223  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 79 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-630-172-8

Query Match 91.6%; Score 87; DB 2; Length 79;  
Best Local Similarity 100.0%; Pred. No. 1.8e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQDVLETFVKSCPD 16  
Db 56 PKQDVLETFVKSCPD 71

RESULT 13  
US-09-375-419-8  
Sequence 8, Application US/09375419  
Patent No. 6264950  
GENERAL INFORMATION:  
APPLICANT: Staerz, Uwe  
TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T  
REGISTRATION NUMBER: LYMPOCYTE VETO  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheridan Ross & McIntosh  
STREET: 1700 Lincoln Street, 35th Floor  
CITY: Denver  
STATE: Colorado  
COUNTRY: U.S.  
ZIP: 80203  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/375,419  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/630,172  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Connell, Gary J.  
REGISTRATION NUMBER: 32,020  
REFERENCE/DOCKET NUMBER: 2879-36

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 863-9700  
TELEFAX: (303) 863-0223  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 79 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-375-419-8

Query Match 91.6%; Score 87; DB 2; Length 79;  
Best Local Similarity 100.0%; Pred. No. 1.8e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQDVLETFVKSCPD 16  
Db 56 PKQDVLETFVKSCPD 71

RESULT 14  
US-08-452-052-2  
Sequence 2, Application US/08452052  
Patent No. 5766922  
GENERAL INFORMATION:  
APPLICANT: Peles, Elior  
TITLE OF INVENTION: FUNCTIONAL LIGANDS FOR THE AXONAL CELL  
TITLE OF INVENTION: RECOGNITION MOLECULE CONTACTIN  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/452,052  
FILING DATE: 26-MAY-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7683-075  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1018 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-452-052-2

Query Match 49.5%; Score 47; DB 1; Length 1018;  
Best Local Similarity 60.0%; Pred. No. 23;  
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 PKQDVLETFVKSCPD 15  
Db 890 PSSDVLETFVKAPP 904

RESULT 15  
US-08-701-380-2

; Sequence 2, Application US/08701380  
; Patent No. 5686598  
; GENERAL INFORMATION:  
; APPLICANT: NORTH, Michael  
; APPLICANT: NISHINA, Patsy  
; APPLICANT: NAGERT, Juergen  
; TITLE OF INVENTION: GENES ASSOCIATED WITH RETINAL  
; TITLE OF INVENTION: DYSTROPHIES  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr, Hohnbach, Test, Albritton & Herbert  
; STREET: 4 Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111-4187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/701,380  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SHERWOOD, Pamela J.  
; REGISTRATION NUMBER: 36,677  
; REFERENCE/DOCKET NUMBER: A-63565/PJS  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-494-8700  
; TELEFAX: 415-494-8771  
; TELEX: 910 277299  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 542 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-701-380-2

Query Match 45.3%; Score 43; DB 1; Length 542;  
Best Local Similarity 56.2%; Pred. No. 54;  
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 KKDVLFTTVKCPDA 17  
| | | | |  
Db 99 KDDPRETFLVARAPDA 114

Search completed: January 20, 2006, 17:23:45  
Job time : 12.6667 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2006, 17:11:18 ; Search time 36.2222 Seconds  
(without alignments)  
207.633 Million cell updates/sec

Title: US-10-619-323-6

Perfect score: 95  
Sequence: 1 PKKDVLETFVKSCPDAL 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	95	100.0	18	4	US-10-619-323-6
2	95	100.0	25	4	US-10-619-323-5
3	95	100.0	74	4	US-10-425-115-240878
4	95	100.0	227	2	US-08-592-711-6
5	95	100.0	227	3	US-09-183-055-6
6	95	100.0	227	3	US-09-350-202-6
7	95	100.0	227	4	US-10-390-330-6
8	95	100.0	227	5	US-10-473-127-1723
9	95	100.0	227	5	US-10-473-127-1726
10	95	100.0	228	4	US-10-156-136-39
11	95	100.0	228	4	US-10-331-496A-41
12	95	100.0	228	4	US-10-619-323-1
13	95	100.0	228	4	US-10-794-899-97
14	95	100.0	228	5	US-10-473-127-1714
15	95	100.0	228	5	US-10-473-127-1715
16	95	100.0	228	5	US-10-473-127-1716
17	95	100.0	228	5	US-10-473-127-1718
18	95	100.0	228	5	US-10-473-127-1719
19	95	100.0	228	5	US-10-473-127-1722
20	95	100.0	228	5	US-10-473-127-1725
21	95	100.0	228	5	US-10-789-378-18
22	95	100.0	228	5	US-10-482-029-144
23	95	100.0	228	5	US-10-852-335A-187
24	95	100.0	228	6	US-11-041-419-39
25	95	100.0	275	3	US-09-925-301-1381
26	95	100.0	275	4	US-10-106-698-5930
27	95	100.0	275	5	US-10-473-127-1720

28	95	100.0	275	5	US-10-473-127-1721	Sequence 1721, Ap
29	95	100.0	454	5	US-10-450-763-44426	Sequence 44426, A
30	87	91.6	79	5	US-10-473-127-1724	Sequence 1724, Ap
31	79	83.2	226	4	US-10-205-194-162	Sequence 162, App
32	61	64.2	30	5	US-10-473-127-1717	Sequence 1717, Ap
33	49.5	52.1	258	4	US-10-437-963-169601	Sequence 169601, A
34	49	51.6	10	5	US-10-473-127-165	Sequence 165, App
35	47	49.5	1020	5	US-10-631-467-1637	Sequence 1637, Ap
36	44.5	46.8	423	4	US-10-282-122A-48428	Sequence 48428, A
37	44	46.3	54	4	US-10-425-115-339548	Sequence 339548, A
38	44	46.3	339	4	US-10-282-122A-48707	Sequence 48707, A
39	44	46.3	475	4	US-10-437-963-155174	Sequence 155174, A
40	43	45.3	364	4	US-10-353-856-14	Sequence 32, Appl
41	43	45.3	364	4	US-10-353-856-32	Sequence 42, Appl
42	43	45.3	364	4	US-10-353-856-42	Sequence 42, Appl
43	43	45.3	542	4	US-10-408-765A-2262	Sequence 2262, Ap
44	43	45.3	542	5	US-10-732-923-19513	Sequence 19513, A
45	43	45.3	542	5	US-10-732-923-19514	Sequence 19514, A

#### ALIGNMENTS

RESULT 1  
US-10-619-323-6  
; Sequence 6, Application US/10619323  
; Publication No. US20040136985A1  
; GENERAL INFORMATION:  
; APPLICANT: Jennings, Lisa K.  
; APPLICANT: Longhurst, Celia M.  
; APPLICANT: Cook, George A.  
; APPLICANT: Bao, Jianxiong  
; APPLICANT: Zhang, Chunxiang  
; APPLICANT: White, Melanie M.  
; APPLICANT: Crosno, Jr., Joseph T.  
; APPLICANT: Lu, Yi  
; TITLE OF INVENTION: METHODS OF MODIFYING BEHAVIOR OF CD9-EXPRESSING CELLS  
; FILE REFERENCE: 20609/241  
; CURRENT APPLICATION NUMBER: US/10/619,323  
; CURRENT FILING DATE: 2003-07-14  
; PRIOR APPLICATION NUMBER: 60/395,864  
; PRIOR FILING DATE: 2002-07-12  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: CD9 peptide  
US-10-619-323-6

Query Match 100.0%; Score 95; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. NO. 7.7e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	PKKDVLETFVKSCPDAL 18
Db	1	PKKDVLETFVKSCPDAL 18

RESULT 2  
US-10-619-323-5  
; Sequence 5, Application US/10619323  
; Publication No. US20040136985A1  
; GENERAL INFORMATION:  
; APPLICANT: Jennings, Lisa K.  
; APPLICANT: Longhurst, Celia M.  
; APPLICANT: Cook, George A.  
; APPLICANT: Bao, Jianxiong  
; APPLICANT: White, Melanie M.  
; APPLICANT: Crosno, Jr., Joseph T.

APPLICANT: Lu, Yi  
TITLE OF INVENTION: METHODS OF MODIFYING BEHAVIOR OF CD9-EXPRESSING CELLS  
FILE REFERENCE: 20609/241  
CURRENT APPLICATION NUMBER: US/10/619,323  
CURRENT FILING DATE: 2003-07-14  
PRIOR APPLICATION NUMBER: 60/395,864  
PRIOR FILING DATE: 2002-07-12  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 5  
LENGTH: 25  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: CD9 peptide  
US-10-619-323-5

Query Match 100.0%; Score 95; DB 4; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.1e-08; Indels 0; Gaps 0;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLFTFTVKSCPDAl 18  
|||||

Db 1 PKKDVLFTFTVKSCPDAl 18  
|||||

RESULT 3  
US-10-425-115-240878  
Sequence 240878, Application US/10425115  
Publication No. US20040214272A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
FILE REFERENCE: 38-21(S3222)B  
CURRENT APPLICATION NUMBER: US/10/425,115  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 369326  
SEQ ID NO 240878  
LENGTH: 74  
TYPE: PRT  
ORGANISM: Zea mays  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (1)..(74)  
OTHER INFORMATION: unsure at all Xaa locations  
FEATURE:  
OTHER INFORMATION: Clone ID: MRT4577\_15125C.1.pep  
US-10-425-115-240878

Query Match 100.0%; Score 95; DB 4; Length 74;  
Best Local Similarity 100.0%; Pred. No. 3.8e-08; Indels 0; Gaps 0;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLFTFTVKSCPDAl 18  
|||||

Db 20 PKKDVLFTFTVKSCPDAl 37  
|||||

RESULT 4  
US-08-592-711-6  
Sequence 6, Application US/08592711  
Publication No. US20020115214A1  
GENERAL INFORMATION:  
APPLICANT: June, Carl H.  
APPLICANT: Thompson, Craig B.  
APPLICANT: Nabel, Gary J.  
APPLICANT: Gray, Gary S.  
APPLICANT: Rennert, Paul D.  
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells

NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/592,711  
FILING DATE: 26-JAN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/435,816  
FILING DATE: 4-MAY-1995  
APPLICATION NUMBER: US 08/403,253  
FILING DATE: 10-MARCH-1995  
APPLICATION NUMBER: US 08/253,964  
FILING DATE: 3-JUNE-1994  
APPLICATION NUMBER: US 08/073,223  
FILING DATE: 4-JUNE-1993  
APPLICATION NUMBER: US 08/200,947  
FILING DATE: 23-FEB-1994  
APPLICATION NUMBER: US 07/864,805  
FILING DATE: 7-APR-1992  
APPLICATION NUMBER: US 08/247,505  
FILING DATE: 23-MAY-1994  
APPLICATION NUMBER: US 07/864,866  
FILING DATE: 7-APR-1992  
APPLICATION NUMBER: US 08/218,155  
FILING DATE: 25-MAR-1994  
APPLICATION NUMBER: US 07/864,807  
FILING DATE: 7-APR-1992  
APPLICATION NUMBER: US 07/902,467  
FILING DATE: 16-JUNE-1992  
APPLICATION NUMBER: US 07/275,433  
FILING DATE: 23-NOV-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: RPI-002CP4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 227 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-592-711-6

Query Match 100.0%; Score 95; DB 2; Length 227;  
Best Local Similarity 100.0%; Pred. No. 1.3e-07; Indels 0; Gaps 0;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLFTFTVKSCPDAl 18  
|||||

Db 167 PKKDVLFTFTVKSCPDAl 184  
|||||

RESULT 5  
US-09-183-055-6  
Sequence 6, Application US/09183055  
Publication No. US20020076407A1  
GENERAL INFORMATION:  
APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.  
APPLICANT: Gray, Gary S., Rennert, Paul D.  
TITLE OF INVENTION: Methods For Selectively Stimulating

## Proliferation Of T-Cells

NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HALE AND DORR LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/183,055  
FILING DATE: 30-Oct-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/403,253  
FILING DATE: March 10, 1995  
APPLICATION NUMBER: US 08/253,964  
FILING DATE: 3 JUNE 1994  
APPLICATION NUMBER: US 08/073,223  
FILING DATE: 4 JUNE 1993  
APPLICATION NUMBER: US 08/200,947  
FILING DATE: 23 FEB 1994  
APPLICATION NUMBER: US 07/864,805  
FILING DATE: 7 APR 1992  
APPLICATION NUMBER: US 08/247,505  
FILING DATE: 23 MAY 1994  
APPLICATION NUMBER: US 07/864,866  
FILING DATE: 7 APR 1992  
APPLICATION NUMBER: US 08/218,155  
FILING DATE: 25 MAR 1994  
APPLICATION NUMBER: US 07/864,807  
FILING DATE: 7 APR 1992  
APPLICATION NUMBER: US 07/902,467  
FILING DATE: 16 JUNE 1992  
APPLICATION NUMBER: US 07/275,433  
FILING DATE: 23 NOV 1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Superko, Colleen  
REGISTRATION NUMBER: 39,850  
REFERENCE/DOCKET NUMBER: 36119-125US8  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6564  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 227 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-183-055-6  
Query Match 100.0%; Score 95; DB 3; Length 227;  
Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 PKKDVLFTFTVKSCPDAl 18  
Db 167 PKKDVLFTFTVKSCPDAl 184  
RESULT 6  
US-09-350-202-6  
Sequence 6, Application US/09350202  
Publication No. US20030099643A1  
GENERAL INFORMATION:  
APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.  
APPLICANT: Gray, Gary S., Rennert, Paul D.

TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/350,202  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/403,253  
FILING DATE: March 10, 1995  
APPLICATION NUMBER: US 08/253,964  
FILING DATE: 3 JUNE 1994  
APPLICATION NUMBER: US 08/073,223  
FILING DATE: 4 JUNE 1993  
APPLICATION NUMBER: US 08/200,947  
FILING DATE: 23 FEB 1994  
APPLICATION NUMBER: US 07/864,805  
FILING DATE: 7 APR 1992  
APPLICATION NUMBER: US 08/247,505  
FILING DATE: 23 MAY 1994  
APPLICATION NUMBER: US 07/864,866  
FILING DATE: 7 APR 1992  
APPLICATION NUMBER: US 08/218,155  
FILING DATE: 25 MAR 1994  
APPLICATION NUMBER: US 07/864,807  
FILING DATE: 7 APR 1992  
APPLICATION NUMBER: US 07/902,467  
FILING DATE: 16 JUNE 1992  
APPLICATION NUMBER: US 07/275,433  
FILING DATE: 23 NOV 1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragoras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: RPI-002CP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 742-4214  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 227 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-350-202-6  
Query Match 100.0%; Score 95; DB 3; Length 227;  
Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 PKKDVLFTFTVKSCPDAl 18  
Db 167 PKKDVLFTFTVKSCPDAl 184  
RESULT 7  
US-10-390-330-6  
Sequence 6, Application US/10390330  
Publication No. US20040001829A1  
GENERAL INFORMATION:  
APPLICANT: June, Carl H.  
APPLICANT: Thompson, Craig B.  
APPLICANT: Nabel, Gary J.

APPLICANT: Gray, Gary S.  
APPLICANT: Remert, Paul D.  
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation  
FILE OF INVENTION: Of T-Cells  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/390,330  
FILING DATE: March 17, 2003  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/435,816A  
FILING DATE: May 4, 1995  
CLASSIFICATION:  
APPLICATION NUMBER: US 08/403,253  
FILING DATE: 10 MARCH 1995  
APPLICATION NUMBER: US 08/253,964  
FILING DATE: 3 JUNE 1994  
APPLICATION NUMBER: US 08/073,223  
FILING DATE: 4 JUNE 1993  
APPLICATION NUMBER: US 08/200,947  
FILING DATE: 23 FEB 1994  
APPLICATION NUMBER: US 07/864,805  
FILING DATE: 7 APR 1992  
APPLICATION NUMBER: US 08/247,505  
FILING DATE: 23 MAY 1994  
APPLICATION NUMBER: US 07/864,866  
FILING DATE: 7 APR 1992  
APPLICATION NUMBER: US 08/218,155  
FILING DATE: 25 MAR 1994  
APPLICATION NUMBER: US 07/864,807  
FILING DATE: 7 APR 1992  
APPLICATION NUMBER: US 07/902,467  
FILING DATE: 16 JUNE 1992  
APPLICATION NUMBER: US 07/275,433  
FILING DATE: 23 NOV 1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: RPI-002CP3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 227 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-10-390-330-6

Query Match 100.0%; Score 95; DB 4; Length 227;  
Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLETFVTKSCPDAl 18  
|||||  
Db 167 PKKDVLETFVTKSCPDAl 184

RESULT 8  
US-10-473-127-1723

Sequence 1723, Application US/10473127  
Publication No. US20040236091A1  
GENERAL INFORMATION:  
APPLICANT: Zycos Inc.  
FILE OF INVENTION: TRANSLATIONAL PROFILING  
FILE REFERENCE: 08191-026WO1  
CURRENT APPLICATION NUMBER: US/10/473,127  
CURRENT FILING DATE: 2003-09-26  
PRIOR APPLICATION NUMBER: 60/279,495  
PRIOR FILING DATE: 2001-03-28  
PRIOR APPLICATION NUMBER: 60/292,544  
PRIOR FILING DATE: 2001-05-21  
PRIOR APPLICATION NUMBER: 60/310,801  
PRIOR FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: 60/326,370  
PRIOR FILING DATE: 2001-10-01  
PRIOR APPLICATION NUMBER: 60/336,780  
PRIOR FILING DATE: 2001-12-04  
PRIOR APPLICATION NUMBER: 60/358,985  
PRIOR FILING DATE: 2002-02-20  
NUMBER OF SEQ ID NOS: 2041  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1723  
LENGTH: 227  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-473-127-1723

Query Match 100.0%; Score 95; DB 5; Length 227;  
Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLETFVTKSCPDAl 18  
|||||  
Db 167 PKKDVLETFVTKSCPDAl 184

## RESULT 9

US-10-473-127-1726  
Sequence 1726, Application US/10473127  
Publication No. US20040236091A1  
GENERAL INFORMATION:  
APPLICANT: Zycos Inc.  
FILE OF INVENTION: TRANSLATIONAL PROFILING  
FILE REFERENCE: 08191-026WO1  
CURRENT APPLICATION NUMBER: US/10/473,127  
CURRENT FILING DATE: 2003-09-26  
PRIOR APPLICATION NUMBER: 60/279,495  
PRIOR FILING DATE: 2001-03-28  
PRIOR APPLICATION NUMBER: 60/292,544  
PRIOR FILING DATE: 2001-05-21  
PRIOR APPLICATION NUMBER: 60/310,801  
PRIOR FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: 60/326,370  
PRIOR FILING DATE: 2001-10-01  
PRIOR APPLICATION NUMBER: 60/336,780  
PRIOR FILING DATE: 2001-12-04  
PRIOR APPLICATION NUMBER: 60/358,985  
PRIOR FILING DATE: 2002-02-20  
NUMBER OF SEQ ID NOS: 2041  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1726  
LENGTH: 227  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-473-127-1726

Query Match 100.0%; Score 95; DB 5; Length 227;  
Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLETFVTKSCPDAl 18  
|||||

Db 167 PKDVLFTFTVKSCPDAl 184

RESULT 10  
US-10-156-136-39  
; Sequence 39, Application US/10156136  
; Publication No. US20030129696A1  
; GENERAL INFORMATION:  
; APPLICANT: Ni, et al.  
; TITLE OF INVENTION: Polynucleotides and Polypeptides Encoding Receptors  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Ave  
; CITY: Rockville  
; STATE: MD  
; COUNTRY: US  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/156,136  
; FILING DATE: 29-May-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/010,146  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: WO US98/00959  
; FILING DATE: 21-JAN-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: A. Anders Brookes  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PF354PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 301-309-8504  
; TELEFAX: 301-309-8439  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 228 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
US-10-156-136-39

Query Match 100.0%; Score 95; DB 4; Length 228;  
Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKDVLFTFTVKSCPDAl 18  
DB 168 PKDVLFTFTVKSCPDAl 185

RESULT 11  
US-10-331-496A-41  
; Sequence 41, Application US/10331496A  
; Publication No. US20030228305A1  
; GENERAL INFORMATION:  
; APPLICANT: FRANTZ, GRETCHEN  
; APPLICANT: HILLAN, KENNETH J.  
; APPLICANT: PHILLIPS, HEIDI S.  
; APPLICANT: POLAKIS, PAUL  
; APPLICANT: SMITH, VICTORIA  
; APPLICANT: SPENCER, SUSAN D.  
; APPLICANT: WILLIAMS, P. MICKEY  
; APPLICANT: WO, THOMAS D.  
; APPLICANT: ZHANG, ZEMIN

Query Match 100.0%; Score 95; DB 4; Length 228;  
Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKDVLFTFTVKSCPDAl 18  
DB 168 PKDVLFTFTVKSCPDAl 185

RESULT 12  
US-10-619-323-1  
; Sequence 1, Application US/10619323  
; Publication No. US20040136985A1  
; GENERAL INFORMATION:  
; APPLICANT: Jennings, Lisa K.  
; APPLICANT: Longhurst, Celia M.  
; APPLICANT: Cook, George A.  
; APPLICANT: Bao, Jianxiong  
; APPLICANT: Zhang, Chunxiang  
; APPLICANT: White, Melanie M.  
; APPLICANT: Crosano, Jr., Joseph T.  
; APPLICANT: Lu, Yi  
; TITLE OF INVENTION: METHODS OF MODIFYING BEHAVIOR OF CD9-EXPRESSING CELLS  
; FILE REFERENCE: 20609/241  
; CURRENT APPLICATION NUMBER: US/10/619,323  
; CURRENT FILING DATE: 2003-07-14  
; PRIOR APPLICATION NUMBER: 60/395,864  
; PRIOR FILING DATE: 2002-07-12  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 228  
; TYPE: PRT  
; ORGANISM: Homosapien  
US-10-619-323-1

Query Match 100.0%; Score 95; DB 4; Length 228;  
Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKDVLFTFTVKSCPDAl 18  
DB 168 PKDVLFTFTVKSCPDAl 185

US-10-331-496A-41

Query Match 100.0%; Score 95; DB 4; Length 228;  
Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKDVLFTFTVKSCPDAl 18  
DB 168 PKDVLFTFTVKSCPDAl 185

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RESULT 13
US-10-794-899-97
; Sequence 97, Application US/10794899
; Publication No. US20040146516A1
; GENERAL INFORMATION:
; APPLICANT: Utah Ventures
; TITLE OF INVENTION: Lumen-Exposed Molecules and Methods Targeted Delivery
; FILE REFERENCE: 27110-715
; CURRENT APPLICATION NUMBER: US/10/794,899
; CURRENT FILING DATE: 2004-03-05
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 97
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-794-899-97
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Query Match      100.0%; Score 95; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 PKKDVLETFVKSCPDAl 18
Db      168 PKKDVLETFVKSCPDAl 185
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RESULT 14
US-10-473-127-1714
; Sequence 1714, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1714
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1714
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Query Match      100.0%; Score 95; DB 5; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      1 PKKDVLETFVKSCPDAl 18
Db      168 PKKDVLETFVKSCPDAl 185
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RESULT 15
US-10-473-127-1715
; Sequence 1715, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
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; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1715
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1715
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Query Match      100.0%; Score 95; DB 5; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 PKKDVLETFVKSCPDAl 18
Db      168 PKKDVLETFVKSCPDAl 185
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Search completed: January 20, 2006, 17:26:39
Job time : 37.2222 secs
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Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:16:18 ; Search time 3.11111 Seconds  
(without alignments)  
58.632 Million cell updates/sec

Title: US-10-619-323-6

Perfect score: 95  
Sequence: 1 PKQVLEFTVKSCPDAl 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 70606 seqs, 10133881 residues

Total number of hits satisfying chosen parameters: 70606

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA\_New.\*  
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2: /cgn2\_6/prodata1/pubpaa/US06\_NEW\_PUB.pep.\*  
3: /cgn2\_6/prodata1/pubpaa/US07\_NEW\_PUB.pep.\*  
4: /cgn2\_6/prodata1/pubpaa/PCT\_NEW\_PUB.pep.\*  
5: /cgn2\_6/prodata1/pubpaa/US09\_NEW\_PUB.pep.\*  
6: /cgn2\_6/prodata1/pubpaa/US10\_NEW\_PUB.pep.\*  
7: /cgn2\_6/prodata1/pubpaa/US11\_NEW\_PUB.pep.\*  
8: /cgn2\_6/prodata1/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	95	100.0	228	6	US-10-821-234-1266
2	43	45.3	364	6	US-10-510-947-2
3	40	42.1	367	6	US-10-467-657-1440
4	38	40.0	959	6	US-10-467-962B-4
5	36.5	38.4	342	6	US-11-129-143-63
6	36	37.9	34	6	US-10-816-768-31
7	36	37.9	98	6	US-10-816-768-42
8	36	37.9	112	7	US-11-082-884-1
9	36	37.9	405	6	US-10-873-528-62
10	36	37.9	645	6	US-10-821-234-1409
11	35.5	37.4	645	6	US-10-763-712A-17
12	35.5	37.4	645	6	US-10-763-712A-105
13	35	36.8	106	7	US-11-008-727-12
14	35	36.8	106	7	US-11-073-222-3
15	35	36.8	129	7	US-11-073-222-2
16	35	36.8	238	7	US-11-008-727-26
17	35	36.8	270	7	US-11-008-727-24
18	35	36.8	289	7	US-11-156-084-108
19	35	36.8	378	7	US-11-152-892-7
20	35	36.8	476	7	US-11-008-727-22
21	35	36.8	509	7	US-11-008-727-16
22	35	36.8	531	7	US-11-008-727-18
23	35	36.8	586	7	US-11-073-112-18
24	35	36.8	662	7	US-11-137-131-2
25	35	36.8	662	7	US-11-137-131-4

26 35 36.8 715 6 US-10-467-657-70 Sequence 70, Appl  
27 35 36.8 715 6 US-10-467-657-3672 Sequence 3672, Ap  
28 35 36.8 1218 7 US-11-052-554A-123 Sequence 123, App  
29 34.5 36.3 130 7 US-11-055-822-690 Sequence 690, App  
30 34.5 36.3 130 7 US-11-055-822-768 Sequence 768, App  
31 34.5 36.3 924 6 US-10-467-657-4290 Sequence 4290, Ap  
32 34 35.8 34 6 US-10-816-768-30 Sequence 30, Appl  
33 34 35.8 98 6 US-10-816-768-41 Sequence 41, Appl  
34 34 35.8 158 6 US-10-821-234-1453 Sequence 1453, Ap  
35 34 35.8 210 7 US-11-103-957-49 Sequence 49, Appl  
36 34 35.8 349 7 US-11-165-024-2 Sequence 2, Appl  
37 34 35.8 383 7 US-11-186-284-183 Sequence 183, App  
38 34 35.8 403 6 US-10-821-234-1490 Sequence 1490, Ap  
39 34 35.8 422 6 US-10-821-234-1313 Sequence 1313, Ap  
40 34 35.8 422 7 US-11-186-284-75 Sequence 75, Appl  
41 34 35.8 467 7 US-11-156-084-115 Sequence 115, App  
42 34 35.8 794 7 US-11-024-959-478 Sequence 478, Appl  
43 34 35.8 870 7 US-11-165-211-48 Sequence 48, Appl  
44 34 35.8 870 7 US-11-165-226-58 Sequence 58, Appl  
45 34 35.8 1616 6 US-10-821-234-1497 Sequence 1497, Ap

#### ALIGNMENTS

RESULT 1  
US-10-821-234-1266  
; Sequence 1266, Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Andarmani, Susan  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
; FILE REFERENCE: 821A  
; CURRENT APPLICATION NUMBER: US/10/821,234  
; CURRENT FILING DATE: 2004-04-07  
; PRIOR APPLICATION NUMBER: US 60/462,047  
; PRIOR FILING DATE: 2003-04-07  
; NUMBER OF SEQ ID NOS: 1704  
; SOFTWARE: pt\_SEQ\_genes Version 1.0  
; SEQ ID NO 1266  
; LENGTH: 228  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-821-234-1266

Query Match 100.0%; Score 95; DB 6; Length 228;  
Best Local Similarity 100.0%; Pred. No. 3.6e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQVLEFTVKSCPDAl 18  
DB 168 PKQVLEFTVKSCPDAl 185

#### RESULT 2

US-10-510-947-2  
; Sequence 2, Application US/10510947  
; Publication No. US20050255123A1  
; GENERAL INFORMATION:  
; APPLICANT: The Trustees of the University of Pennsylvania  
; APPLICANT: Wilson, James M.  
; APPLICANT: Medina, Maria Fe C.  
; APPLICANT: Kobinger, Gary  
; TITLE OF INVENTION: Chimeric Ebola Virus Envelopes and Uses Therefor  
; FILE REFERENCE: UPN-02811PCT  
; CURRENT APPLICATION NUMBER: US/10/510,947  
; CURRENT FILING DATE: 2004-10-28  
; PRIOR APPLICATION NUMBER: US 60/376,480  
; PRIOR FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/385,704

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; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/427,752
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Ebola virus
US-10-510-947-2

Query Match      45.3%; Score 43; DB 6; Length 364;
Best Local Similarity 69.2%; Pred. No. 4.1;
Matches 9; Conservative 0; Mismatches 4; Indels 4; Gaps 0;

QY 2 KKDVLFTFTVKSC 14
   |||||
Db 294 KNTSLEKFAVKSC 306

RESULT 3
US-10-467-657-1440
; Sequence 1440, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1440
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1440

Query Match      42.1%; Score 40; DB 6; Length 367;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 8; Conservative 3; Mismatches 5; Indels 5; Gaps 0;

QY 1 PKKDVLFTFTVKSCPD 16
   |:|||:|:|:|
Db 197 PKRTVLELFLKLNPD 212

RESULT 4
US-10-467-962B-4
; Sequence 4, Application US/10467962B
; Publication No. US20050246784A1
; GENERAL INFORMATION:
; APPLICANT: Plesch, Gunnar
; APPLICANT: Blau, Astrid
; APPLICANT: Daeschner, Klaus
; APPLICANT: Klein, Mathieu
; TITLE OF INVENTION: Identification of Herbicidally Active Substances
; FILE REFERENCE: 2000 857
; CURRENT APPLICATION NUMBER: US/10/467,962B
; CURRENT FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: PCT/EP02/01466
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn Vers. 2.0
; SEQ ID NO 4
; LENGTH: 959
; TYPE: PRT

; ORGANISM: Arabidopsis thaliana
US-10-467-962B-4

Query Match      40.0%; Score 38; DB 6; Length 959;
Best Local Similarity 80.0%; Pred. No. 84;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18
   |||||
Db 840 FTKSVDPDAI 849

RESULT 5
US-11-129-143-63
; Sequence 63, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBELIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Rickettsia prowazekii
US-11-129-143-63

Query Match      38.4%; Score 36.5; DB 7; Length 342;
Best Local Similarity 50.0%; Pred. No. 48;
Matches 8; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY 2 KKDVLFTFTVKSC-CPD 16
   ||:||||:|
Db 106 KPDTIKTFTVRHVAPD 121

RESULT 6
US-10-816-768-31
; Sequence 31, Application US/10816768
; Publication No. US20050250936A1
; GENERAL INFORMATION:
; APPLICANT: Oppermann, Hermann
; APPLICANT: Tai, Mei-Sheng
; APPLICANT: McCartney, John
; TITLE OF INVENTION: Modified TGF-beta Superfamily Proteins
; FILE REFERENCE: STK-075
; CURRENT APPLICATION NUMBER: US/10/816,768
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 31
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: TGF-Beta3
US-10-816-768-31

Query Match      37.9%; Score 36; DB 6; Length 34;
Best Local Similarity 50.0%; Pred. No. 4.6;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKKDVLFTFTVKSC 14
   ||:|
Db 18 PRVEQLSNMVKSC 31
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	US-10-816-768-42	PRIOR APPLICATION NUMBER: US/09/769,787
	; Sequence 42, Application US/10816768	PRIOR FILING DATE: 2001-01-26
	; Publication No. US20050250936A1	PRIOR APPLICATION NUMBER: GB 9816337.1
	; GENERAL INFORMATION:	PRIOR FILING DATE: 1998-03-27
	; APPLICANT: Oppermann, Hermann	PRIOR APPLICATION NUMBER: US 60/125164
	; APPLICANT: Tai, Mei-Sheng	PRIOR FILING DATE: 1999-03-19
	; APPLICANT: McCartney, John	NUMBER OF SEQ ID NOS: 388
	; FILE REFERENCE: STK-075	SOFTWARE: PatentIn ver. 2.1
	; CURRENT APPLICATION NUMBER: US/10/816,768	SEQ ID NO 62
	; CURRENT FILING DATE: 2004-04-02	LENGTH: 405
	; NUMBER OF SEQ ID NOS: 124	TYPE: PRT
	; SOFTWARE: PatentIn version 2.0	ORGANISM: Streptococcus pneumoniae
	; SEQ ID NO 42	US-10-873-528-62
	; LENGTH: 98	
	; TYPE: PRT	
	; ORGANISM: Homo sapiens	
	; FEATURE:	
	; OTHER INFORMATION: TGF-Beta3	
	US-10-816-768-42	
	Query Match	37.9%; Score 36; DB 6; Length 98;
	Best Local Similarity	50.0%; Pred. No. 15;
	Matches	7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
	QY	1 PKDVLFTFTVKSC 14
	DB	82 PKVEQLSNWVWSC 95
	RESULT 8	
	US-11-082-884-1	
	; Sequence 1, Application US/11082884	
	; Publication No. US2005027636A1	
	; GENERAL INFORMATION:	
	; APPLICANT: ROBERTSON, Sarah et al.	
	; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF A REPRODUCTIVE DISORDER BY MEASURING	
	; FILE REFERENCE: 0641-0269PUS1	
	; CURRENT APPLICATION NUMBER: US/11/082,884	
	; CURRENT FILING DATE: 2005-03-18	
	; NUMBER OF SEQ ID NOS: 13	
	; SOFTWARE: PatentIn version 3.3	
	; SEQ ID NO 1	
	; LENGTH: 112	
	; TYPE: PRT	
	; ORGANISM: Homo sapiens	
	US-11-082-884-1	
	Query Match	37.9%; Score 36; DB 7; Length 112;
	Best Local Similarity	50.0%; Pred. No. 17;
	Matches	7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
	QY	1 PKDVLFTFTVKSC 14
	DB	96 PKVEQLSNWVWSC 109
	RESULT 9	
	US-10-873-528-62	
	; Sequence 62, Application US/10873528	
	; Publication No. US2005027681A1	
	; GENERAL INFORMATION:	
	; APPLICANT: Microbial Technics Limited	
	; APPLICANT: Gilbert, Christophe FG	
	; APPLICANT: Hanabro, Philip M	
	; TITLE OF INVENTION: Proteins	
	; FILE REFERENCE: PWC/P21129WO	
	; CURRENT APPLICATION NUMBER: US/10/873,528	
	; CURRENT FILING DATE: 2004-06-23	

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; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 645
; TYPE: PRT
; ORGANISM: Thermotoga maritima
US-10-763-712A-17

Query Match      37.4%; Score 35.5; DB 6; Length 645;
Best Local Similarity 45.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 4; Mismatches 4; Indels 3; Gaps 1;

QY      2 KKDVLFTFKVSC---PDAI 18
Db      604 KIEVLGTCVNGGASPNVI 623

RESULT 12
US-10-763-712A-105
; Sequence 105, Application US/10763712A
; Publication No. US20050266541A1
; GENERAL INFORMATION:
; APPLICANT: Solazyme, Inc.
; TITLE OF INVENTION: Methods and Compositions for Evolving Microbial Hydrogen
; TITLE OF INVENTION: Production
; FILE REFERENCE: H2042101-CIP
; CURRENT APPLICATION NUMBER: US/10/763,712A
; CURRENT FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: US 10/287,750
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 10/411,910
; PRIOR FILING DATE: 2003-04-12
; PRIOR APPLICATION NUMBER: US 60/500,032
; PRIOR FILING DATE: 2003-09-03
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 105
; LENGTH: 645
; TYPE: PRT
; ORGANISM: T. maritima
US-10-763-712A-105

Query Match      37.4%; Score 35.5; DB 6; Length 645;
Best Local Similarity 45.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 4; Mismatches 4; Indels 3; Gaps 1;

QY      2 KKDVLFTFKVSC---PDAI 18
Db      604 KIEVLGTCVNGGASPNVI 623

RESULT 13
US-11-008-727-12
; Sequence 12, Application US/11008727
; Publication No. US20050250185A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Andrew J.
; APPLICANT: Macdonald, Lynn
; APPLICANT: Sleeman, Mark W.
; TITLE OF INVENTION: OGH Fusion Polypeptides and Therapeutic
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 2010A
; CURRENT APPLICATION NUMBER: US/11/008,727
; CURRENT FILING DATE: 2004-12-09
; PRIOR APPLICATION NUMBER: US 60/529,036
; PRIOR FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: US 60/548,415
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 106

; TYPE: PRT
; ORGANISM: homo sapiens
US-11-008-727-12

Query Match      36.8%; Score 35; DB 7; Length 106;
Best Local Similarity 38.5%; Pred. No. 24;
Matches 5; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY      2 KKDVLFTFKVSC 14
Db      84 RREELEIFTARAC 96

RESULT 14
US-11-073-222-3
; Sequence 3, Application US/11073222
; Publication No. US20050272635A1
; GENERAL INFORMATION:
; APPLICANT: KELLY, JAMES D.
; TITLE OF INVENTION: USE OF CORTICOTROPH-DERIVED
; TITLE OF INVENTION: GLYCOPROTEIN HORMONE TO TREAT LIVER STEATOSIS
; FILE REFERENCE: 04-02
; CURRENT APPLICATION NUMBER: US/11/073,222
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 60/550,623
; PRIOR FILING DATE: 2004-03-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-222-3

Query Match      36.8%; Score 35; DB 7; Length 106;
Best Local Similarity 38.5%; Pred. No. 24;
Matches 5; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY      2 KKDVLFTFKVSC 14
Db      84 RREELEIFTARAC 96

RESULT 15
US-11-073-222-2
; Sequence 2, Application US/11073222
; Publication No. US20050272635A1
; GENERAL INFORMATION:
; APPLICANT: KELLY, JAMES D.
; TITLE OF INVENTION: USE OF CORTICOTROPH-DERIVED
; TITLE OF INVENTION: GLYCOPROTEIN HORMONE TO TREAT LIVER STEATOSIS
; FILE REFERENCE: 04-02
; CURRENT APPLICATION NUMBER: US/11/073,222
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 60/550,623
; PRIOR FILING DATE: 2004-03-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-222-2

Query Match      36.8%; Score 35; DB 7; Length 129;
Best Local Similarity 38.5%; Pred. No. 30;
Matches 5; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY      2 KKDVLFTFKVSC 14
Db      107 RREELEIFTARAC 119
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Search completed: January 20, 2006, 17:27:03  
Job time : 3.11111 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2006, 17:06:32 ; Search time 12.6667 Seconds  
(without alignments)  
136.729 Million cell updates/sec

Title: US-10-619-323-6

Perfect score: 95

Sequence: 1 PKKDVLETFVKCPDAI 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 80:\*

2: pir1:\*

3: pir2:\*

4: pir3:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	100.0	228	1 A40402	CD9 antigen [valid
2	94	98.9	228	1 A42929	CD9 antigen - gre
3	79	83.2	226	1 S3262	CD9 antigen - rat
4	67	70.5	226	2 I49589	antigen - mouse
5	48	50.5	1057	2 T15720	hypothetical prote
6	47	49.5	159	2 AE2547	hypothetical prote
7	47	49.5	1020	2 S05944	neuronal cell surf
8	47	49.5	1021	2 A57112	contactin precurs
9	44	46.3	226	1 JX0221	CD9 antigen - bovi
10	44	46.3	402	2 D70602	probable arginine
11	43	45.3	399	2 T16634	hypothetical prote
12	42	44.2	92	2 A98054	ferredoxin [import
13	42	44.2	581	2 G71520	proline-tRNA ligas
14	42	44.2	630	2 A49556	estrogen-responsiv
15	41.5	43.7	1980	2 S54307	myosin heavy chain
16	41	43.2	68	2 H95186	ferredoxin [import
17	41	43.2	220	2 T26518	hypothetical prote
18	41	43.2	342	2 T08837	probable gamma-glu
19	41	43.2	398	2 JC4254	ribosomal protein
20	41	43.2	439	2 F83746	hypothetical prote
21	41	43.2	1018	2 JC4211	neural adhesion pr
22	41	43.2	1217	2 T13996	pol protein - frui
23	40.5	42.6	244	2 T41676	hypothetical prote
24	40	42.1	336	2 JC4102	hypothetical prote
25	40	42.1	367	2 AB1974	probable DNA-direc
26	40	42.1	367	2 C81030	DNA polymerase III
27	40	42.1	439	2 T29587	hypothetical prote
28	40	42.1	823	2 T29644	hypothetical prote
29	40	42.1	836	2 B96716	probable serine/th

30	40	42.1	1160	2 T31688	Ca2+-transporting
31	40	42.1	1905	2 I51553	Plexin - African c
32	40	42.1	3396	2 T22613	hypothetical prote
33	39	41.1	64	2 H91000	hypothetical prote
34	39	41.1	64	2 B90779	hypothetical prote
35	39	41.1	175	2 F82486	conserved hypothet
36	39	41.1	201	2 B90114	hypothetical prote
37	39	41.1	211	2 B84066	hypothetical prote
38	39	41.1	274	2 B70020	conserved hypothet
39	39	41.1	294	2 G87366	enoyl-CoA hydratase
40	39	41.1	329	2 D86329	Fl4Pl.1 protein -
41	39	41.1	340	2 E72739	conserved hypothet
42	39	41.1	343	2 H84607	hypothetical prote
43	39	41.1	521	2 T01923	hypothetical prote
44	39	41.1	573	2 T48584	auxin-regulated pr
45	39	41.1	798	2 F98134	hypothetical prote

ALIGNMENTS

RESULT 1

A40402

CD9 antigen [validated] - human

N:Alternate names: motility-related protein-1

C:Species: Homo sapiens (man)

C>Date: 06-Dec-1991 #sequence revision 07-Jul-1995 #text\_change 09-Jul-2004

C:Accession: A46123, A40402; JH0555; A39029; S10564

R:Rubinstein, E.; Benoist, P.; Billard, M.; Plaisance, S.; Prenant, M.; Uzan, G.; Bouche

Genomics 16, 132-138, 1993

A:Title: Organization of the human CD9 gene.

A:Reference number: A46123; MUID:93252369; PMID:8486348

A:Accession: A46123

A:Molecule type: DNA

A:Residues: 1-228 <RUB>

A:Cross-references: UNIPROT:P21926; UNIPARC:UPI00003B45A; GB:S60489; NID:G300112; PIDN

A:Experimental source: leukocyte

A>Note: sequence extracted from NCBI backbone (NCBIN:131318, NCBIN:131326, NCBIN:131328,

R:Lanza, P.; Wolf, D.; Fox, C.F.; Kieffer, N.; Seyer, J.M.; Fried, V.A.; Coughlin, S.R.,

J. Biol. Chem. 266, 10638-10645, 1991

A:Title: CDNA cloning and expression of platelet p24/CD9. Evidence for a new family of

A:Reference number: A40402; MUID:91244846; PMID:2037603

A:Accession: A40402

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-228 <LAN>

A:Cross-references: UNIPARC:UPI000003B45A; GB:L34068; GB:M61880; NID:G508495; PIDN:AAA5

A>Note: parts of this sequence, including the amino end of the mature protein, were con

R:Miyake, M.; Koyama, M.; Seno, M.; Ikegawa, S.

J. Exp. Med. 174, 1347-1354, 1991

A:Title: Identification of the motility-related protein (MRP-1), recognized by monoclon.

A:Reference number: JH0555; MUID:92078843; PMID:1720807

A:Accession: JH0555

A:Molecule type: mRNA

A:Residues: 1-228 <MIY>

A:Cross-references: UNIPARC:UPI000003B45A; GB:X60111; NID:G34768; PIDN:CAA42708.1; PID

A:Experimental source: breast carcinoma

A>Note: this protein has the epitope defined by cell motility-inhibiting monoclonal ant

R:Bouchaix, C.; Benoist, P.; Frachet, P.; Billard, M.; Worthington, R.E.; Gagnon, J.; Uz

J. Biol. Chem. 266, 117-122, 1991

A:Title: Molecular cloning of the CD9 antigen. A new family of cell surface proteins.

A:Reference number: A39029; MUID:91093112; PMID:1840589

A:Accession: A39029

A:Molecule type: mRNA

A:Residues: 1-8, 'S', 10-66, 'A', 68-193, 195-228 <BOU>

A:Cross-references: UNIPARC:UPI000017414B; GB:M38690

A>Note: parts of this sequence, including the amino end of the mature protein, were con

R:Higashihara, M.; Takahata, K.; Yatomi, Y.; Nakahara, K.; Kurokawa, K.

FEBS Lett. 264, 270-274, 1990

A:Title: Purification and partial characterization of CD9 antigen of human platelets.

A:Reference number: S10564; MUID:90292223; PMID:2358073

A:Accession: S10564

A:Molecule type: protein



```

Qy      1 PKDVLSTFTVKSCP 15
      |  |  |  |  |  |  |
Db      893 PSSDVIETFTRKAPP 907

RESULT 8
A57112
contactin precursor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jan-2000
C/Accession: A57112
R/Peles, E.; Nativ, M.; Campbell, P.L.; Sakurai, T.; Martinez, R.; Lev, S.; Clary, D.O.
Cell 82, 251-260, 1995
A/Title: The carbonic anhydrase domain of receptor tyrosine phosphatase beta is a func-
A/Reference number: A57112; MUID:95354206; PMID:7628014
A/Accession: A57112
A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr.
A/Molecule type: mRNA
A/Residues: 1-1021 <PEL>
A/Cross-references: UNIPARC:UPI0000178925
C/Superfamily: contactin; fibronectin type III repeat homology; immunoglobulin homology
C/Keywords: membrane protein; phosphatidylinositol linkage
F/256-312/Domain: immunoglobulin homology <IMM>

Query Match      49.5%; Score 47; DB 2; Length 1021;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      1 PKDVLSTFTVKSCP 15
      |  |  |  |  |  |  |
Db      893 PSSDVIETFTRKAPP 907

RESULT 9
JX0221
CD9 antigen - bovine
C/Species: Bos primigenius taurus (cattle)
C/Date: 09-Oct-1992 #sequence_revision 09-Aug-1996 #text_change 09-Jul-2004
C/Accession: JX0221
R/Martin-Alonso, J.M.; Hernando, N.; Ghosh, S.; Coca-Prados, M.
J. Biochem. 112, 63-67, 1992
A/Title: Molecular cloning of the bovine CD9 antigen from ocular ciliary epithelial cel
A/Reference number: JX0221; MUID:93054422; PMID:1339429
A/Accession: JX0221
A/Molecule type: mRNA
A/Residues: 1-226 <WAR>
A/Cross-references: UNIPROT:P30932; UNIPARC:UPI0000167C21; GB:M81720; NID:g162820; PIDN
A/Experimental source: ocular ciliary epithelial cell
C/Superfamily: CD9 antigen
C/Keywords: glycoprotein; transmembrane protein
F/2-226/Product: CD9 antigen #status predicted <MAT>
F/2-11/Domain: intracellular #status predicted <CV1>
F/12-55/Domain: transmembrane #status predicted <TM1>
F/36-53/Domain: extracellular #status predicted <EX1>
F/54-76/Domain: transmembrane #status predicted <TM2>
F/77-80/Domain: intracellular #status predicted <CY2>
F/81-109/Domain: transmembrane #status predicted <TM3>
F/110-192/Domain: extracellular #status predicted <EX2>
F/193-219/Domain: transmembrane #status predicted <TM4>
F/220-226/Domain: intracellular #status predicted <CY3>
F/50/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      46.3%; Score 44; DB 1; Length 226;
Best Local Similarity 33.3%; Pred. No. 14;
Matches 6; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy      1 PKDVLSTFTVKSCPDAI 18
      |  |  |  |  |  |  |
Db      166 PPKVLIDSLKTRCPDAI 183

RESULT 10
D70602

```

probable arginine deiminase - Mycobacterium tuberculosis (strain H37RV)  
C:Species: Mycobacterium tuberculosis  
C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004  
C:Accession: D70602  
R: Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, K.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A:Reference number: A70500; MUID:98295987; PMID:9634230  
A:Accession: D70602  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-402 <COL>  
A:Cross-references: UNIPROT:O05585; UNIPARC:UPI0000125D93; GB:Z94752; GB:AL123456; NID:9  
A:Experimental source: strain H37RV  
C:Genetics:  
A:Gene: arca  
C:Superfamily: arginine deiminase arca

Query Match 46.3%; Score 44; DB 2; Length 402;  
Best Local Similarity 46.7%; Pred. NO. 25;  
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 4 DVLEFTTVKSCPDAl 18  
DB 289 DTLEAFTIQTPDGV 303

RESULT 11  
T16634  
hypothetical protein M02F4.1 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: T16634  
R: Wu, X.  
submitted to the EMBL Data Library, November 1995  
A:Description: The sequence of C. elegans cosmid M02F4.  
A:Reference number: Z18550  
A:Accession: T16634  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-399 <WUX>  
A:Cross-references: UNIPROT:Q21472; UNIPARC:UPI000007B6B2; EMBL:U41548; NID:g1109912; PI  
C:Genetics:  
A:Gene: CBSP:M02F4.1  
A:Introns: 50/3; 234/3; 298/3; 336/1; 381/3

Query Match 45.3%; Score 43; DB 2; Length 399;  
Best Local Similarity 45.0%; Pred. NO. 36;  
Matches 9; Conservative 3; Mismatches 6; Indels 2; Gaps 1;

QY 1 PKKDVLLE--TFTVKSCPDAl 18  
DB 274 PKREVLDLPPLCPDCPDGI 293

RESULT 12  
A98054  
ferredoxin [imported] - Streptococcus pneumoniae (strain R6)  
C:Species: Streptococcus pneumoniae  
C:Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 09-Jul-2004  
C:Accession: A98054  
R: Hoskins, J.A.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; B  
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M  
y, P.; Sun, P.M.; Winkler, M.E.  
J. Bacteriol. 183, 5703-5717, 2001  
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;  
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.  
A:Reference number: A97872; MUID:21429245; PMID:11544234  
A:Accession: A98054  
A:Status: preliminary

A:Molecule type: DNA  
A:Residues: 1-92 <KUR>  
A:Cross-references: UNIPROT:Q8DNY8; UNIPARC:UPI00000E3668; GB:AE007317; PIDN:AAL00262.1  
C:Genetics:  
A:Gene: fer

Query Match 44.2%; Score 42; DB 2; Length 92;  
Best Local Similarity 60.0%; Pred. NO. 13;  
Matches 9; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 1 PKKDVLFTTVKSCP 15  
DB 70 FSDQVLE--AVKNCP 82

RESULT 13  
G71520  
proline-tRNA ligase (EC 6.1.1.15) - Chlamydia trachomatis (serotype D, strain UW3/Cx)  
C:Species: Chlamydia trachomatis  
C:Date: 13-Sep-1998 #sequence\_revision 13-Sep-1998 #text\_change 09-Jul-2004  
C:Accession: G71520  
R: Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,  
Science 282, 754-759, 1998  
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tra  
A:Reference number: A71570; MUID:99000809; PMID:9784136  
A:Accession: G71520  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-581 <ARN>  
A:Cross-references: UNIPROT:P36431; UNIPARC:UPI0000136607; GB:AE001312; GB:AE001273; NID  
A:Experimental source: serotype D, strain UW-3/Cx  
C:Genetics:  
A:Gene: pros  
C:Superfamily: proline-tRNA ligase  
C:Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 44.2%; Score 42; DB 2; Length 581;  
Best Local Similarity 50.0%; Pred. NO. 74;  
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 PKKDVLFTTVKSC 14  
DB 273 PKHKILKTLVVKTC 286

RESULT 14  
A49656  
estrogen-responsive finger protein, efp (RING finger, coiled-coil domains) - human  
C:Species: Homo sapiens (man)  
C:Date: 07-Apr-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C:Accession: A49656  
R: Inoue, S.; Orimo, A.; Hosoi, T.; Kondo, S.; Toyoshima, H.; Kondo, T.; Ikegami, A.; Ouc  
Proc. Natl. Acad. Sci. U.S.A. 90, 11117-11121, 1993  
A:Title: Genomic binding-site cloning reveals an estrogen-responsive gene that encodes a  
A:Reference number: A49656; MUID:94068555; PMID:8248217  
A:Accession: A49656  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-630 <INO>  
A:Cross-references: UNIPROT:Q14258; UNIPARC:UPI000000D9E6; GB:D21205; NID:g458725; PIDN  
A:Experimental source: placenta  
A:Note: sequence extracted from NCBI backbone (NCBIN:140455, NCBIP:140456)  
C:Superfamily: rfp transforming protein  
C:Keywords: zinc  
P:9-59/Domain: RING finger homology <RNG>

Query Match 44.2%; Score 42; DB 2; Length 630;  
Best Local Similarity 52.9%; Pred. NO. 80;  
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 KKDVLFTTVKSCPDAl 18  
DB 437 KAKVLETFKSRPELL 453



```

RESULT 15
S54307
myosin heavy chain - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S54307
R;Reinhard, J.; Scheel, A.A.; Diekmann, D.; Hall, A.; Ruppert, C.; Baehler, M.
EMBO J. 14, 697-704, 1995
A;Title: A novel type of myosin implicated in signalling by rho family GTPases.
A;Reference number: S54307; MUID:95188874; PMID:7882973
A;Accession: S54307
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1980 <REI>
A;Cross-references: UNIPROT:Q63359; UNIPARC:UPI000012PAD6; EMBL:X77609; NID:9639998; PID
C;Superfamily: rat myosin heavy chain; myosin motor domain homology; protein kinase C zeta
C;Keywords: nucleotide binding; P-loop
F;149-942/Domain: myosin motor domain homology <MMOT>
F;239-246/Region: nucleotide-binding motif A (P-loop)
F;1593-1641/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match 43.7%; Score 41.5; DB 2; Length 1980;
Best Local Similarity 42.9%; Pred. No. 2.8e+02;
Matches 9; Conservative 4; Mismatches 5; Indels 3; Gaps 1;

QY 1 PKKDVLETTT---VKSCPDAI 18
Db 1191 FREDGLETTWTAAAPCPKQV 1211

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Search completed: January 20, 2006, 17:22:38  
Job time : 13.6667 secs

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OM protein - protein search, using sw model

Run on: January 20, 2006, 17:05:21 ; Search time 68.4444 Seconds  
(without alignments)  
185.545 Million cell updates/sec

Title: US-10-619-323-6  
Perfect score: 95  
Sequence: 1 PKKDVLETFVKSCPDAL 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	100.0	227	1	CD9 HUMAN
2	95	100.0	228	2	Q5J7W6 homo sapien
3	94	98.9	227	1	CD9 CERAE
4	79	83.2	225	1	CD9 RAT
5	67	70.5	225	1	CD9 MOUSE
6	66	69.5	225	1	CD9 FELCA
7	63	66.3	227	2	Q6NWG7 BRARE
8	62	65.3	227	2	Q4RWM0 TETNG
9	58	61.1	226	2	Q8MJ48 PIG
10	55	57.9	225	1	CD9 PIG
11	53.5	56.3	398	2	Q6OKA7 CABER
12	52	54.7	224	2	Q91BC9 CHICK
13	49.5	52.1	218	2	Q851Q5 ORYSA
14	48	50.5	144	2	Q5Y296 NOCPA
15	48	50.5	694	2	Q9SDY4 PETCR
16	48	50.5	1057	2	Q18331 CABEL
17	47	49.5	159	2	Q8ZS48 ANASP
18	47	49.5	1020	1	CNTN1 MOUSE
19	47	49.5	1021	1	CNTN1 RAT
20	46	48.4	178	2	Q46130 LEUMA
21	46	48.4	262	1	PYRK METKA
22	46	48.4	497	2	Q6B111 DEBHA
23	46	48.4	497	2	Q7RDN7 PLAYO
24	46	48.4	892	2	Q5AT76 EMENI
25	45.5	47.9	236	2	Q7ZTR5 XENLA
26	45	47.4	91	2	Q6OHW9 RAT
27	45	47.4	112	2	Q8EJ87 SHEON
28	45	47.4	150	2	Q5J183 PYRKO
29	45	47.4	331	2	Q8GP11 STAAU
30	45	47.4	365	2	Q51CE4 ENTHI
31	45	47.4	373	2	Q60119 RAT

32	45	47.4	642	2	Q4LOF6 9EUGL	Q4LOF6 ichthyobodo
33	45	47.4	721	2	Q4WCK2 ASPFU	Q4WCK2 aspergillus
34	45	47.4	819	2	Q5BDF5 EMENI	Q5BDF5 aspergillus
35	45	47.4	849	2	Q4WL27 ASPFU	Q4WL27 aspergillus
36	45	47.4	885	2	Q53KP9 ORYSA	Q53KP9 oryza sativ
37	44.5	46.8	308	2	Q6ABBI PROAC	Q6ABBI propionibac
38	44.5	46.8	423	1	PURA BACTN	Q8A6N4 bacteroides
39	44.5	46.8	423	2	Q5LAD5 BACFN	Q5LAD5 bacteroides
40	44.5	46.8	423	2	Q64QR7 BACFR	Q64QR7 bacteroides
41	44.5	46.8	1025	2	Q5CM51 CRYHO	Q5CM51 cryptospori
42	44.5	46.8	1633	2	Q5CKY0 CRYPV	Q5CKY0 cryptospori
43	44	46.3	206	2	Q877D1 9CREN	Q877D1 pyrobaculum
44	44	46.3	225	1	CD9 BOVIN	P30932 bos taurus
45	44	46.3	306	2	Q81KH1 BACAN	Q81KH1 bacillus an

## ALIGNMENTS

RESULT 1

CD9\_HUMAN  
ID CD9\_HUMAN STANDARD; PRT; 227 AA.  
AC P21926; Q96BS4;  
DT 01-MAY-1991 (Rel. 18, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE CD9 antigen (p24) (Leukocyte antigen MIC3) (Motility-related protein) (MRP-1) (tetraspanin-29) (TSPAN-29).  
DB (MRP-1) (tetraspanin-29) (TSPAN-29).  
GN Name=CD9; Synonyms=MIC3, TSPAN29;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 1-4.  
RX MEDLINE=91093112; PubMed=1840589;  
RA Boucheix C., Benoit P., Frachet P., Billard M., Worthington R.E., Gagnon J., Uzan G.;  
RA "Molecular cloning of the CD9 antigen. A new family of cell surface proteins.";  
RL J. Biol. Chem. 266:117-122 (1991).  
RN [2]  
RP NUCLEOTIDE SEQUENCE [MRNA], AND PARTIAL PROTEIN SEQUENCE.  
RX MEDLINE=91244846; PubMed=2037603;  
RA Lanza F., Wolf D., Fox C.F., Kieffer N., Seyer J.M., Fried V.A., Coughlin S.R., Phillips D.R., Jennings L.K.;  
RT "cDNA cloning and expression of platelet p24/CD9. Evidence for a new family of multiple membrane-spanning proteins.";  
RL J. Biol. Chem. 266:10638-10645 (1991).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=92078843; PubMed=1720807; DOI=10.1084/jem.174.6.1347;  
RA Miyake M., Koyama M., Seno M., Ikegawa S.;  
RT "Identification of the motility-related protein (MRP-1), recognized by monoclonal antibody M31-15, which inhibits cell motility.";  
RL J. Exp. Med. 174:1347-1354 (1991).  
RN [4]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RX MEDLINE=93252369; PubMed=8486348;  
RC TISSUE=Leukocyte;  
RA Rubinstein E., Benoit P., Billard M., Plaisance S., Prenant M., Uzan G., Boucheix C.;  
RT "Organization of the human CD9 gene.";  
RL Genomics 16:132-138 (1993).  
RN [5]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RA Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O., Rajkumar N., Yi Q., Nickerson D.A.;  
RT "seattlesnp. NHBI HL66682 program for genomic applications, UW-FHRC, Seattle, WA (URL: http://pga.gs.washington.edu).";  
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
RN [6]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RC TISSUE=Ovary;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smillius D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [17]  
RP PROTEIN SEQUENCE OF 1-20.  
RC TISSUE=Platelet;  
RX MEDLINE=90292223; PubMed=2358073; DOI=10.1016/0014-5793(90)80265-K;  
RA Higashihara M., Takahata K., Yatomi Y., Nakahara K., Kurokawa K.;  
RT "Purification and partial characterization of CD9 antigen of human  
platelets.";  
RL FEBS Lett. 264:270-274(1990).  
RN [8]  
RP ROLE IN CELL MOTILITY AND METASTASIS.  
RX PubMed=8478605; DOI=10.1084/jem.177.5.1231;  
RA Ikegama S., Koyama M., Yamaoka M., Sasada R., Miyake M.;  
RT "Suppression of cell motility and metastasis by transfection with  
human motility-related protein (MRP-1/CD9) DNA.";  
RL J. Exp. Med. 177:1231-1237(1993).  
RN [9]  
RP ROLE IN CELL ADHESION.  
RX PubMed=7511626;  
RA Masellis-Smith A., Shaw A.R.;  
RT "CD9-regulated adhesion. Anti-CD9 monoclonal antibody induce pre-B  
cell adhesion to bone marrow fibroblasts through de novo recognition  
of fibronectin.";  
RL J. Immunol. 152:2768-2777(1994).  
RN [10]  
RP ROLE IN GAMETE FUSION.  
RX PubMed=14575715; DOI=10.1016/j.bbrc.2003.09.196;  
RA Higginbottom A., Takahashi Y., Bolling L., Coonrod S.A., White J.M.,  
RA Partridge L.J., Monk P.N.;  
RT "Structural requirements for the inhibitory action of the CD9 large  
extracellular domain in sperm/oocyte binding and fusion.";  
RL Biochem. Biophys. Res. Commun. 311:208-214(2003).  
RN [11]  
RP SUBUNIT.  
RX PubMed=14556650; DOI=10.1042/BJ20031037;  
RA Kovalevsk O.V., Yang X., Kolesnikova T.V., Hemler M.E.;  
RT "Evidence for specific tetraspanin homodimers: inhibition of  
palmitoylation makes cysteine residues available for cross-linking.";  
RL Biochem. J. 377:407-417(2004).  
RN [12]  
RP PHOSPHORYLATION.  
RX MEDLINE=93327758; PubMed=7687539;  
RA Chalupny N.J., Kanner S.B., Schieven G.L., Wee S., Gilliland L.K.,  
RA Aruffo A., Ledbetter J.A.;  
RT "Tyrosine phosphorylation of CD19 in pre-B and mature B cells.";  
RL EMBO J. 12:2691-2696(1993).  
RN [13]  
RP PALMITOYLATION, AND MUTAGENESIS OF CVS-8; CVS-77; CVS-78; CVS-86;  
CY5-217 AND CVS-218.  
RX PubMed=11959120; DOI=10.1016/S0014-5793(02)02522-X;  
RA Charrin S., Manie S., Oualid M., Billard M., Boucheix C.,  
Rubinstein E.;  
RT "Differential stability of tetraspanin/tetraspanin interactions: role  
of palmitoylation.";  
RL FEBS Lett. 516:139-144(2002).  
RN [14]  
RP INTERACTION WITH PTGFRN.  
RX MEDLINE=21216740; PubMed=11279880; DOI=10.1074/jbc.M011297200;  
RA Charrin S., Le Nour F., Oualid M., Billard M., Faure G., Hanash S.M.,  
RA Boucheix C., Rubinstein E.;  
RT "The major CD9 and CD81 molecular partner. Identification and  
characterization of the complexes.";  
RL J. Biol. Chem. 276:14329-14337(2001).  
CC -!- FUNCTION: Involved in platelet activation and aggregation.  
CC Regulates paranodal junction formation. Required for gamete  
fusion. Involved in cell adhesion, cell motility and tumor  
metastasis.  
CC -!- SUBUNIT: Forms both disulfide-linked homodimers and higher  
homooligomers as well as heterooligomers with other members of the  
tetraspanin family. Associates with CR2/CD21 and with  
PTGFRN/CD9P1.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: Expressed by a variety of hematopoietic and  
epithelial cells.  
CC -!- PTM: Protein exists in three forms with molecular masses between  
22 and 27 kDa, and is known to carry covalently linked fatty  
acids.  
CC -!- PTM: Phosphorylated on tyrosine following B-cell activation.  
CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.  
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between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use as long as its content is in no way modified and this statement is not  
removed.  
CC EMBL; S60489; AACG0586.1; -; Genomic DNA.  
DR EMBL; S60462; AACG0586.1; JOINED; Genomic DNA.  
DR EMBL; S60463; AACG0586.1; JOINED; Genomic DNA.  
DR EMBL; S60464; AACG0586.1; JOINED; Genomic DNA.  
DR EMBL; S60700; AACG0586.1; JOINED; Genomic DNA.  
DR EMBL; S60699; AACG0586.1; JOINED; Genomic DNA.  
DR EMBL; S60465; AACG0586.1; JOINED; Genomic DNA.  
DR EMBL; S60472; AACG0586.1; JOINED; Genomic DNA.  
DR EMBL; M38690; AACG0586.1; -; mRNA.  
DR EMBL; L34068; AACG0586.1; -; mRNA.  
DR EMBL; X60111; CAA42708.1; -; mRNA.  
DR EMBL; L08118; -; NOT ANNOTATED CDS; Genomic DNA.  
DR EMBL; L08119; AAA51954.1; ALT\_SEQ; Genomic DNA.  
DR EMBL; L08120; AAA51955.1; ALT\_SEQ; Genomic DNA.  
DR EMBL; L08121; AAA51956.1; -; Genomic DNA.  
DR EMBL; L08122; AAA51957.1; -; Genomic DNA.  
DR EMBL; L08123; AAA51958.1; -; Genomic DNA.  
DR EMBL; L08124; AAA51959.1; -; Genomic DNA.  
DR EMBL; L08125; -; NOT ANNOTATED CDS; Genomic DNA.  
DR EMBL; AY422198; AAC87878.1; -; Genomic DNA.  
DR EMBL; BC011988; AAH11988.1; -; mRNA.  
DR PIR; A46123; A40402.  
DR Ensembl; ENSG00000010278; Homo sapiens.  
DR HGNC; HGNC:1709; CD9.  
DR H-InvDB; HIX0010357; -.  
DR Reactome; R12926; -.  
DR MIM; 143030; -.  
DR GO; GO:0005887; C:integral to plasma membrane; NAS.  
DR GO; GO:0005886; C:plasma membrane; NAS.  
DR GO; GO:0005515; P:protein binding; IPI.  
DR GO; GO:0007155; P:cell adhesion; IDA.  
DR GO; GO:0006928; P:cell motility; IDA.  
DR GO; GO:0007342; P:fusion of sperm to egg plasma membrane; IDA.  
DR GO; GO:0030913; P:paranodal junction formation; ISS.  
DR GO; GO:0030168; P:platelet activation; NAS.  
DR InterPro; IPR00301; Transmem 4.  
DR Pfam; PF00335; Tetraspanin; I.  
DR PRINTS; PR00259; TMFOUR.

DR PROSITE; PS00421; TM4\_1; 1.  
 KW Antigen; Cell adhesion; Direct protein sequencing; Fertilization;  
 Query Match 100.0%; Score 95; DB 1; Length 227;  
 Best Local Similarity 100.0%; Pred. No. 2e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLETFVKSCPDAl 18  
 |||||  
 DB 167 PKKDVLETFVKSCPDAl 184

RESULT 2  
 Q5J7W6 HUMAN  
 ID Q5J7W6 HUMAN PRELIMINARY; PRT; 228 AA.  
 AC Q5J7W6;  
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
 DE Growth-inhibiting gene 2 protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa;  
 OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Homiidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Kim J. W.;  
 RT "Identification of a human growth inhibition gene 2 (GIG2).";  
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
 RQ EMBL; AY423720; AA500483.1; -; mRNA.  
 SQ SEQUENCE 228 AA; 25416 MW; F68333E0C20611D8 CRC64;

Query Match 100.0%; Score 95; DB 2; Length 228;  
 Best Local Similarity 100.0%; Pred. No. 2e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLETFVKSCPDAl 18  
 |||||  
 DB 168 PKKDVLETFVKSCPDAl 185

RESULT 3  
 CD9 CERAE  
 ID CD9 CERAE STANDARD; PRT; 227 AA.  
 AC P30409;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE CD9 antigen (27 kDa diphtheria toxin receptor-associated protein) (DRAP27).  
 DE Names=CD9;  
 OS Cercopithecus aethiops (Green monkey) (Grivet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini;  
 OC Cercopithecidae; Cercopithecinae; Cercopithecus.  
 OX NCBI\_TaxID=9534;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE (MRNA).  
 RX MEDLINE=92394967; PubMed=1522113; DOI=10.1083/jcb.118.6.1389;  
 RA Mitamura T., Iwamoto R., Umata T., Yomo T., Urabe I., Tsuneoka M.,  
 RA Mekada E.;  
 RT "The 27-kD diphtheria toxin receptor-associated protein (DRAP27) from  
 RT vero cells is the monkey homologue of human CD9 antigen: expression of  
 RT DRAP27 elevates the number of diphtheria toxin receptors on toxin-  
 RT sensitive cells.";  
 RL J. Cell Biol. 118:1389-1399(1992).  
 CC -1- FUNCTION: Involved in platelet activation and aggregation.  
 CC Regulates paranodal junction formation. Required for gamete  
 CC fusion. Involved in cell adhesion, cell motility and tumor  
 CC metastasis (By similarity).  
 CC -1- FUNCTION: Expression of DRAP27 elevates the number of diphtheria  
 CC toxin receptors on toxin-sensitive cells.

CC -1- SUBUNIT: Forms both disulfide-linked homodimers and higher  
 CC homooligomers as well as heterooligomers with other members of the  
 CC tetraspanin family. Associates with CR2/CD21 and with PTGFRN/CD9P1  
 CC (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- PTM: Phosphorylated on tyrosine following B-cell activation (By  
 CC similarity).  
 CC -1- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.  
 CC  
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 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.

EMBL; D10726; BAA01569.1; -; mRNA.  
 DR PIR; A42929; A42929.  
 DR GO; GO:0005887; C:integral to plasma membrane; ISS.  
 DR GO; GO:0005515; P:protein binding; ISS.  
 DR GO; GO:0007155; P:cell adhesion; ISS.  
 DR GO; GO:0006928; P:cell motility; ISS.  
 DR GO; GO:0007342; P:fusion of sperm to egg plasma membrane; ISS.  
 DR GO; GO:0030913; P:paranodal junction formation; ISS.  
 DR GO; GO:0030168; P:platelet activation; ISS.  
 DR InterPro; IPR000301; Transmem\_4.  
 DR Pfam; PF00335; Tetraspannin; 1.  
 DR PRINTS; PR00259; TMFOUR.  
 DR PROSITE; PS00421; TM4\_1; 1.  
 KW Antigen; Cell adhesion; Fertilization; Glycoprotein; Lipoprotein;  
 KW Palmitate; Phosphorylation; Transmembrane.  
 FT INIT MET 0  
 FT TOPO\_DOM 1 11 Cytoplasmic (Potential).  
 FT TRANSMEM 12 32 Potential.  
 FT TOPO\_DOM 33 54 Extracellular (Potential).  
 FT TRANSMEM 55 75 Potential.  
 FT TOPO\_DOM 76 86 Cytoplasmic (Potential).  
 FT TRANSMEM 87 110 Potential.  
 FT TOPO\_DOM 111 194 Extracellular (Potential).  
 FT TRANSMEM 195 220 Potential.  
 FT TOPO\_DOM 221 227 Cytoplasmic (Potential).  
 FT LIPID 8 8 S-palmitoyl cysteine (By similarity).  
 FT LIPID 77 77 S-palmitoyl cysteine (By similarity).  
 FT LIPID 78 78 S-palmitoyl cysteine (By similarity).  
 FT LIPID 86 86 S-palmitoyl cysteine (By similarity).  
 FT LIPID 217 217 S-palmitoyl cysteine (By similarity).  
 FT LIPID 218 218 S-palmitoyl cysteine (By similarity).  
 FT CARBOHYD 51 51 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 52 52 N-linked (GlcNAc...) (Potential).  
 SQ SEQUENCE 227 AA; 25300 MW; 8E3474E7A590374A CRC64;

Query Match 98.9%; Score 94; DB 1; Length 227;  
 Best Local Similarity 94.4%; Pred. No. 3e-07;  
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLETFVKSCPDAl 18  
 |||||  
 DB 167 PKKDVLETFVKSCPDAl 184

RESULT 4  
 CD9 RAT  
 ID CD9 RAT STANDARD; PRT; 225 AA.  
 AC P40241;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE CD9 antigen.  
 DE Name=CD9;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;

RN NUCLEOTIDE SEQUENCE [MRNA]  
 RP STRAIN=Sprague-Dawley; TISSUE=Sciatic nerve;  
 RC MEDLINE=95123481; PubMed=7823164;  
 RX Kaprielian Z., Cho K.O., Hadjiargyrou M., Patterson P.H.;  
 RT "CD9, a major platelet cell surface glycoprotein, is a ROCA antigen  
 RT and is expressed in the nervous system.";  
 RL J. Neurosci. 15:562-573(1995).  
 CC -!- FUNCTION: Involved in platelet activation and aggregation.  
 CC Regulates paranodal junction formation. Required for gamete  
 CC fusion. Involved in cell adhesion, cell motility and tumor  
 CC metastasis (By similarity).  
 CC -!- SUBUNIT: Forms both disulfide-linked homodimers and higher  
 CC homooligomers as well as heterooligomers with other members of the  
 CC tetraspanin family. Associates with CR2/CD21 and with PTGFRN/CD9P1  
 CC (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- TISSUE SPECIFICITY: Expressed in the peripheral nervous system.  
 CC -!- PTM: Phosphorylated on tyrosine following B-cell activation (By  
 CC similarity).  
 CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.  
 CC -----  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 DR EMBL; X76489; CAA54027.1; -; mRNA.  
 DR PIR; I56562; S39262.  
 DR Ensembl; ENSRNOG0000019556; Rattus norvegicus.  
 DR RGD; 2318; Cd9.  
 DR GO; GO:0009986; C:cell surface; IDA.  
 DR GO; GO:0005887; C:integral to plasma membrane; ISS.  
 DR GO; GO:0005515; F:protein binding; IPI.  
 DR GO; GO:0007155; P:cell adhesion; ISS.  
 DR GO; GO:0006928; P:cell motility; ISS.  
 DR GO; GO:0007342; P:fusion of sperm to egg plasma membrane; ISS.  
 DR GO; GO:0030913; P:paranodal junction formation; ISS.  
 DR GO; GO:0030168; P:platelet activation; ISS.  
 DR InterPro; IPR000301; Transmem 4.  
 DR Pfam; PF00335; Tetraspanin; 1.  
 DR PRINTS; PR00259; TMFOUR.  
 DR PROSITE; PS00421; TM4\_1, 1.  
 KW Antigen; Cell adhesion; Fertilization; Glycoprotein; Lipoprotein;  
 KW Palmitate; Phosphorylation; Transmembrane.  
 FT INIT MET 0 0 By similarity.  
 FT TOPO\_DOM 1 11 Cytoplasmic (Potential).  
 FT TRANSMEM 12 32 Potential.  
 FT TOPO\_DOM 33 52 Extracellular (Potential).  
 FT TRANSMEM 53 73 Potential.  
 FT TOPO\_DOM 74 84 Cytoplasmic (Potential).  
 FT TRANSMEM 85 108 Potential.  
 FT TOPO\_DOM 109 192 Extracellular (Potential).  
 FT TRANSMEM 193 218 Potential.  
 FT TOPO\_DOM 219 225 Cytoplasmic (Potential).  
 FT LIPID 8 8 S-palmitoyl cysteine (By similarity).  
 FT LIPID 75 75 S-palmitoyl cysteine (By similarity).  
 FT LIPID 76 76 S-palmitoyl cysteine (By similarity).  
 FT LIPID 84 84 S-palmitoyl cysteine (By similarity).  
 FT LIPID 215 215 S-palmitoyl cysteine (By similarity).  
 FT LIPID 216 216 S-palmitoyl cysteine (By similarity).  
 FT CARBOHYD 49 49 N-linked (GlcNAc...) (Potential).  
 SQ SEQUENCE 225 AA; 25084 MW; 7889619F99A59C9D CRC64;

Query Match 83.2%; Score 79; DB 1; Length 225;

Best Local Similarity 83.3%; Pred. No. 9.8e-05;

Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PKKQVLETFVKSCPDAI 18

Db 165 PKKQVLESFQVKSCPDAI 182

RESULT 5  
 CD9\_MOUSE  
 ID CD9\_MOUSE STANDARD; PRT; 225 AA.  
 AC P40240;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE CD9 antigen.  
 GN Name=CD9;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [MRNA].  
 RC STRAIN=BALB/c; TISSUE=Kidney;  
 RX MEDLINE=94054345; PubMed=8236164; DOI=10.1016/0049-3848(93)90162-H;  
 RA Rubinstein E., Billard M., Plaisance S., Prenant M., Boucheix C.;  
 RT "Molecular cloning of the mouse equivalent of CD9 antigen.";  
 RL Thromb. Res. 71:377-383(1993).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RC STRAIN=C57BL/6J; TISSUE=Kidney;  
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Bradt D., Bruscia V., Chothia C., Corbani L.E., Cousins S.,  
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Mikki H.,  
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,  
 RA Ravasi T., Reed J.C., Reid J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilming L.G., Wyszynski-Boris A., Yanagisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs";  
 RL Nature 420:563-573(2002).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prance C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.N., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).  
 RN [4]

RA ROLE IN GAMETE FUSION.  
 RX PubMed=10700183; DOI=10.1038/73502;  
 RX Kajji K., Oda S., Shikano T., Ohnuki T., Uematsu Y., Sakagami J.,  
 RX Tada N., Miyazaki S., Kudo A.;  
 RA "The gamete fusion process is defective in eggs of Cd9-deficient  
 RT mice";  
 RL Nat. Genet. 24:279-282(2000).  
 RN [5]

RA ROLE IN PARANODAL FORMATION, AND TISSUE SPECIFICITY.  
 RX PubMed=14715942; DOI=10.1523/JNEUROSCI.1484-03.2004;  
 RX Ishibashi T., Ding L., Ikenaka K., Inoue Y., Miyado K., Mekada E.,  
 RA Baba H.;  
 RA "Tetraspanin protein Cd9 is a novel paranodal component regulating  
 RT paranodal junctional formation";  
 RL J. Neurosci. 24:96-102(2004).  
 RN [6]

RA FUNCTION AS RECEPTOR FOR PSG17.  
 RX PubMed=11805154; DOI=10.1084/jem.20011741;  
 RX Waterhouse R., Ha C., Dvorkin G.S.;  
 RA "Murine Cd9 is the receptor for pregnancy-specific glycoprotein 17";  
 RL J. Exp. Med. 195:277-282(2002).  
 CC -!- FUNCTION: Involved in platelet activation and aggregation.  
 CC Regulates paranodal junction formation. Required for gamete  
 CC fusion. Involved in cell adhesion, cell motility and tumor  
 CC metastasis. Acts as a receptor for PSG17.  
 CC -!- SUBUNIT: Forms both disulfide-linked homodimers and higher  
 CC tetraspanin family. Associates with CR2/CD21 and with PTGERN/CD9P1  
 CC (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- TISSUE SPECIFICITY: Expressed predominantly in the peripheral  
 CC nervous system.  
 CC -!- PTM: Phosphorylated on tyrosine following B-cell activation (By  
 CC similarity).  
 CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.

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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.

DR EMBL; L08115; AAA37405.1; -; mRNA.  
 DR EMBL; AK002251; BAB21965.1; -; mRNA.  
 DR EMBL; AK012793; BAB28473.1; -; mRNA.  
 DR EMBL; BC070474; AAB70474.1; -; mRNA.  
 DR F1R; I49589; I49589.  
 DR Ensembl; ENSMUSG00000030342; Mus musculus.  
 DR MGI; MGI:88348; Cd9.  
 DR GO; GO:0005887; C: integral to plasma membrane; ISS.  
 DR GO; GO:0005886; C: plasma membrane; TAS.  
 DR GO; GO:0005515; P: protein binding; IPI.  
 DR GO; GO:0007155; P: cell adhesion; ISS.  
 DR GO; GO:0006928; P: cell motility; ISS.  
 DR GO; GO:0007342; P: fusion of sperm to egg plasma membrane; IDA.  
 DR GO; GO:0030913; P: paranodal junction formation; IDA.  
 DR GO; GO:0030168; P: platelet activation; ISS.  
 DR InterPro; IPR000301; Transmem 4.  
 DR Pfam; PF00335; Tetraspanin; 1.  
 DR PRINTS; PR00259; TMFOUR.  
 DR PROSITE; PS00421; TM4 1; 1.  
 DR Antigen; Cell adhesion; Fertilization; Glycoprotein; Lipoprotein;  
 KW Palmitate; Phosphorylation; Transmembrane.  
 FT INIT\_MET 0 0 By similarity.  
 FT TOPO\_DOM 1 11 Cytoplasmic (Potential).  
 FT TRANSMEM 12 32 Potential.

FT TOPO\_DOM 33 52 Extracellular (Potential).  
 FT TRANSMEM 53 73 Potential.  
 FT TOPO\_DOM 74 84 Cytoplasmic (Potential).  
 FT TRANSMEM 85 108 Potential.  
 FT TOPO\_DOM 109 192 Extracellular (Potential).  
 FT TRANSMEM 193 218 Potential.  
 FT TOPO\_DOM 219 225 Cytoplasmic (Potential).  
 FT LIPID 8 8 S-palmitoyl cysteine (By similarity).  
 FT LIPID 75 75 S-palmitoyl cysteine (By similarity).  
 FT LIPID 76 76 S-palmitoyl cysteine (By similarity).  
 FT LIPID 84 84 S-palmitoyl cysteine (By similarity).  
 FT LIPID 215 215 S-palmitoyl cysteine (By similarity).  
 FT LIPID 216 216 S-palmitoyl cysteine (By similarity).  
 FT CARBOHYD 49 49 N-linked (GlcNAc...) (Potential).  
 SQ SEQUENCE 225 AA; 25127 MW; 2BBE40B8D7C31B5C0 CRC64;

Query Match 70.5%; Score 67; DB 1; Length 225;  
 Best Local Similarity 66.7%; Pred. No. 0.01;  
 Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 PKQVLETFVKSCPDAL 18  
 |||:||||:||||:|  
 Db 165 PKQQLLESFQVPCPEAI 182

RESULT 6  
 CD9\_FELCA STANDARD; PRT; 225 AA.  
 ID CD9\_FELCA  
 AC F40239;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE CD9 antigen.  
 GN Name=CD9;  
 OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Felidae;  
 OC Felinae; Felis.  
 OX NCBI\_TaxID=9685;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [MRNA].  
 RX PubMed=7753050; DOI=10.1016/0161-5890(95)00008-3;  
 RA Willett B.J., Neil J.C.;  
 RT "cDNA cloning and eukaryotic expression of feline CD9";  
 RL Mol. Immunol. 32:417-423(1995).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE [MRNA].  
 RA Morikawa S.;  
 RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Involved in platelet activation and aggregation.  
 CC Regulates paranodal junction formation. Required for gamete  
 CC fusion. Involved in cell adhesion, cell motility and tumor  
 CC metastasis (By similarity).  
 CC -!- SUBUNIT: Forms both disulfide-linked homodimers and higher  
 CC homooligomers as well as heterooligomers with other members of the  
 CC tetraspanin family. Associates with CR2/CD21 and with PTGERN/CD9P1  
 CC (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- PTM: Phosphorylated on tyrosine following B-cell activation (By  
 CC similarity).  
 CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.

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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.

DR EMBL; L35275; AAA92867.1; -; mRNA.  
 DR EMBL; D30786; BAA06452.1; -; mRNA.  
 DR GO; GO:0005887; C: integral to plasma membrane; ISS.  
 DR GO; GO:0005515; P: protein binding; ISS.  
 DR GO; GO:0007155; P: cell adhesion; ISS.

DR GO; GO:0006928; P:cell motility; ISS.  
 DR GO; GO:0007342; P:fusion of sperm to egg plasma membrane; ISS.  
 DR GO; GO:0030913; P:paranodal junction formation; ISS.  
 DR GO; GO:0030168; P:platelet activation; ISS.  
 DR InterPro; IPR000301; Transmem 4.  
 DR Pfam; PF00335; Tetraepannin; 1.  
 DR PRINTS; PR00259; TMFOUR.  
 DR PROSITE; PS00421; TM4\_1; 1.  
 KW Antigen; Cell adhesion; Fertilization; Lipoprotein; Palmitate;  
 KW Phosphorylation; Transmembrane.  
 FT INIT MET 0 0 By similarity.  
 FT TOPO\_DOM 1 11 Cytoplasmic (Potential).  
 FT TRANSMEM 12 22 Potential.  
 FT TOPO\_DOM 33 52 Extracellular (Potential).  
 FT TRANSMEM 53 73 Potential.  
 FT TOPO\_DOM 74 84 Cytoplasmic (Potential).  
 FT TRANSMEM 85 108 Potential.  
 FT TOPO\_DOM 109 192 Extracellular (Potential).  
 FT TRANSMEM 193 218 Potential.  
 FT TOPO\_DOM 219 225 Cytoplasmic (Potential).  
 FT LIPID 8 8 S-palmitoyl cysteine (By similarity).  
 FT LIPID 75 75 S-palmitoyl cysteine (By similarity).  
 FT LIPID 76 76 S-palmitoyl cysteine (By similarity).  
 FT LIPID 84 84 S-palmitoyl cysteine (By similarity).  
 FT LIPID 215 215 S-palmitoyl cysteine (By similarity).  
 FT LIPID 216 216 S-palmitoyl cysteine (By similarity).  
 FT CONFLICT 82 82 S -> Y (in Ref. 2).  
 SQ SEQUENCE 225 AA; 24927 MW; 5A049774501B03B3 CRC64;

Query Match 69.5%; Score 66; DB 1; Length 225;  
 Best Local Similarity 61.1%; Pred. No. 0.015; 3; Indels 0; Gaps 0;  
 Matches 11; Conservative 4; Mismatches 3

QY 1 PKKDVLFTFTVKSCPDAI 18  
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 Db 165 PQKDILSSITVKCPDAI 182

RESULT 7  
 Q6NWG7 BRARE PRELIMINARY; PRT; 227 AA.  
 AC Q6NWG7  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
 DE Hypothetical protein cd9.  
 GN Name=cd9;  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Wild-type; TISSUE=Eye, and Kidney;  
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smillius D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Kidney;  
 RC Director MGC Project;  
 RA Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=Wild-type; TISSUE=Eye;  
 RA Director MGC Project;  
 RA Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; BC067597; AAH67597.1; -; mRNA.  
 DR EMBL; BC059691; AAH59691.1; -; mRNA.  
 DR ZFIN; ZDB-GENE-030131-1175; cd9.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR InterPro; IPR000301; Transmem 4.  
 DR Pfam; PF00335; Tetraepannin; 1.  
 DR PRINTS; PR00259; TMFOUR.  
 DR PROSITE; PS00421; TM4\_1; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 227 AA; 25116 MW; 26E5BC25F4E638B8 CRC64;

Query Match 66.3%; Score 63; DB 2; Length 227;  
 Best Local Similarity 61.1%; Pred. No. 0.049;  
 Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 PKKDVLFTFTVKSCPDAI 18  
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 Db 167 PQKGLDNLIIKSCPDAI 184

RESULT 8  
 Q4REW0 TETNG PRELIMINARY; PRT; 227 AA.  
 AC Q4REW0  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Chromosome 13 SCAP15122, whole genome shotgun sequence.  
 DE (Fragment).  
 GN ORFNames=GSTENG00035589001;  
 OS Tetraodon nigroviridis (Green puffer).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
 OC Tetraodontidae; Tetraodontidae; Tetraodon.  
 OX NCBI\_TaxID=99883;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RA Jaillon O., Aury J.M., Brunet P., Petit J.L., Stange-Thomann N.,  
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dessat C., Segurens B.,  
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
 RA Anthouard V., Jubin C., Castellani V., Katinka J., Vacherie B.,  
 RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,  
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,  
 RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,  
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,  
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
 RA Laudet V., Schachter V., Quetier P., Saurin W., Scarpelli C.,  
 RA Winkler P., Landier E.S., Weissenbach J., Roest Crolius H.,  
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
 the early vertebrate proto-karyotype.";  
 RL Nature 431:946-957(2004).  
 RN [2]

RP NUCLEOTIDE SEQUENCE.  
 RG Genoscope; Whitehead Institute Centre for Genome Research;  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 preliminary data.



DR EMBL; CAAE01015122; CAGI3072.1; -; Genomic\_DNA.  
FT NON\_TER 227  
SQ SEQUENCE 227 AA; 25021 MW; 9CBE48C405F33996 CRC64;  
  
Query Match 65.3%; Score 62; DB 2; Length 227;  
Best Local Similarity 61.1%; Pred No. 0.072; Mismatches 2; Indels 0; Gaps 0;  
Matches 11; Conservative 2;  
  
QY 1 PKKDVLETFVTKSCPDAI 18  
| : | | | : | | | |  
Db 167 PSRDLLEQLITKSCPDPI 184  
| : | | | : | | | |  
  
RESULT 9 Q8MJ48\_PIG PRELIMINARY; PRT; 226 AA.  
ID Q8MJ48\_PIG AC  
AC Q8MJ48;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Transmembrane protein CD9.  
GN Name=CD9;  
GC Name=CD9;  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
OC Sus.  
NCBI\_TaxID=9823;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Heinz M., Huang C.A., Emery D.W., Giovino M.A., LeGuern A.,  
RA Kurilla-Mahon B., Theodore P., Arn J.S., Sykes M., Mulligan R.C.,  
RA Down J.D., Sachs D.H., Goodell M.A.;  
RA "Use of CD9 Expression to Enrich for Porcine Hematopoietic  
RT Progenitors.";  
RL Exp. Hematol. 0:0-0(2002).  
DR EMBL; AF252029; AM81376.1; -; mRNA.  
DR HSSP; P60033; IG8Q.  
GO; GO:0016021; C:integral to membrane; IEA.  
DR InterPro; IPR000301; Transmem 4.  
DR Pfam; PF00335; Tetraspannin; I.  
DR PRINTS; PR00259; TMFOUR.  
DR PROSITE; PS00421; TM4\_1; 1.  
SQ TRANSMEMBRANE.  
KW TRANSMEMBRANE.  
FT TOPO\_DOM 74 84  
FT TOPO\_DOM 85 108  
FT TOPO\_DOM 109 192  
FT TOPO\_DOM 193 218  
FT TOPO\_DOM 219 225  
FT LIPID 8 8  
FT LIPID 75 75  
FT LIPID 76 76  
FT LIPID 84 84  
FT LIPID 215 215  
FT LIPID 216 216  
FT CARBOHYD 49 49  
FT CARBOHYD 50 50  
SQ SEQUENCE 226 AA; 25127 MW; 885C244477F95C23 CRC64;  
  
Query Match 61.1%; Score 58; DB 2; Length 226;  
Best Local Similarity 55.6%; Pred No. 0.34; Mismatches 4; Indels 0; Gaps 0;  
Matches 10; Conservative 4;  
  
QY 1 PKKDVLETFVTKSCPDPI 18  
| : | | | : | | | |  
Db 166 PQKDVLSLPKPCPEAI 183  
| : | | | : | | | |  
  
RESULT 10 CD9\_PIG STANDARD; PRT; 225 AA.  
ID CD9\_PIG AC  
AC Q8WQ03;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE CD9 antigen.  
GN Name=CD9;  
GC Name=CD9;  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
OC Sus.  
NCBI\_TaxID=9823;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [MRNA].  
RA Tissue-Smooth muscle;  
RC PubMed=14610335; DOI=10.1159/000074170;  
RA Yubero N., Jimenez-Marín A., Verle M., Morera L., Barbancho M.J.,

```

DE Hypothetical protein CBG24151.
GN Name=CBG24151;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]_TaxID=6238;
RP NUCLEOTIDE SEQUENCE.
RL The C.briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (by similarity).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAC0100244; CAB56446.1; -; Genomic_DNA.
DR GO; GO:0005856; Cytoskeleton; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000535; MSP.
DR Pfam; PF00635; Motile_Sperm; 1.
DR PROSITE; PS0202; MSP; 1.
KW Cytoskeleton; Hypothetical protein; Nuclear protein.
SQ SEQUENCE 398 AA; 44537 MW; EB3639FD23BD6FD2 CRC64;

Query Match 56.3%; Score 53.5; DB 2; Length 398;
Best Local Similarity 54.5%; Pred. No. 3.5;
Matches 12; Conservative 2; Mismatches 3; Indels 5; Gaps 1;

QY 1 PKKDVLFTVTKV-----SCPDA 17
Db |||||:|||||:|||||:
24 PKKTVIETSKSLFSCPS 45

RESULT 12
Q9IBC9 CHICK
ID Q9IBC9_CHICK PRELIMINARY; PRT; 224 AA.
AC Q9IBC9
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CD9 antigen.
GN Names=CD9;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]_TaxID=9031;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spinal cord;
RA Kobayashi T., Mekada E.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB032767; BAA93011.1; -; mRNA.
DR HSP; P60033; IG80.
DR Ensembl; ENSGALG0000017274; Gallus gallus.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR000301; Transmem_4.
DR Pfam; PF00335; Tetraspannin; 1.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM4_1; 1.
SQ SEQUENCE 224 AA; 24969 MW; AE64BDF849516151 CRC64;

Query Match 54.7%; Score 52; DB 2; Length 224;
Best Local Similarity 55.6%; Pred. No. 3.4;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKKDVLFTVTKVSCPDAI 18
Db |||||:|||||:|||||:
164 PKKTLPESTTMPCKAI 181

RESULT 13
Q851Q5_ORYSA

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ID Q851Q5_ORYSA PRELIMINARY; PRT; 218 AA.
AC Q851Q5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative DNA-binding protein.
GN Name=OSJNBa0052F07.18;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]_TaxID=39947;
RP NUCLEOTIDE SEQUENCE.
RA Buell R.;
RA Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
RA Padrosh D.W., Tallon L.J., Koo H., Ziemann V., Hsiao J., Blunt S.,
RA Vanaken S.S., Riedmuller S.B., Utterback T.T., Feildblyum T.V.,
RA Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
RA White O., Salzberg S.L., Fraser C.M.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Buell R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC104321; AAO37525.1; -; Genomic_DNA.
DR Gramene; Q851Q5; -.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001025; BAH.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001965; Znf_PHD.
DR Pfam; PF01426; BAH; 1.
DR Pfam; PF00628; PHD; 1.
DR SMART; SM00439; BAH; 1.
DR SMART; SM00249; PHD; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS01359; ZF_PHD_1; UNKNOWN_1.
DR PROSITE; PS00016; ZF_PHD_2; 1.
KW DNA-binding.
SQ SEQUENCE 218 AA; 25047 MW; D82DEFB3F116D057 CRC64;

Query Match 52.1%; Score 49.5; DB 2; Length 218;
Best Local Similarity 55.6%; Pred. No. 8.7;
Matches 10; Conservative 4; Mismatches 3; Indels 1; Gaps 1;

QY 1 PKKDVLFTVTKVSCPDAI 18
Db |||||:|||||:|||||:
7 PKRVLESFTYKG-PDGV 23

RESULT 14
Q5YZ96 NOCPA
ID Q5YZ96_NOCPA PRELIMINARY; PRT; 144 AA.
AC Q5YZ96;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=nfal6490;
OS Nocardia farcinica.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Nocardiaceae; Nocardia.
OX NCBI_TaxID=37329;
RN [1]_TaxID=37329;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=IFM 10152;
RX PubMed=15466710; DOI=10.1073/pnas.0406410101;
RX Ishikawa J., Yamashita A., Mikami Y., Hoshino Y., Kurita H., Hotta K.,
RX Shiba T., Hattori M.;
RT "The complete genomic sequence of Nocardia farcinica IFM 10152.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14925-14930(2004).
DR EMBL; AP006618; BAD56495.1; -; Genomic_DNA.

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Search completed: January 20, 2006, 17:21:31  
Job time : 69.4444 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2006, 17:38:26 ; Search time 29.2308 Seconds  
(without alignments)  
226.270 Million cell updates/sec

Title: US-10-619-323-1\_COPY\_113\_192  
Perfect score: 80  
Sequence: 1 HKDEVIKEVQEPYKDTYKNL.....LEFTTVKSCPDAlKEVFDNK 80

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size : 0

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/prodata/1/taa/5 COMB.pep.\*

2: /cgn2\_6/prodata/1/taa/6 COMB.pep.\*

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5: /cgn2\_6/prodata/1/taa/RE COMB.pep.\*

6: /cgn2\_6/prodata/1/taa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	80	100.0	227	1 US-08-254-493-1	Sequence 1, Appli
2	80	100.0	227	1 US-08-253-751-6	Sequence 6, Appli
3	80	100.0	227	1 US-08-453-925-6	Sequence 6, Appli
4	80	100.0	227	2 US-08-403-253A-6	Sequence 6, Appli
5	80	100.0	227	2 US-08-435-816A-6	Sequence 6, Appli
6	80	100.0	227	2 US-09-350-202-6	Sequence 6, Appli
7	80	100.0	227	2 US-08-592-711-6	Sequence 6, Appli
8	80	100.0	227	2 US-09-349-915B-6	Sequence 6, Appli
9	80	100.0	228	1 US-08-408-222B-1	Sequence 1, Appli
10	47	58.8	79	2 US-08-630-172-8	Sequence 8, Appli
11	47	58.8	79	2 US-09-375-419-8	Sequence 8, Appli
12	30	37.5	30	1 US-08-254-493-4	Sequence 4, Appli
13	30	37.5	30	1 US-08-408-222B-4	Sequence 4, Appli
14	29	36.2	29	1 US-08-254-493-5	Sequence 5, Appli
15	29	36.2	29	1 US-08-254-493-6	Sequence 5, Appli
16	29	36.2	29	1 US-08-408-222B-5	Sequence 5, Appli
17	29	36.2	29	1 US-08-408-222B-6	Sequence 6, Appli
18	8	10.0	303	2 US-09-134-001C-5215	Sequence 5215, Ap
19	8	10.0	361	2 US-09-248-796A-16765	Sequence 16765, A
20	7	8.8	321	2 US-09-252-991A-26003	Sequence 26003, A
21	7	8.8	589	2 US-09-328-352-6901	Sequence 6901, Ap
22	7	8.8	770	2 US-09-252-991A-26865	Sequence 26865, A
23	7	8.8	781	2 US-09-252-991A-28926	Sequence 28926, A
24	7	8.8	919	2 US-09-248-796A-17485	Sequence 17485, A
25	7	8.8	1196	2 US-09-107-532A-3944	Sequence 3944, Ap
26	6	7.5	62	2 US-09-621-976-5649	Sequence 5649, Ap
27	6	7.5	75	2 US-09-489-039A-12814	Sequence 12814, A

28	7.5	76	2	US-09-107-532A-4420	Sequence 4420, Ap
29	7.5	90	2	US-09-397-787-17	Sequence 17, Appl
30	7.5	90	2	US-09-270-767-59503	Sequence 59503, A
31	7.5	100	2	US-09-583-110-3743	Sequence 3743, Ap
32	7.5	109	2	US-09-107-532A-5605	Sequence 5605, Ap
33	7.5	110	2	US-09-084-303B-200	Sequence 200, App
34	7.5	119	2	US-09-270-767-47551	Sequence 47551, A
35	7.5	120	2	US-09-949-016-8529	Sequence 8529, Ap
36	7.5	120	2	US-09-949-016-9471	Sequence 9471, Ap
37	7.5	122	2	US-09-134-001C-4533	Sequence 4533, Ap
38	7.5	123	2	US-09-949-016-10319	Sequence 10319, A
39	7.5	134	1	US-08-482-728A-14	Sequence 14, Appl
40	7.5	134	2	US-09-949-016-8720	Sequence 8720, Ap
41	7.5	144	2	US-09-107-433-3320	Sequence 3320, Ap
42	7.5	155	2	US-09-270-767-44087	Sequence 44087, A
43	7.5	155	2	US-09-248-796A-21136	Sequence 21136, A
44	7.5	156	2	US-09-902-540-10151	Sequence 10151, A
45	7.5	169	2	US-09-134-000C-3649	Sequence 3649, Ap
46	7.5	176	1	US-08-145-995A-4	Sequence 4, Appli
47	7.5	176	1	US-08-451-747-4	Sequence 4, Appli
48	7.5	176	2	US-09-134-852-4	Sequence 4, Appli
49	7.5	183	2	US-09-248-796A-15732	Sequence 15732, A
50	7.5	186	2	US-10-104-047-2159	Sequence 2159, Ap
51	7.5	194	2	US-09-489-039A-9776	Sequence 9776, Ap
52	7.5	196	2	US-09-543-681A-5304	Sequence 5304, Ap
53	7.5	202	2	US-09-248-796A-22355	Sequence 22355, A
54	7.5	207	2	US-09-134-001C-4488	Sequence 4488, Ap
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56	7.5	222	1	US-08-292-550-1	Sequence 1, Appli
57	7.5	222	1	US-07-927-661A-1	Sequence 1, Appli
58	7.5	245	2	US-09-252-991A-26304	Sequence 26304, A
59	7.5	248	2	US-09-252-991A-34788	Sequence 34788, A
60	7.5	252	2	US-09-252-991A-20598	Sequence 20598, A
61	7.5	261	2	US-08-975-762-72	Sequence 72, Appl
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64	7.5	261	2	US-09-159-469-72	Sequence 72, Appl
65	7.5	261	2	US-09-693-542-72	Sequence 72, Appl
66	7.5	265	2	US-09-614-069-1	Sequence 1, Appli
67	7.5	265	2	US-09-855-323-16	Sequence 16, Appl
68	7.5	279	2	US-09-704-725-8	Sequence 8, Appli
69	7.5	281	2	US-09-270-767-35423	Sequence 35423, A
70	7.5	281	2	US-09-103-664A-5	Sequence 5, Appli
71	7.5	294	2	US-09-134-000C-5262	Sequence 5262, Ap
72	7.5	300	2	US-09-247-155-107	Sequence 107, App
73	7.5	303	2	US-09-903-190-107	Sequence 107, App
74	7.5	306	2	US-09-634-238-231	Sequence 231, App
75	7.5	307	2	US-09-134-000C-5830	Sequence 5830, Ap
76	7.5	312	2	US-09-107-532A-6219	Sequence 6219, Ap
77	7.5	314	2	US-09-551-826D-6	Sequence 6, Appli
78	7.5	316	2	US-09-551-826D-2	Sequence 2, Appli
79	7.5	318	2	US-09-551-826D-10	Sequence 10, Appl
80	7.5	319	2	US-09-615-192A-323	Sequence 323, App
81	7.5	324	2	US-09-304-967-81	Sequence 81, Appl
82	7.5	327	2	US-09-543-681A-6219	Sequence 6219, Ap
83	7.5	334	2	US-09-252-991A-27369	Sequence 27369, A
84	7.5	334	2	US-09-489-039A-14184	Sequence 14184, A
85	7.5	344	2	US-09-252-991A-16717	Sequence 16717, A
86	7.5	351	2	US-09-270-767-41311	Sequence 41311, A
87	7.5	351	2	US-09-270-767-56527	Sequence 56527, A
88	7.5	355	2	US-09-270-767-44300	Sequence 44300, A
89	7.5	362	2	US-10-164-595-68	Sequence 68, Appl
90	7.5	362	2	US-09-248-796A-14994	Sequence 14994, A
91	7.5	372	2	US-09-328-352-5630	Sequence 5630, Ap
92	7.5	386	1	US-08-455-968E-7	Sequence 7, Appli
93	7.5	387	1	US-08-823-516-140	Sequence 140, App
94	7.5	387	2	US-09-940-244-140	Sequence 140, App
95	7.5	387	2	US-09-381-212-140	Sequence 140, App
96	7.5	387	2	US-09-713-601A-140	Sequence 140, App
97	7.5	400	2	US-09-949-016-6387	Sequence 6387, Ap
98	7.5	403	2	US-08-311-731A-104	Sequence 104, App
99	7.5	405	2	US-09-769-787-62	Sequence 62, Appl
100	7.5	405	2		

101	6	7.5	406	2	US-09-328-352-6564	Sequence 6564, Ap	174	6	7.5	591	2	US-09-252-991A-19506	Sequence 19506, A
102	6	7.5	410	2	US-09-949-016-8783	Sequence 8783, Ap	175	6	7.5	698	2	US-09-134-001C-3632	Sequence 3632, Ap
103	6	7.5	413	2	US-08-942-572-2	Sequence 2, Appli	176	6	7.5	700	2	US-09-252-991A-28344	Sequence 28344, A
104	6	7.5	413	2	US-09-614-069-13	Sequence 13, Appl	177	6	7.5	719	2	US-08-975-762-59	Sequence 59, Appl
105	6	7.5	413	2	US-09-614-069-14	Sequence 14, Appl	178	6	7.5	719	2	US-09-295-028-59	Sequence 59, Appl
106	6	7.5	413	2	US-09-821-803A-7	Sequence 7, Appli	179	6	7.5	719	2	US-09-106-582-59	Sequence 59, Appl
107	6	7.5	413	2	US-09-821-803A-8	Sequence 8, Appli	180	6	7.5	719	2	US-09-153-489-59	Sequence 59, Appl
108	6	7.5	416	2	US-09-252-991A-28396	Sequence 28396, A	181	6	7.5	719	2	US-09-693-542-59	Sequence 59, Appl
109	6	7.5	419	2	US-09-248-796A-17396	Sequence 17396, A	182	6	7.5	735	2	US-09-999-833A-74	Sequence 74, Appl
110	6	7.5	438	2	US-09-252-991A-16791	Sequence 16791, A	183	6	7.5	735	2	US-10-020-445A-74	Sequence 74, Appl
111	6	7.5	452	2	US-09-489-039A-12558	Sequence 12558, A	184	6	7.5	736	2	US-09-252-991A-31194	Sequence 31194, A
112	6	7.5	460	2	US-09-199-637A-132	Sequence 132, App	185	6	7.5	736	2	US-09-902-540-10958	Sequence 10958, A
113	6	7.5	460	2	US-09-949-016-7994	Sequence 7994, App	186	6	7.5	740	2	US-09-252-991A-20586	Sequence 20586, A
114	6	7.5	462	2	US-09-538-092-769	Sequence 769, App	187	6	7.5	745	1	US-08-887-518-3	Sequence 3, Appli
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118	6	7.5	482	2	US-09-252-991A-19130	Sequence 19130, A	191	6	7.5	745	1	US-09-099-125A-4	Sequence 4, Appli
119	6	7.5	491	2	US-09-252-991A-22394	Sequence 22394, A	192	6	7.5	745	1	US-09-099-124A-4	Sequence 4, Appli
120	6	7.5	495	2	US-09-198-484-4	Sequence 4, Appli	193	6	7.5	745	2	US-09-032-476-4	Sequence 4, Appli
121	6	7.5	495	2	US-09-543-681A-5589	Sequence 5589, Ap	194	6	7.5	745	2	US-08-890-854-4	Sequence 4, Appli
122	6	7.5	495	2	US-09-902-540-15518	Sequence 15518, A	195	6	7.5	745	2	US-09-023-324-4	Sequence 4, Appli
123	6	7.5	499	2	US-09-252-991A-28010	Sequence 28010, A	196	6	7.5	745	2	US-09-168-629-2	Sequence 2, Appli
124	6	7.5	501	2	US-09-538-092-707	Sequence 707, App	197	6	7.5	745	2	US-08-910-820-10	Sequence 10, Appl
125	6	7.5	502	2	US-09-949-016-10218	Sequence 10218, A	198	6	7.5	745	2	US-08-810-131A-2	Sequence 2, Appli
126	6	7.5	504	1	US-08-441-139-18	Sequence 18, Appl	199	6	7.5	745	2	US-09-109-986-4	Sequence 4, Appli
127	6	7.5	508	2	US-08-956-171E-5241	Sequence 5241, Ap	200	6	7.5	745	2	US-09-844-908-10	Sequence 10, Appl
128	6	7.5	508	2	US-08-781-986A-5241	Sequence 5241, Ap	201	6	7.5	745	2	US-09-868-758-3	Sequence 3, Appli
129	6	7.5	509	2	US-09-134-000C-4807	Sequence 4807, Ap	202	6	7.5	745	2	US-09-796-872-2	Sequence 2, Appli
130	6	7.5	510	2	US-09-744-016A-5	Sequence 6, Appli	203	6	7.5	755	2	US-09-097-767A-38	Sequence 38, Appl
131	6	7.5	520	2	US-09-252-991A-23797	Sequence 23797, A	204	6	7.5	761	2	US-09-585-858-27	Sequence 27, Appl
132	6	7.5	521	1	US-08-557-122A-32	Sequence 32, Appl	205	6	7.5	761	2	US-10-270-878-27	Sequence 27, Appl
133	6	7.5	521	2	US-09-262-666-32	Sequence 32, Appl	206	6	7.5	811	2	US-09-540-236-2412	Sequence 2412, Ap
134	6	7.5	521	2	US-09-538-092-1283	Sequence 1283, Ap	207	6	7.5	815	2	US-09-328-352-4284	Sequence 4284, Ap
135	6	7.5	522	2	US-09-368-588-2	Sequence 2, Appli	208	6	7.5	879	2	US-09-872-733A-16	Sequence 16, Appl
136	6	7.5	523	2	US-09-744-016A-21	Sequence 21, Appl	209	6	7.5	903	2	US-09-543-681A-4186	Sequence 4186, Ap
137	6	7.5	529	2	US-09-949-016-10714	Sequence 10714, A	210	6	7.5	904	2	US-09-198-484-2	Sequence 2, Appli
138	6	7.5	529	6	5217865-2	Patent No. 5217865	211	6	7.5	909	2	US-09-949-016-6370	Sequence 6370, Ap
139	6	7.5	530	1	US-08-557-122A-35	Sequence 35, Appl	212	6	7.5	916	2	US-09-543-681A-5205	Sequence 5205, Ap
140	6	7.5	530	2	US-09-262-666-35	Sequence 35, Appl	213	6	7.5	916	2	US-09-489-039A-14125	Sequence 14125, A
141	6	7.5	533	2	US-09-744-016A-18	Sequence 18, Appl	214	6	7.5	952	2	US-09-252-991A-32183	Sequence 32183, A
142	6	7.5	534	2	US-09-103-664A-2	Sequence 2, Appli	215	6	7.5	971	2	US-09-248-796A-19531	Sequence 19531, A
143	6	7.5	536	2	US-10-104-047-2780	Sequence 2780, Ap	216	6	7.5	996	2	US-09-417-197-123	Sequence 123, App
144	6	7.5	541	2	US-09-107-532A-5648	Sequence 5648, Ap	217	6	7.5	997	2	US-09-417-197-121	Sequence 121, App
145	6	7.5	549	2	US-09-344-510B-2	Sequence 2, Appli	218	6	7.5	1003	1	US-07-991-867B-6	Sequence 6, Appli
146	6	7.5	550	2	US-09-344-510B-4	Sequence 4, Appli	219	6	7.5	1003	1	US-08-107-755A-6	Sequence 6, Appli
147	6	7.5	570	1	US-08-967-364-1	Sequence 1, Appli	220	6	7.5	1003	1	US-08-544-332-6	Sequence 6, Appli
148	6	7.5	570	1	US-09-368-408-1	Sequence 7, Appli	221	6	7.5	1003	2	US-09-370-861A-6	Sequence 6, Appli
149	6	7.5	570	2	US-09-368-408-7	Sequence 7, Appli	222	6	7.5	1011	2	US-09-602-362E-27	Sequence 27, Appl
150	6	7.5	570	2	US-09-368-408-7	Sequence 7, Appli	223	6	7.5	1012	2	US-09-344-510B-1	Sequence 1, Appli
151	6	7.5	572	2	US-09-252-991A-23996	Sequence 23996, A	224	6	7.5	1014	2	US-09-344-510B-3	Sequence 3, Appli
152	6	7.5	572	2	US-09-252-991A-25086	Sequence 25086, A	225	6	7.5	1082	2	US-10-164-595-28	Sequence 28, Appl
153	6	7.5	586	2	US-08-419-810-12	Sequence 12, Appl	226	6	7.5	1095	2	US-09-112-096-15	Sequence 15, Appl
154	6	7.5	586	6	5405775-11	Patent No. 5405775	227	6	7.5	1095	2	US-09-636-215-778	Sequence 778, App
155	6	7.5	595	2	US-09-949-016-9801	Sequence 9801, Ap	228	6	7.5	1095	2	US-09-636-215-780	Sequence 780, App
156	6	7.5	600	2	US-09-252-991A-21703	Sequence 21703, A	229	6	7.5	1095	2	US-09-685-166A-778	Sequence 778, App
157	6	7.5	618	2	US-09-252-991A-22418	Sequence 22418, A	230	6	7.5	1095	2	US-09-685-166A-780	Sequence 780, App
158	6	7.5	630	2	US-09-902-540-11085	Sequence 11085, A	231	6	7.5	1095	2	US-09-679-426-778	Sequence 778, App
159	6	7.5	631	2	US-09-252-991A-20418	Sequence 20418, A	232	6	7.5	1095	2	US-09-679-426-780	Sequence 780, App
160	6	7.5	632	2	US-09-354-129-8	Sequence 8, Appli	233	6	7.5	1095	2	US-09-759-143-778	Sequence 778, App
161	6	7.5	632	2	US-09-504-357-8	Sequence 8, Appli	234	6	7.5	1095	2	US-09-759-143-780	Sequence 780, App
162	6	7.5	638	1	US-08-557-122A-38	Sequence 38, Appli	235	6	7.5	1095	2	US-09-651-236-778	Sequence 778, App
163	6	7.5	638	2	US-09-262-666-38	Sequence 38, Appl	236	6	7.5	1095	2	US-09-651-236-780	Sequence 780, App
164	6	7.5	645	2	US-09-538-092-920	Sequence 920, App	237	6	7.5	1095	2	US-09-657-279-778	Sequence 778, App
165	6	7.5	650	2	US-09-252-991A-32334	Sequence 32334, A	238	6	7.5	1095	2	US-09-657-279-780	Sequence 780, App
166	6	7.5	652	2	US-09-636-215-818	Sequence 818, App	239	6	7.5	1095	2	US-10-012-896-778	Sequence 778, App
167	6	7.5	652	2	US-09-685-166A-818	Sequence 818, App	240	6	7.5	1095	2	US-10-012-896-780	Sequence 780, App
168	6	7.5	652	2	US-09-679-426-818	Sequence 818, App	241	6	7.5	1231	2	US-09-071-035-420	Sequence 420, App
169	6	7.5	652	2	US-09-759-143-818	Sequence 818, App	242	6	7.5	1231	2	US-10-206-576-420	Sequence 420, App
170	6	7.5	652	2	US-09-651-236-818	Sequence 818, App	243	6	7.5	1239	2	US-10-076-622-577	Sequence 577, App
171	6	7.5	652	2	US-09-657-279-818	Sequence 818, App	244	6	7.5	1265	2	US-09-071-035-418	Sequence 418, App
172	6	7.5	652	2	US-10-012-896-818	Sequence 818, App	245	6	7.5	1265	2	US-10-206-576-418	Sequence 418, App
173	6	7.5	662	2	US-09-252-991A-31942	Sequence 31942, A	246	6	7.5	1278	2	US-09-134-000C-6043	Sequence 6043, Ap

247	6	7.5	1462	2	US-09-538-092-1043	Sequence 1043, Ap	320	5	6.2	20	2	US-09-724-062-65	Sequence 65, Appl
248	6	7.5	1462	2	US-09-949-002-381	Sequence 381, App	321	5	6.2	20	2	US-09-724-065-64	Sequence 64, Appl
249	6	7.5	1504	2	US-09-252-991A-26608	Sequence 26608, A	322	5	6.2	20	2	US-09-724-065-65	Sequence 65, Appl
250	6	7.5	1514	1	US-08-853-310-4	Sequence 4, Appli	323	5	6.2	20	2	US-09-724-481-64	Sequence 64, Appl
251	6	7.5	1524	2	US-09-949-002-495	Sequence 495, App	324	5	6.2	20	2	US-09-724-481-65	Sequence 65, Appl
252	6	7.5	1566	2	US-09-581-472B-2	Sequence 2, Appli	325	5	6.2	20	6	5204097-3	Patent No. 5204097
253	6	7.5	1581	2	US-09-110-517-2	Sequence 2, Appli	326	5	6.2	22	2	US-10-038-612-79	Sequence 79, Appl
254	6	7.5	1596	2	US-09-328-352-5542	Sequence 2, Appli	327	5	6.2	22	2	US-10-038-612-80	Sequence 80, Appl
255	6	7.5	1650	2	US-09-252-991A-21798	Sequence 21798, A	328	5	6.2	22	2	US-09-479-479-29	Sequence 29, Appl
256	6	7.5	1659	2	US-09-487-558B-118	Sequence 118, App	329	5	6.2	23	2	US-09-297-851-29	Sequence 29, Appl
257	6	7.5	1706	1	US-08-459-568-2	Sequence 2, Appli	330	5	6.2	25	2	US-09-200-757-5	Sequence 5, Appli
258	6	7.5	1706	1	US-08-399-411-2	Sequence 2, Appli	331	5	6.2	26	4	PCT-US95-13841-1	Sequence 1, Appli
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263	6	7.5	2220	2	US-09-949-016-9730	Sequence 9730, Ap	336	5	6.2	28	2	US-09-827-960-2	Sequence 2, Appli
264	6	7.5	2273	2	US-09-426-998-5	Sequence 5, Appli	337	5	6.2	28	2	US-09-837-886-2	Sequence 2, Appli
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266	6	7.5	3522	2	US-09-262-666-26	Sequence 26, Appl	339	5	6.2	30	1	US-08-287-959-14	Sequence 14, Appl
267	6	7.5	3724	1	US-08-804-227C-10	Sequence 10, Appl	340	5	6.2	31	2	US-09-227-357-398	Sequence 398, App
268	6	7.5	3724	1	US-08-804-198-4	Sequence 4, Appli	341	5	6.2	31	2	US-09-973-278-508	Sequence 508, App
269	6	7.5	3913	2	US-09-949-016-10933	Sequence 10933, A	342	5	6.2	39	2	US-09-270-767-58213	Sequence 58213, A
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272	5	6.2	6	2	US-09-634-496-9	Sequence 9, Appli	345	5	6.2	43	2	US-09-057-363C-59	Sequence 59, Appl
273	5	6.2	6	2	US-09-635-145A-9	Sequence 9, Appli	346	5	6.2	43	2	US-09-265-107-59	Sequence 59, Appl
274	5	6.2	8	2	US-09-200-757-1	Sequence 1, Appli	347	5	6.2	43	2	US-09-270-767-62022	Sequence 62022, A
275	5	6.2	8	2	US-09-200-757-3	Sequence 3, Appli	348	5	6.2	43	4	PCT-US95-13841-36	Sequence 36, Appl
276	5	6.2	10	2	US-09-200-757-4	Sequence 4, Appli	349	5	6.2	46	1	US-08-639-857-30	Sequence 30, Appl
277	5	6.2	10	2	US-09-926-163B-18	Sequence 18, Appl	350	5	6.2	46	1	US-09-270-767-56973	Sequence 56973, A
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279	5	6.2	10	2	US-10-394-980-452	Sequence 452, App	352	5	6.2	47	2	US-09-904-615-88	Sequence 88, Appl
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281	5	6.2	13	1	US-08-305-871A-28	Patent No. 5204097	354	5	6.2	47	2	US-08-054-988-88	Sequence 88, Appl
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284	5	6.2	15	2	US-09-767-460-15	Sequence 15, Appl	357	5	6.2	49	2	US-08-829-525-38	Sequence 38, Appl
285	5	6.2	16	2	US-08-602-999A-384	Sequence 384, App	358	5	6.2	49	2	US-08-310-367-38	Sequence 38, Appl
286	5	6.2	16	2	US-09-500-124-384	Sequence 384, App	359	5	6.2	51	6	5274075-11	Patent No. 5274075
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288	5	6.2	17	2	US-09-297-851-23	Sequence 23, Appl	361	5	6.2	52	2	US-08-836-500A-8	Sequence 8, Appli
289	5	6.2	19	2	US-09-441-502B-90	Sequence 90, Appl	362	5	6.2	53	2	US-09-678-750-8	Sequence 8, Appli
290	5	6.2	19	2	US-09-441-502B-91	Sequence 91, Appl	363	5	6.2	54	2	US-09-270-767-36652	Sequence 36652, A
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293	5	6.2	20	2	US-08-825-852-64	Sequence 64, Appl	366	5	6.2	61	1	US-08-290-448A-61	Sequence 61, Appl
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295	5	6.2	20	2	US-09-052-888-65	Sequence 65, Appl	368	5	6.2	61	1	US-08-290-448A-57	Sequence 57, Appl
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297	5	6.2	20	2	US-09-723-890-65	Sequence 65, Appl	370	5	6.2	61	1	US-08-446-137B-12	Sequence 12, Appl
298	5	6.2	20	2	US-09-723-890-65	Sequence 65, Appl	371	5	6.2	61	2	US-08-461-939B-57	Sequence 57, Appl
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314	5	6.2	20	2	US-09-723-912-65	Sequence 65, Appl	387	5	6.2	65	2	US-09-337-501-10	Sequence 10, Appl
315	5	6.2	20	2	US-09-724-095-64	Sequence 64, Appl	388	5	6.2	65	2	US-09-621-976-4513	Sequence 4513, Ap
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319	5	6.2	20	2	US-09-724-062-64	Sequence 64, Appl	392	5	6.2	65	2		

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394	5	6.2	66	1	US-08-437-607A-44	Sequence 44, Appl	467	5	6.2	89	2	US-09-295-028-26	Sequence 26, Appl
395	5	6.2	66	2	US-08-446-137B-10	Sequence 10, Appl	468	5	6.2	89	2	US-09-106-582-26	Sequence 26, Appl
396	5	6.2	66	2	US-09-540-236-2981	Sequence 2981, Ap	469	5	6.2	89	2	US-09-159-469-26	Sequence 26, Appl
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399	5	6.2	67	2	US-09-248-796A-22622	Sequence 22622, A	472	5	6.2	89	2	US-09-334-477-4	Sequence 4, Appli
400	5	6.2	67	2	US-08-180-761B-3	Sequence 3, Appli	473	5	6.2	89	2	US-09-334-477-8	Sequence 8, Appli
401	5	6.2	68	1	US-09-248-796A-26169	Sequence 26169, A	474	5	6.2	89	2	US-09-693-542-26	Sequence 26, Appl
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405	5	6.2	69	2	US-08-467-936-21	Sequence 21, Appl	478	5	6.2	91	2	US-09-621-976-4864	Sequence 4864, Ap
406	5	6.2	69	2	US-09-082-514-21	Sequence 21, Appl	479	5	6.2	92	2	US-09-248-796A-16829	Sequence 16829, A
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410	5	6.2	70	6	5204097-1	Patent No. 5204097	483	5	6.2	93	2	US-09-902-540-14770	Sequence 14770, A
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412	5	6.2	72	2	US-08-836-500A-6	Sequence 6, Appli	485	5	6.2	94	2	US-09-270-767-62094	Sequence 62094, A
413	5	6.2	72	2	US-09-679-750-6	Sequence 6, Appli	486	5	6.2	95	2	US-09-902-540-10228	Sequence 10228, A
414	5	6.2	73	2	US-09-366-887A-24	Sequence 24, Appl	487	5	6.2	97	2	US-08-816-977-23	Sequence 23, Appl
415	5	6.2	73	2	US-09-248-796A-24220	Sequence 24220, A	488	5	6.2	97	2	US-08-816-977-27	Sequence 27, Appl
416	5	6.2	73	2	US-09-517-204-24	Sequence 24, Appl	489	5	6.2	97	2	US-09-366-887A-6	Sequence 6, Appl
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423	5	6.2	76	2	US-09-583-110-3419	Sequence 3419, Ap	496	5	6.2	97	2	US-09-513-999C-5617	Sequence 5617, Ap
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426	5	6.2	77	2	US-09-134-001C-3386	Sequence 3386, Ap	499	5	6.2	99	2	US-09-583-110-3188	Sequence 3188, Ap
427	5	6.2	77	2	US-09-248-796A-23767	Sequence 23767, A	500	5	6.2	99	2	US-09-107-433-4418	Sequence 4418, Ap
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436	5	6.2	80	2	US-09-270-767-59415	Sequence 59415, A	509	5	6.2	101	1	US-08-967-038-1	Sequence 1, Appli
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444	5	6.2	83	2	US-09-489-039A-7547	Sequence 7547, Ap	517	5	6.2	102	2	US-09-583-110-2880	Sequence 2880, Ap
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447	5	6.2	83	2	US-09-270-767-48821	Sequence 48821, A	520	5	6.2	102	2	US-09-902-540-12779	Sequence 12779, A
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687	5	6.2	144	1	US-08-133-979A-11	Sequence 11, Appli	760	5	6.2	158	2	US-09-438-486A-82	Sequence 85, Appli
688	5	6.2	144	1	US-08-436-890-11	Sequence 11, Appli	761	5	6.2	158	2	US-09-438-486A-85	Sequence 85, Appli
689	5	6.2	144	1	US-08-451-213-11	Sequence 11, Appli	762	5	6.2	159	2	US-09-252-991A-21119	Sequence 21119, A
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694	5	6.2	145	2	US-09-461-325-438	Sequence 438, App	767	5	6.2	160	2	US-09-370-838-189	Sequence 189, App
695	5	6.2	145	2	US-10-012-542-438	Sequence 438, App	768	5	6.2	160	2	US-09-252-991A-27416	Sequence 27416, A
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697	5	6.2	145	2	US-10-115-123-438	Sequence 438, App	770	5	6.2	160	2	US-09-583-110-3449	Sequence 3449, Ap
698	5	6.2	146	2	US-09-227-357-396	Sequence 396, App	771	5	6.2	160	2	US-08-884-133-189	Sequence 189, App
699	5	6.2	146	2	US-09-134-001C-3406	Sequence 3406, Ap	772	5	6.2	161	2	US-08-493-071-20	Sequence 20, Appli
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701	5	6.2	146	2	US-09-973-278-506	Sequence 506, App	774	5	6.2	162	2	US-09-732-210-768	Sequence 768, App
702	5	6.2	147	2	US-09-383-586-35	Sequence 35, Appli	775	5	6.2	163	2	US-09-134-001C-4131	Sequence 4131, Ap
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710	5	6.2	149	2	US-09-732-210-843	Sequence 843, App	783	5	6.2	166	2	US-09-107-532A-5004	Sequence 5004, Ap
711	5	6.2	149	2	US-09-488-039A-3279	Sequence 3279, Ap	784	5	6.2	166	2	US-09-248-796A-17285	Sequence 17285, A
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## ALIGNMENTS

RESULT 1  
 US-08-254-493-1  
 ; Sequence 1, Application US/08254493  
 ; Patent No. 5439886  
 ; GENERAL INFORMATION:  
 ; APPLICANT: IKEYAMA, SHUICHI  
 ; APPLICANT: KOYAMA, MASARU  
 ; APPLICANT: MIYAKE, MASAYUKI  
 ; APPLICANT: SENOO, MASAHARU  
 ; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND  
 ; TITLE OF INVENTION: PRODUCTION THEREOF  
 ; NUMBER OF SEQUENCES: 7  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &  
 ; STREET: 130 WATER STREET  
 ; CITY: BOSTON  
 ; STATE: MASSACHUSETTS  
 ; COUNTRY: US  
 ; ZIP: 02109  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/254,493  
 ; FILING DATE:  
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 ; FILING DATE: 09-APR-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: JP 079996-1991  
 ; FILING DATE: 12-APR-1991  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: JP 085396-1991  
 ; FILING DATE: 17-APR-1991  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: JP 022321-1992  
 ; FILING DATE: 07-FEB-1992  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: RESNICK, DAVID S.  
 ; REGISTRATION NUMBER: 34235  
 ; REFERENCE/DOCKET NUMBER: 41777

```

;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-254-493-1

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Query Match	100.0%;	Score 80;	DB 1;	Length 227;
Best Local Similarity	100.0%;	Pred. No. 8.3e-79;		
Matches 80;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	HKDEVKEVQEFYKDTYNTKLTQDDEPQRETLKAIHYALNCCGLAGGVEQFISDTCPKKDV	60	
Db	112	HKDEVKEVQEFYKDTYNTKLTQDDEPQRETLKAIHYALNCCGLAGGVEQFISDTCPKKDV	171	
Qy	61	LETFTVKSCPDAIKEVFDNK	80	
Db	172	LETFTVKSCPDAIKEVFDNK	191	

RESULT 2  
 US-08-253-751-6  
 Sequence 6, Application US/08253751  
 Patent No. 5858358  
 GENERAL INFORMATION:  
 APPLICANT: June, Carl H.  
 APPLICANT: Thompson, Craig B.  
 APPLICANT: Nabel, Gary J.  
 APPLICANT: Gray, Gary S.  
 APPLICANT: Rennert, Paul D.  
 APPLICANT: Freeman, Gordon J.  
 TITLE OF INVENTION: METHODS FOR SELECTIVELY STIMULATING  
 TITLE OF INVENTION: PROLIFERATION OF T-CELLS  
 NUMBER OF SEQUENCES: 10  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LAHIVE & COCKFIELD  
 STREET: 60 STATE STREET, SUITE 510  
 CITY: BOSTON  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: ASCII TEXT  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/253,751  
 FILING DATE: 3 JUNE 1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/073,223  
 FILING DATE: 4 JUNE 1993  
 APPLICATION NUMBER: US 08/200,947  
 FILING DATE: 23 FEB 1994  
 APPLICATION NUMBER: US 07/864,805  
 FILING DATE: 7 APR 1992  
 APPLICATION NUMBER: US 08/247,505  
 FILING DATE: 23 MAY 1994  
 APPLICATION NUMBER: US 07/864,866  
 FILING DATE: 7 APR 1992  
 APPLICATION NUMBER: 08/218,155  
 FILING DATE: 25 MAR 1994  
 APPLICATION NUMBER: US 07/864,807  
 FILING DATE: 7 APR 1992  
 APPLICATION NUMBER: US 07/902,467  
 FILING DATE: 16 JUNE 1992  
 APPLICATION NUMBER: US 07/275,433

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/
/ FILING DATE: 23 NOV 1988
/ ATTORNEY/AGENT INFORMATION:
/ NAME: MANDRAGOURAS, AMY E.
/ REGISTRATION NUMBER: 36,207
/ REFERENCE/DOCKET NUMBER: RPI-002CPB
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 227-7400
/ TELEFAX: (617) 227-5941
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 227 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/
US-08-253-751-6

Query Match 100.0%; Score 80; DB 1; Length 227;
Best Local Similarity 100.0%; Pred. No. 8.3e-79;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVIKEVQEFYKDTYNKLTKEDEPQRETLLKAIHYALNCCGLAGGVEQFISDIPCCKDV 60
Db 112 HKDEVIKEVQEFYKDTYNKLTKEDEPQRETLLKAIHYALNCCGLAGGVEQFISDIPCCKDV 171

QY 61 LETFTVKSCPDAIKEVFDNK 80
Db 172 LETFTVKSCPDAIKEVFDNK 191

RESULT 3
US-08-453-925-6
/ Sequence 6, Application US/08453925
/ Patent No. 5883223
/ GENERAL INFORMATION:
/ APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.
/ APPLICANT: Gray, Gary S., Rennert, Paul D., Freeman, Gordon J.
/ TITLE OF INVENTION: METHODS FOR SELECTIVELY STIMULATING
/ TITLE OF INVENTION: PROLIFERATION OF T-CELLS
/ NUMBER OF SEQUENCES: 10
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: LAHIVE & COCKFIELD
/ STREET: 60 STATE STREET, SUITE 510
/ CITY: BOSTON
/ STATE: MA
/ COUNTRY: USA
/ ZIP: 02109
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: ASCII TEXT
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/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/453,925
/ FILING DATE: 30 MAY 1995
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/253,751
/ FILING DATE: 3 JUNE 1994
/ APPLICATION NUMBER: US 08/073,223
/ FILING DATE: 4 JUNE 1993
/ APPLICATION NUMBER: US 08/200,947
/ FILING DATE: 23 FEB 1994
/ APPLICATION NUMBER: US 07/864,805
/ FILING DATE: 7 APR 1992
/ APPLICATION NUMBER: US 08/247,505
/ FILING DATE: 23 MAY 1994
/ APPLICATION NUMBER: US 07/864,866
/ FILING DATE: 7 APR 1992
/ APPLICATION NUMBER: 08/218,155
/ FILING DATE: 25 MAR 1994
/ APPLICATION NUMBER: US 07/864,807
/ FILING DATE: 7 APR 1992
/ APPLICATION NUMBER: US 07/902,467
/ FILING DATE: 16 JUNE 1992
```

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/
/ APPLICATION NUMBER: US 07/275,433
/ FILING DATE: 23 NOV 1988
/ ATTORNEY/AGENT INFORMATION:
/ NAME: MANDRAGOURAS, AMY E.
/ REGISTRATION NUMBER: 36,207
/ REFERENCE/DOCKET NUMBER: RPI-002CPB
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 227-7400
/ TELEFAX: (617) 227-5941
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 227 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/
US-08-453-925-6

Query Match 100.0%; Score 80; DB 1; Length 227;
Best Local Similarity 100.0%; Pred. No. 8.3e-79;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVIKEVQEFYKDTYNKLTKEDEPQRETLLKAIHYALNCCGLAGGVEQFISDIPCCKDV 60
Db 112 HKDEVIKEVQEFYKDTYNKLTKEDEPQRETLLKAIHYALNCCGLAGGVEQFISDIPCCKDV 171

QY 61 LETFTVKSCPDAIKEVFDNK 80
Db 172 LETFTVKSCPDAIKEVFDNK 191

RESULT 4
US-08-403-253A-6
/ Sequence 6, Application US/08403253A
/ Patent No. 6352694
/ GENERAL INFORMATION:
/ APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.
/ APPLICANT: Gray, Gary S., Rennert, Paul D.
/ TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
/ NUMBER OF SEQUENCES: 14
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: LAHIVE & COCKFIELD
/ STREET: 28 State Street
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: USA
/ ZIP: 02109
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/403,253A
/ FILING DATE: March 10, 1995
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/253,964
/ FILING DATE: 3 JUNE 1994
/ APPLICATION NUMBER: US 08/073,223
/ FILING DATE: 4 JUNE 1993
/ APPLICATION NUMBER: US 08/200,947
/ FILING DATE: 23 FEB 1994
/ APPLICATION NUMBER: US 07/864,805
/ FILING DATE: 7 APR 1992
/ APPLICATION NUMBER: US 08/247,505
/ FILING DATE: 23 MAY 1994
/ APPLICATION NUMBER: US 07/864,866
/ FILING DATE: 7 APR 1992
/ APPLICATION NUMBER: US 08/218,155
/ FILING DATE: 25 MAR 1994
/ APPLICATION NUMBER: US 07/864,807
/ FILING DATE: 7 APR 1992
/ APPLICATION NUMBER: US 07/902,467
/ FILING DATE: 16 JUNE 1992
```

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;
; FILING DATE: 16 JUNE 1992
; APPLICATION NUMBER: US 07/275,433
; FILING DATE: 23 NOV 1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-403-253A-6

Query Match          100.0%; Score 80; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 8.3e-79;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVIKEVQEFYKDTYNNKLTQDEPQRETLKAIHYALNCCGLAGGVQFISDIPCCKDV 60
Db 112 HKDEVIKEVQEFYKDTYNNKLTQDEPQRETLKAIHYALNCCGLAGGVQFISDIPCCKDV 171

QY 61 LETFTVKSCPDAIKEVFDNK 80
Db 172 LETFTVKSCPDAIKEVFDNK 191

RESULT 5
US-08-435-816A-6
; Sequence 6, Application US/08435816A
; Patent No. 6534055
; GENERAL INFORMATION:
; APPLICANT: June, Carl H.
; APPLICANT: Thompson, Craig B.
; APPLICANT: Nabel, Gary S.
; APPLICANT: Gray, Gary S.
; APPLICANT: Rennert, Paul D.
; TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,816A
; FILING DATE: May 4, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/403,253
; FILING DATE: 10 MARCH 1995
; APPLICATION NUMBER: US 08/253,964
; FILING DATE: 3 JUNE 1994
; APPLICATION NUMBER: US 08/073,223
; FILING DATE: 4 JUNE 1993
; APPLICATION NUMBER: US 08/200,947
; FILING DATE: 23 FEB 1994
; APPLICATION NUMBER: US 07/864,805
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/247,505
; FILING DATE: 23 MAY 1994
; APPLICATION NUMBER: US 07/864,866
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; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/218,155
; FILING DATE: 25 MAR 1994
; APPLICATION NUMBER: US 07/864,807
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 07/902,467
; FILING DATE: 16 JUNE 1992
; APPLICATION NUMBER: US 07/275,433
; FILING DATE: 23 NOV 1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-435-816A-6

Query Match          100.0%; Score 80; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 8.3e-79;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVIKEVQEFYKDTYNNKLTQDEPQRETLKAIHYALNCCGLAGGVQFISDIPCCKDV 60
Db 112 HKDEVIKEVQEFYKDTYNNKLTQDEPQRETLKAIHYALNCCGLAGGVQFISDIPCCKDV 171

QY 61 LETFTVKSCPDAIKEVFDNK 80
Db 172 LETFTVKSCPDAIKEVFDNK 191

RESULT 6
US-09-350-202-6
; Sequence 6, Application US/09350202
; Patent No. 6887466
; GENERAL INFORMATION:
; APPLICANT: June, Carl H.; Thompson, Craig B.; Nabel, Gary J.
; APPLICANT: Gray, Gary S.; Rennert, Paul D.
; TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/350,202
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/403,253
; FILING DATE: March 10, 1995
; APPLICATION NUMBER: US 08/253,964
; FILING DATE: 3 JUNE 1994
; APPLICATION NUMBER: US 08/073,223
; FILING DATE: 4 JUNE 1993
; APPLICATION NUMBER: US 08/200,947
; FILING DATE: 23 FEB 1994
; APPLICATION NUMBER: US 07/864,805
; FILING DATE: 7 APR 1992
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APPLICATION NUMBER: US 08/247,505  
FILING DATE: 23 MAY 1994  
APPLICATION NUMBER: US 07/864,866  
FILING DATE: 7 APR 1992  
APPLICATION NUMBER: US 08/218,155  
FILING DATE: 25 MAR 1994  
APPLICATION NUMBER: US 07/864,807  
FILING DATE: 7 APR 1992  
APPLICATION NUMBER: US 07/902,467  
FILING DATE: 16 JUNE 1992  
APPLICATION NUMBER: US 07/275,433  
FILING DATE: 23 NOV 1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: RPI-002CP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 742-4214  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 227 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-350-202-6

Query Match 100.0%; Score 80; DB 2; Length 227;  
Best Local Similarity 100.0%; Pred. No. 8.3e-79;  
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVKIQVQFYKDTYNKLTQDEPQRTLKAIHYALNCCGLAGGVEQFISDIPCCKDV 60  
DB 112 HKDEVKIQVQFYKDTYNKLTQDEPQRTLKAIHYALNCCGLAGGVEQFISDIPCCKDV 171

QY 61 LETFTVKSCPDAIKEVFNK 80  
DB 172 LETFTVKSCPDAIKEVFNK 191

RESULT 7  
US-08-592-711-6  
Sequence 6, Application US/08592711  
Patent No. 6905680  
GENERAL INFORMATION:  
APPLICANT: June, Carl H.  
APPLICANT: Thompson, Craig B.  
APPLICANT: Nabel, Gary J.  
APPLICANT: Gray, Gary S.  
APPLICANT: Rennert, Paul D.  
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESS: LAHIVE & COCKFIELD  
STREET: 60 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/592,711  
FILING DATE: 26-JAN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/435,816  
FILING DATE: 4-MAY-1995  
APPLICATION NUMBER: US 08/403,253  
FILING DATE: 10-MARCH-1995  
APPLICATION NUMBER: US 08/253,964

FILING DATE: 3-JUNE-1994  
APPLICATION NUMBER: US 08/073,223  
FILING DATE: 4-JUNE-1993  
APPLICATION NUMBER: US 08/200,947  
FILING DATE: 23-FEB-1994  
APPLICATION NUMBER: US 07/864,805  
FILING DATE: 7-APR-1992  
APPLICATION NUMBER: US 08/247,505  
FILING DATE: 23-MAY-1994  
APPLICATION NUMBER: US 07/864,866  
FILING DATE: 7-APR-1992  
APPLICATION NUMBER: US 08/218,155  
FILING DATE: 25-MAR-1994  
APPLICATION NUMBER: US 07/864,807  
FILING DATE: 7-APR-1992  
APPLICATION NUMBER: US 07/902,467  
FILING DATE: 16-JUNE-1992  
APPLICATION NUMBER: US 07/275,433  
FILING DATE: 23-NOV-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: RPI-002CP4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 227 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-592-711-6

Query Match 100.0%; Score 80; DB 2; Length 227;  
Best Local Similarity 100.0%; Pred. No. 8.3e-79;  
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVKIQVQFYKDTYNKLTQDEPQRTLKAIHYALNCCGLAGGVEQFISDIPCCKDV 60  
DB 112 HKDEVKIQVQFYKDTYNKLTQDEPQRTLKAIHYALNCCGLAGGVEQFISDIPCCKDV 171

QY 61 LETFTVKSCPDAIKEVFNK 80  
DB 172 LETFTVKSCPDAIKEVFNK 191

RESULT 8  
US-09-349-915B-6  
Sequence 6, Application US/09349915B  
Patent No. 6905681  
GENERAL INFORMATION:  
APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.  
APPLICANT: Gray, Gary S., Rennert, Paul D.  
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESS: HALE AND DORR LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/349,915B  
FILING DATE: 01-Aug-2000  
CLASSIFICATION: <Unknown>



;;  
;; PRIORITY APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/403,253  
;; FILING DATE: March 10, 1995  
;; APPLICATION NUMBER: US 08/253,964  
;; FILING DATE: 3 JUNE 1994  
;; APPLICATION NUMBER: US 08/073,223  
;; FILING DATE: 4 JUNE 1993  
;; APPLICATION NUMBER: US 08/200,947  
;; FILING DATE: 23 FEB 1994  
;; APPLICATION NUMBER: US 07/864,805  
;; FILING DATE: 7 APR 1992  
;; APPLICATION NUMBER: US 08/247,505  
;; FILING DATE: 23 MAY 1994  
;; APPLICATION NUMBER: US 07/864,866  
;; FILING DATE: 7 APR 1992  
;; APPLICATION NUMBER: US 08/218,155  
;; FILING DATE: 25 MAR 1994  
;; APPLICATION NUMBER: US 07/864,807  
;; FILING DATE: 7 APR 1992  
;; APPLICATION NUMBER: US 07/902,467  
;; FILING DATE: 16 JUNE 1992  
;; APPLICATION NUMBER: US 07/275,433  
;; FILING DATE: 23 NOV 1988  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Superko, Colleen  
;; REGISTRATION NUMBER: 39,850  
;; REFERENCE/DOCKET NUMBER: 36119-125 (US10)  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617) 526-6564  
;; TELEFAX: (617) 526-5000  
;; INFORMATION FOR SEQ ID NO: 6:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 227 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; ANTI-SENSE: NO  
;; FRAGMENT TYPE: internal  
;; ORIGINAL SOURCE:  
;; US-09-349-915B-6

Query Match 100.0%; Score 80; DB 2; Length 227;  
Best Local Similarity 100.0%; Pred. No. 8.3e-79;  
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVIKEVQEFYKDYTKLTKDPEQRETLKAIHYALNCCGLAGGVQFISDIPCKDV 60  
DB 112 HKDEVIKEVQEFYKDYTKLTKDPEQRETLKAIHYALNCCGLAGGVQFISDIPCKDV 171

QY 61 LETFTVKSCPDAIKEVFNK 80  
DB 172 LETFTVKSCPDAIKEVFNK 191

RESULT 9  
US-08-408-222B-1  
; Sequence 1, Application US/08408222B  
; Patent No. 5776727  
; GENERAL INFORMATION:  
; APPLICANT: Ikeyama, Shuichi  
; APPLICANT: Koyama, Masaru  
; APPLICANT: Miyake, Masayuki  
; APPLICANT: Senoo, Masaharu  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: 130 Water Street  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; SOFTWARE: IBM Compatible

;;  
;; OPERATING SYSTEM: DOS  
;; SOFTWARE: FastSeq Version 1.5  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/408,222B  
;; FILING DATE: 22-MAR-1995  
;; CLASSIFICATION: 536  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/254,493  
;; FILING DATE: 06-JUN-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: JP-079996-1991  
;; FILING DATE: 12-APR-1991  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: JP-085396-1991  
;; FILING DATE: 14-APR-1991  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: JP-022321-1992  
;; FILING DATE: 07-FEB-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Resnick, David S.  
;; REGISTRATION NUMBER: 34,235  
;; REFERENCE/DOCKET NUMBER: 41777-DIV  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 617-523-3400  
;; TELEFAX: 617-523-6440  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 228 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
;; FRAGMENT TYPE: internal  
;; ORIGINAL SOURCE:  
;; US-08-408-222B-1

Query Match 100.0%; Score 80; DB 1; Length 228;  
Best Local Similarity 100.0%; Pred. No. 8.3e-79;  
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVIKEVQEFYKDYTKLTKDPEQRETLKAIHYALNCCGLAGGVQFISDIPCKDV 60  
DB 113 HKDEVIKEVQEFYKDYTKLTKDPEQRETLKAIHYALNCCGLAGGVQFISDIPCKDV 172

QY 61 LETFTVKSCPDAIKEVFNK 80  
DB 173 LETFTVKSCPDAIKEVFNK 192

RESULT 10  
US-08-630-172-8  
; Sequence 8, Application US/08630172  
; Patent No. 6060054  
; GENERAL INFORMATION:  
; APPLICANT: Staerz, Uwe  
; TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T  
; TITLE OF INVENTION: LYMPHOCYTE VETO  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sheridan Ross & McIntosh  
; STREET: 1700 Lincoln Street, 35th Floor  
; CITY: Denver  
; STATE: Colorado  
; COUNTRY: U.S.  
; ZIP: 80203  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:



APPLICATION NUMBER: US/08/630,172  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Connell, Gary J.  
REGISTRATION NUMBER: 32,020  
REFERENCE/DOCKET NUMBER: 2879-36  
TELEPHONE: (303) 863-9700  
TELEFAX: (303) 863-0223  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 79 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-630-172-8

Query Match 58.8%; Score 47; DB 2; Length 79;  
Best Local Similarity 100.0%; Pred. No. 1.9e-43;  
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVKEVQEFYKDTYNKLTQKDBPQRETLKAIHYALNCCGLAGV 47  
DB 1 HKDEVKEVQEFYKDTYNKLTQKDBPQRETLKAIHYALNCCGLAGV 47

RESULT 11  
US-09-375-419-8  
Sequence 8, Application US/09375419  
Patent No. 6264950  
GENERAL INFORMATION:  
APPLICANT: Staerz, Uwe  
TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T  
TITLE OF INVENTION: LYMPHOCYTE VETO  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheridan Ross & McIntosh  
STREET: 1700 Lincoln Street, 35th Floor  
CITY: Denver  
STATE: Colorado  
COUNTRY: U.S.  
ZIP: 80203  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/375,419  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/630,172  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Connell, Gary J.  
REGISTRATION NUMBER: 32,020  
REFERENCE/DOCKET NUMBER: 2879-36  
TELEPHONE: (303) 863-9700  
TELEFAX: (303) 863-0223  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 79 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-375-419-8

Query Match 58.8%; Score 47; DB 2; Length 79;  
Best Local Similarity 100.0%; Pred. No. 1.9e-43;  
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVKEVQEFYKDTYNKLTQKDBPQRETLKAIHYALNCCGLAGV 47  
DB 1 HKDEVKEVQEFYKDTYNKLTQKDBPQRETLKAIHYALNCCGLAGV 47

RESULT 12  
US-08-254-493-4  
Sequence 4, Application US/08254493  
Patent No. 5439886  
GENERAL INFORMATION:  
APPLICANT: IKEYAMA, SHUICHI  
APPLICANT: KOYAMA, MASARU  
APPLICANT: MIYAKE, MASAYUKI  
APPLICANT: SENOO, MASAHARU  
TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND  
TITLE OF INVENTION: PRODUCTION THEREOF  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
STREET: 130 WATER STREET  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: US  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/254,493  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/865552  
FILING DATE: 09-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 079996-1991  
FILING DATE: 12-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 085396-1991  
FILING DATE: 17-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 022321-1992  
FILING DATE: 07-FEB-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: RESNICK, DAVID S.  
REGISTRATION NUMBER: 34235  
REFERENCE/DOCKET NUMBER: 41777  
TELEPHONE: (617) 523-3400  
TELEFAX: (617) 523-6440  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-254-493-4

Query Match 37.5%; Score 30; DB 1; Length 30;  
Best Local Similarity 100.0%; Pred. No. 2.1e-25;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KDEVKEVQEFYKDTYNKLTQKDBPQRETL 31  
DB 1 KDEVKEVQEFYKDTYNKLTQKDBPQRETL 30

RESULT 13

US-08-408-222B-4  
; Sequence 4, Application US/08408222B  
; Patent No. 5776727  
; GENERAL INFORMATION:  
; APPLICANT: Ikeyama, Shuichi  
; APPLICANT: Koyama, Masaru  
; APPLICANT: Miyake, Masayuki  
; APPLICANT: Senoo, Masaharu  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/408,222B  
; FILING DATE: 22-MAR-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/254,493  
; FILING DATE: 06-JUN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP-079996-1991  
; FILING DATE: 12-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP-085396-1991  
; FILING DATE: 07-FEB-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Resnick, David S.  
; REGISTRATION NUMBER: 34,235  
; REFERENCE/DOCKET NUMBER: 41777-DIV  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-523-6440  
; TELEFAX: 617-523-6440  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 30 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-408-222B-4  
Query Match 37.5%; Score 30; DB 1; Length 30;  
Best Local Similarity 100.0%; Pred. No. 2.1e-25;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 KDEVIKEVQEFYKOTYKTKDEPQRETL 31  
Db 1 KDEVIKEVQEFYKOTYKTKDEPQRETL 30  
RESULT 14  
US-08-254-493-5  
; Sequence 5, Application US/08254493  
; Patent No. 5439886  
; GENERAL INFORMATION:  
; APPLICANT: IKEYAMA, SHUICHI  
; APPLICANT: KOYAMA, MASARU  
; APPLICANT: MIYAKE, MASAYUKI  
; APPLICANT: SENOO, MASAHARU  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
; STREET: 130 WATER STREET  
; CITY: BOSTON  
; STATE: MASSACHUSETTS  
; COUNTRY: US

; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
; STREET: 130 WATER STREET  
; CITY: BOSTON  
; STATE: MASSACHUSETTS  
; COUNTRY: US  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/254,493  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/865552  
; FILING DATE: 09-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 079996-1991  
; FILING DATE: 12-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 085396-1991  
; FILING DATE: 17-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 022321-1992  
; FILING DATE: 07-FEB-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: RESNICK, DAVID S.  
; REGISTRATION NUMBER: 34235  
; REFERENCE/DOCKET NUMBER: 41777  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 523-3400  
; TELEFAX: (617) 523-6440  
; TELEX: 200291 STRE UR  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 29 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-254-493-5  
Query Match 36.2%; Score 29; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 2.5e-24;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 27 QRETLKAIHYALNCCGLAGVGEQFISDIC 55  
Db 1 QRETLKAIHYALNCCGLAGVGEQFISDIC 29  
RESULT 15  
US-08-254-493-6  
; Sequence 6, Application US/08254493  
; Patent No. 5439886  
; GENERAL INFORMATION:  
; APPLICANT: IKEYAMA, SHUICHI  
; APPLICANT: KOYAMA, MASARU  
; APPLICANT: MIYAKE, MASAYUKI  
; APPLICANT: SENOO, MASAHARU  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
; STREET: 130 WATER STREET  
; CITY: BOSTON  
; STATE: MASSACHUSETTS  
; COUNTRY: US

;  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/254,493  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/865552  
; FILING DATE: 09-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 079996-1991  
; FILING DATE: 12-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 085396-1991  
; FILING DATE: 17-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 022321-1992  
; FILING DATE: 07-FEB-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: RESNICK, DAVID S.  
; REGISTRATION NUMBER: 34235  
; REFERENCE/DOCKET NUMBER: 41777  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 523-3400  
; TELEFAX: (617) 523-6440  
; TELEX: 200291 STRE UR  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 29 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-254-493-6

Query Match 36.2%; Score 29; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 2.5e-24;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 52 SDICPKQVLETFYTKSCPDAIKEVFDNK 80  
|||  
Db 1 SDICPKQVLETFYTKSCPDAIKEVFDNK 29

Search completed: January 20, 2006, 17:45:25  
Job time : 35.2308 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2006, 17:44:47 ; Search time 76 Seconds  
(without alignments)  
462.504 Million cell updates/sec

Title: US-10-619-323-1\_COPY\_113\_192

Perfect score: 80

Sequence: 1 HKDEVIKEQVEFYKDYTNKL.....LEFTVKSCPDAIKVFDPNK 80

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1293556

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Listing first 1000 summaries

Database : A\_Geneseq\_21.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*
- 9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	47	58.8	79	6	Abu05058 Human exp
3	38	47.5	38	8	Adj57561 Human CD9
4	32	40.0	30	6	Abp76310 Human GEN
5	30	37.5	30	6	Abu05051 Human exp
6	25	31.2	25	8	Adj57562 Human CD9
7	22	27.5	22	8	Adj57564 Human CD9
8	22	27.5	24	8	Adj57578 Human CD9
9	18	22.5	18	8	Adj57563 Human CD9
10	10	12.5	10	6	Abu03385 Human exp
11	8	10.0	33	5	ABP43064 Human ova
12	7	8.8	58	5	Abu51670 Helicobac
13	6	7.5	16	6	ABR67406 Human pro
14	6	7.5	16	2	Aaw31082 Mugwort p
15	6	7.5	18	9	Adj67376 Amino aci
16	6	7.5	20	8	Adj95249 OSPF-rela
17	6	7.5	20	8	Adi95250 OSPF-rela
18	6	7.5	25	9	Ady28634 Novel mod
19	6	7.5	25	9	Ady28635 Novel mod
20	6	7.5	29	7	ADG14386 Cytochrom
21	6	7.5	31	7	Adi49210 Human HMG
22	6	7.5	33	6	Abu18835 Human Bcl
23	6	7.5	37	7	Adf13922 Human end
24	6	7.5	42	3	Aag55485 Arabidops

98	5	6.2	10	6	ABP75115	Abp75115 Proteome	171	5	6.2	15	7	ADE70504	Adc70504 Human 161
99	5	6.2	10	7	AD223868	Ad223868 Breast ca	172	5	6.2	15	7	ADE70503	Adc70503 Human 161
100	5	6.2	10	7	AD66418	Ad66418 Human 161	173	5	6.2	15	7	ADE70820	Adc70820 Human 161
101	5	6.2	10	7	AD69278	Ad69278 Human 161	174	5	6.2	15	7	ADW33381	Adw33381 HLA bindi
102	5	6.2	10	7	AD69292	Ad69292 Human 161	175	5	6.2	15	7	ADW34614	Adw34614 HLA bindi
103	5	6.2	10	7	AD67636	Ad67636 Human 161	176	5	6.2	15	8	ADP26486	Adp26486 Plaemodiu
104	5	6.2	10	7	AD666384	Ad666384 Human 161	177	5	6.2	15	8	ADR19120	Adr19120 Type IV c
105	5	6.2	10	7	AD666679	Ad666679 Human 161	178	5	6.2	15	8	ADR19111	Adr19111 Type IV c
106	5	6.2	10	7	AD667382	Ad667382 Human 161	179	5	6.2	15	9	ADV21817	Adv21817 SIV pol p
107	5	6.2	10	7	ADW30960	Adw30960 HLA bindi	180	5	6.2	15	9	ADV21818	Adv21818 SIV pol p
108	5	6.2	10	8	ADG94770	Adg94770 Human JAM	181	5	6.2	15	9	ADV21819	Adv21819 SIV pol p
109	5	6.2	10	8	ADI47144	Adi47144 Human-der	182	5	6.2	15	9	ADW86218	Adw86218 Human mus
110	5	6.2	10	8	ADK05372	Adk05372 Hepatitis	183	5	6.2	15	9	ADZ88943	Adz88943 Human mus
111	5	6.2	10	8	ADK06991	Adk06991 Hepatitis	184	5	6.2	16	2	AAW38987	Aaw38987 Peptide r
112	5	6.2	10	8	ADP87345	Adp87345 Human cla	185	5	6.2	17	2	AAR54389	Aar54389 RAE 29.1-
113	5	6.2	11	1	AAW33025	Aaw33025 Shiga tox	186	5	6.2	17	2	AAR54389	Aar54389 RAE 29.1-
114	5	6.2	11	4	ABW88297	Abw88297 Hsp-65 pe	187	5	6.2	17	2	AAW02473	Aaw02473 RAE 29.1-
115	5	6.2	11	4	ABW88232	Abw88232 Hsp-65 pe	188	5	6.2	17	4	ABW88288	Abw88288 Hsp-65 pe
116	5	6.2	11	4	ABW88298	Abw88298 Hsp-65 pe	189	5	6.2	17	8	ADW96816	Adw96816 Tissue fa
117	5	6.2	11	6	ABU36793	Abu36793 G protein	190	5	6.2	17	8	ADM96915	Adm96915 Tissue fa
118	5	6.2	11	8	ADT51214	Adt51214 G protein	191	5	6.2	18	2	AAR94845	Aar94845 Peptide f
119	5	6.2	12	7	ADW35524	Adw35524 HLA bindi	192	5	6.2	18	2	AAW43523	Aaw43523 Mycobacte
120	5	6.2	12	7	ADW34291	Adw34291 HLA bindi	193	5	6.2	18	4	ABW51354	Abw51354 Bovine HS
121	5	6.2	12	8	ADT40727	Adt40727 hSARS vir	194	5	6.2	18	4	ABW88292	Abw88292 Hsp-65 pe
122	5	6.2	12	8	ADW80143	Adw80143 SARS viru	195	5	6.2	18	4	ABW88287	Abw88287 Hsp-65 pe
123	5	6.2	12	8	ADT38257	Adt38257 hSARS vir	196	5	6.2	18	4	ADW17673	Adw17673 Type IV c
124	5	6.2	12	9	ADV25827	Adv25827 SARS coro	197	5	6.2	18	8	ADR19195	Adr19195 SRP plus
125	5	6.2	12	9	ADV12954	Adv12954 Human pho	198	5	6.2	18	8	ADR84049	Adr84049 S. pyogen
126	5	6.2	13	2	AAW50131	Aaw50131 Pan DR bi	199	5	6.2	19	4	ABW88286	Abw88286 Hsp-65 pe
127	5	6.2	13	4	ABW88296	Abw88296 Hsp-65 pe	200	5	6.2	19	4	ABW88291	Abw88291 Hsp-65 pe
128	5	6.2	13	5	ADG66141	Adg66141 Human pro	201	5	6.2	19	5	AAU8289	Aau8289 Insulin/i
129	5	6.2	13	5	ADG66144	Adg66144 Human pro	202	5	6.2	19	6	ABU13493	Abu13493 Zona pell
130	5	6.2	13	5	ADG66142	Adg66142 Human pro	203	5	6.2	19	6	ABU13494	Abu13494 Zona pell
131	5	6.2	13	5	ADG66143	Adg66143 Human pro	204	5	6.2	19	7	ABW74372	Abw74372 DNA clone
132	5	6.2	13	5	ADG66140	Adg66140 Human pro	205	5	6.2	19	7	ADC17676	Adc17676 Type IV c
133	5	6.2	13	7	ADP23246	Adp23246 Breast ca	206	5	6.2	19	8	ADR19198	Adr19198 SRP plus
134	5	6.2	14	1	APB3024	Apb3024 Shiga tox	207	5	6.2	20	1	APB3023	Apb3023 Shiga Cox
135	5	6.2	14	2	ARK54390	Ark54390 RAE 29.1-	208	5	6.2	20	2	AAW54386	Aaw54386 RAE 29.1-
136	5	6.2	14	2	AAW02474	Aaw02474 RAE 29.1-	209	5	6.2	20	2	AAW54387	Aaw54387 RAE 29.1-
137	5	6.2	14	2	AAW02474	Aaw02474 RAE 29.1-	210	5	6.2	20	2	AAW13200	Aaw13200 Fragment
138	5	6.2	14	3	AAW99191	Aaw99191 HLA class	211	5	6.2	20	2	AAW02471	Aaw02471 RAE 29.1-
139	5	6.2	14	3	ABW30019	Abw30019 Scaffold	212	5	6.2	20	2	AAW02470	Aaw02470 RAE 29.1-
140	5	6.2	14	4	AAW99099	Aaw99099 Vaccine r	213	5	6.2	20	2	AAW67520	Aaw67520 IGF-1/IGF
141	5	6.2	14	8	ADO40746	Ado40746 Human A6	214	5	6.2	20	2	AAW67521	Aaw67521 IGF-1/IGF
142	5	6.2	14	8	ADO40742	Ado40742 Human A6	215	5	6.2	20	2	AAW67521	Aaw67521 IGF-1/IGF
143	5	6.2	14	8	ADO40756	Ado40756 Human A6	216	5	6.2	20	3	AAW66841	Aaw66841 T cell an
144	5	6.2	14	8	ADO40754	Ado40754 Human A6	217	5	6.2	20	4	AAE12279	Aae12279 Mycobacte
145	5	6.2	14	8	ADO40736	Ado40736 Human A6	218	5	6.2	20	4	AAW63758	Aaw63758 Synthetic
146	5	6.2	14	8	ADO40744	Ado40744 Human A6	219	5	6.2	20	4	AAW63757	Aaw63757 Synthetic
147	5	6.2	15	2	ARK94846	Ark94846 Peptide f	220	5	6.2	20	5	ABB57679	Abb57679 IGFBP-3 b
148	5	6.2	15	2	AAW43524	Aaw43524 Mycobacte	221	5	6.2	20	5	ABB57677	Abb57677 IGFBP-3 b
149	5	6.2	15	3	ABW30318	Abw30318 Human epi	222	5	6.2	20	5	AAU73539	Aau73539 Vascular
150	5	6.2	15	3	ABW30318	Abw30318 Human epi	223	5	6.2	20	5	ABB96959	Abb96959 Human tum
151	5	6.2	15	3	ABW30328	Abw30328 Human epi	224	5	6.2	20	5	ABB96960	Abb96960 Human tum
152	5	6.2	15	4	ABW83346	Abw83346 Dopamine	225	5	6.2	20	7	ADD12335	Add12335 PDZ ligan
153	5	6.2	15	5	AAU73469	Aau73469 Vascular	226	5	6.2	20	7	ADD84840	Add84840 Synthetic
154	5	6.2	15	6	ABR38255	Abw38255 Human can	227	5	6.2	20	7	ADD84841	Add84841 Synthetic
155	5	6.2	15	6	ABR38255	Abw38255 Human can	228	5	6.2	20	7	ADH48153	Adh48153 IGFBP-3 b
156	5	6.2	15	6	ABR38226	Abw38226 Human can	229	5	6.2	20	7	ADH48154	Adh48154 IGFBP-3 b
157	5	6.2	15	6	ABR38106	Abw38106 Human can	230	5	6.2	20	8	ADP47645	Adp47645 Insulin-1
158	5	6.2	15	6	ABR38056	Abw38056 Human can	231	5	6.2	20	8	ADP47644	Adp47644 Insulin-1
159	5	6.2	15	6	ABR38064	Abw38064 Human can	232	5	6.2	20	8	ADG39591	Adg39591 IGFBP-3 b
160	5	6.2	15	6	ABR38091	Abw38091 Human can	233	5	6.2	20	8	ADG39590	Adg39590 IGFBP-3 b
161	5	6.2	15	6	ABP83158	Abp83158 G protein	234	5	6.2	20	8	ADI62073	Adi62073 IGFBP-3 b
162	5	6.2	15	7	ADC17598	Adc17598 Type IV c	235	5	6.2	20	8	ADI62074	Adi62074 IGFBP-3 b
163	5	6.2	15	7	ADW17589	Adw17589 Type IV c	236	5	6.2	20	8	ADI57584	Adi57584 Inhibitor
164	5	6.2	15	7	ADW70454	Adw70454 Human 161	237	5	6.2	20	8	ADI57585	Adi57585 Inhibitor
165	5	6.2	15	7	ADW70205	Adw70205 Human 161	238	5	6.2	20	8	ADI57477	Adi57477 Inhibitor
166	5	6.2	15	7	ADW70643	Adw70643 Human 161	239	5	6.2	20	8	ADI57478	Adi57478 Inhibitor
167	5	6.2	15	7	ADW70354	Adw70354 Human 161	240	5	6.2	20	8	ADJ56634	Adj56634 Inhibitor
168	5	6.2	15	7	ADW70728	Adw70728 Human 161	241	5	6.2	20	8	ADJ56633	Adj56633 Inhibitor
169	5	6.2	15	7	ADW70068	Adw70068 Human 161	242	5	6.2	20	8	ADJ58155	Adj58155 Insulin-1
170	5	6.2	15	7	ADW70355	Adw70355 Human 161	243	5	6.2	20	8	ADJ58156	Adj58156 Insulin-1

244	5	6.2	20	8	ADJ45156	Adj45156 Inhibitor	317	5	6.2	33	2	AAW29234	Aaw29234 Membrane
245	5	6.2	20	8	ADJ45155	Adj45155 Inhibitor	318	5	6.2	33	9	ADV13248	Adv13248 Human pho
246	5	6.2	20	8	ADM86651	Adm86651 E. coli p	319	5	6.2	34	9	Aaw29230	Aaw29230 Membrane
247	5	6.2	20	8	ADM76502	Adm76502 IGFBP-3 b	320	5	6.2	34	9	ADV56005	Adv56005 G protein
248	5	6.2	20	8	ADM76501	Adm76501 IGFBP-3 b	321	5	6.2	34	9	ADV55451	Adv55451 G protein
249	5	6.2	20	8	ADL08270	Adl08270 Inhibitor	322	5	6.2	34	9	ADV55963	Adv55963 G protein
250	5	6.2	20	8	ADL08269	Adl08269 Inhibitor	323	5	6.2	36	2	AAR54449	Aar54449 Amb a I.1
251	5	6.2	20	8	ADN32752	Adn32752 Insulin-1	324	5	6.2	36	2	AAW02504	Aaw02504 Peptide c
252	5	6.2	20	8	ADN32753	Adn32753 Insulin-1	325	5	6.2	36	2	AAV35985	Aav35985 Extended
253	5	6.2	20	8	ADU63739	Adu63739 SARS coro	326	5	6.2	36	4	AAW99616	Aaw99616 Human exc
254	5	6.2	21	4	AA888285	Aab88285 Hsp-65 pe	327	5	6.2	36	4	AAW96738	Aag76738 Human col
255	5	6.2	21	5	ABG69737	Abg69737 Polypteti	328	5	6.2	36	4	ABG26327	Abg26327 Novel hum
256	5	6.2	22	3	AAV98364	Aay98364 Alpha D p	329	5	6.2	36	4	AAW42431	Aam42431 Human kid
257	5	6.2	22	3	AAV98365	Aay98365 Alpha D p	330	5	6.2	36	7	ADD69608	Add69608 Human REM
258	5	6.2	22	5	ABP62321	Abp62321 Human inm	331	5	6.2	36	8	ADP19293	Adp19293 Human sec
259	5	6.2	22	5	ABP62322	Abp62322 Human inm	332	5	6.2	37	2	AAV20292	Aay20292 Human apo
260	5	6.2	22	5	ABP62320	Abp62320 Human inm	333	5	6.2	37	2	AAV07047	Aay07047 Breat ca
261	5	6.2	22	5	ABP62319	Abp62319 Human inm	334	5	6.2	37	3	AAW28204	Aab28204 Novel hum
262	5	6.2	22	6	ABR54847	AbR54847 Human inm	335	5	6.2	37	6	ABU61207	Abu61207 Human A d
263	5	6.2	22	9	AEB19163	Aeb19163 Igm heavy	336	5	6.2	37	8	ADP21429	Adp21429 Human LDL
264	5	6.2	23	2	AAR54385	Aar54385 RAE 74.1-	337	5	6.2	38	4	AAW17291	Aam17291 Peptide #
265	5	6.2	23	2	AAW02469	Aaw02469 RAE 74.1-	338	5	6.2	38	4	ABW36296	Abb36296 Peptide #
266	5	6.2	23	4	AA888295	Aab88295 Hsp-65 pe	339	5	6.2	38	4	ABB42598	Abb42598 Peptide #
267	5	6.2	23	5	ABG47126	Abg47126 Human pep	340	5	6.2	38	4	AAW36414	Aam36414 Peptide #
268	5	6.2	23	6	ABO12075	Abol12075 Human zin	341	5	6.2	38	4	AAW29790	Aam29790 Peptide #
269	5	6.2	24	4	AA888284	Aab88284 Hsp-65 pe	342	5	6.2	38	4	ABW64809	Aab64809 Human sec
270	5	6.2	24	9	ADV13017	Adv13017 Human pho	343	5	6.2	38	4	ABB31099	Abb31099 Peptide #
271	5	6.2	25	2	AAW64578	Aaw64578 Human Fac	344	5	6.2	38	4	ABB21657	Abb21657 Protein #
272	5	6.2	25	2	AAW00362	Aay00362 Fragment	345	5	6.2	38	4	AAW69454	Aam69454 Human bon
273	5	6.2	25	3	AA844341	Aab44341 Human sec	346	5	6.2	38	4	AAW76304	Aam76304 Human bon
274	5	6.2	25	4	AAW15499	Aam15499 Peptide #	347	5	6.2	38	4	AAW57067	Aam57067 Human bra
275	5	6.2	25	4	ABW34505	Abb34505 Peptide #	348	5	6.2	38	4	AAW63489	Aam63489 Human bra
276	5	6.2	25	4	AAW27987	Aam27987 Peptide #	349	5	6.2	38	4	ABW51130	Abw51130 Human liv
277	5	6.2	25	4	ABW29333	Abb29333 Peptide #	350	5	6.2	38	4	ABW58014	Abw58014 Human liv
278	5	6.2	25	4	ABW19216	Abb19216 Protein #	351	5	6.2	38	4	AAW04976	Aam04976 Peptide #
279	5	6.2	25	4	AAW67690	Aam67690 Human bon	352	5	6.2	38	5	ABG39078	Abg39078 Human pep
280	5	6.2	25	4	AAW55292	Aam55292 Human bra	353	5	6.2	38	5	ABG45607	Abg45607 Human pep
281	5	6.2	25	4	AAW64064	Aab64064 Human Cla	354	5	6.2	39	7	ADD88693	Add88693 Malarial
282	5	6.2	25	4	AAW64063	Aab64063 Human Cla	355	5	6.2	39	7	ADG18458	Adg18458 P. falcip
283	5	6.2	25	4	ABG49323	Abg49323 Human liv	356	5	6.2	39	9	ADW92620	Adw92620 P. falcip
284	5	6.2	25	4	AAW03356	Aam03356 Peptide #	357	5	6.2	40	4	ABB41573	Abb41573 Peptide #
285	5	6.2	25	7	ADW90427	Adw90427 Novel hum	358	5	6.2	40	4	ABB37513	Abb37513 Peptide #
286	5	6.2	25	7	ADG90246	Adg90246 Human sec	359	5	6.2	40	4	AAW35365	Aam35365 Peptide #
287	5	6.2	25	9	ADY25586	Ady25586 Novel hum	360	5	6.2	40	4	AAW70626	Aam70626 Human bon
288	5	6.2	26	2	AAR54435	Aar54435 AMB 4-9.1	361	5	6.2	40	4	AAW75253	Aam75253 Human bon
289	5	6.2	26	2	AAR54384	Aar54384 RAE 74.1.	362	5	6.2	40	4	AAW05085	Aao05085 Human pol
290	5	6.2	26	2	AAW02468	Aaw02468 RAE 74.1.	363	5	6.2	40	4	AAW58175	Aam58175 Human bra
291	5	6.2	26	2	AAW02416	Aaw02416 AMB 4-9.1	364	5	6.2	40	4	AAW62444	Aam62444 Human liv
292	5	6.2	26	2	AAW05595	Aaw05595 Membrane	365	5	6.2	40	4	ABG57015	Abg57015 Human liv
293	5	6.2	26	4	AA888310	Aab88310 Hsp-65 pe	366	5	6.2	40	5	AAW06061	Aam06061 Peptide #
294	5	6.2	26	6	ABW99526	Abw99526 Amino aci	367	5	6.2	40	5	ABG44901	Abg44901 Human pep
295	5	6.2	27	4	AAW17891	Aam17891 Peptide #	368	5	6.2	41	2	AAV49097	Aay49097 Amino aci
296	5	6.2	27	4	ABB36916	Abb36916 Peptide #	369	5	6.2	41	3	AAW53229	Aab53229 Protein c
297	5	6.2	27	4	AAW30400	Aam30400 Peptide #	370	5	6.2	41	3	AAW29580	Aag29580 Arabidops
298	5	6.2	27	4	ABB31700	Abb31700 Peptide #	371	5	6.2	41	4	AAU29908	Aau29908 Novel hum
299	5	6.2	27	4	ABB22241	Abb22241 Protein #	372	5	6.2	41	7	ADL11747	Adl11747 Human sec
300	5	6.2	27	4	AAW70068	Aam70068 Human bon	373	5	6.2	42	2	AAW05617	Aaw05617 MVFlth-GG
301	5	6.2	27	4	AAW57659	Aam57659 Human bra	374	5	6.2	42	2	AAW05621	Aaw05621 HBSTH-GG-
302	5	6.2	27	4	ABG51759	Abg51759 Human liv	375	5	6.2	42	3	AAV76125	Aay76125 Human sec
303	5	6.2	27	4	AAW05544	Aam05544 Peptide #	376	5	6.2	43	2	AAW05618	Aaw05618 mIGB1-GG-
304	5	6.2	27	5	ABG39700	Abg39700 Human pep	377	5	6.2	43	2	AAW05622	Aaw05622 mIGB1-GG-
305	5	6.2	28	2	AAR54434	Aar54434 AMB 4-8.1	378	5	6.2	43	2	AAW91058	Aaw91058 Flanking
306	5	6.2	28	4	AAW99100	Aam99100 Vaccine r	379	5	6.2	43	2	AAV49096	Aay49096 Amino aci
307	5	6.2	28	4	AAE07404	Aae07404 Synthetic	380	5	6.2	43	3	AAW27072	Aab27072 Beta-cate
308	5	6.2	28	5	AAE15758	Aae15758 pda8d pep	381	5	6.2	43	3	AAW39250	Aab39250 Human sec
309	5	6.2	28	5	AAU76766	Aau76766 pda8d pep	382	5	6.2	43	4	AAU22457	Aau22457 Human car
310	5	6.2	28	5	ABG75545	Abg75545 Opt.imised	383	5	6.2	43	7	ABE46425	Ade46425 Human car
311	5	6.2	29	2	AAW02415	Aaw02415 AMB 4-8.1	384	5	6.2	43	8	ADJ07843	Adj07843 Human car
312	5	6.2	30	2	AAW54388	Aar54388 RAE 28+29	385	5	6.2	43	9	ADX25649	Adx25649 Potato pa
313	5	6.2	30	2	AAW02472	Aaw02472 RAE 28+29	386	5	6.2	44	4	AAW74910	Aag74910 Human col
314	5	6.2	31	7	ADA07577	Ada07577 Human sec	387	5	6.2	44	4	AAW95874	Aam95874 Human rep
315	5	6.2	31	8	ADN41386	Adn41386 Novel hum	388	5	6.2	44	4	ABB96405	Abb96405 Human tee
316	5	6.2	32	8	ADH18893	Adh18893 Human cel	389	5	6.2	44	6	ABB99525	Abb99525 Amino aci

390	5	6.2	45	4	ABR17677	Abb17677 Human ner	463	5	6.2	55	2	AAR13464	Aar13464 Membrane
391	5	6.2	45	5	ABR40588	Abf40588 Human sec	464	5	6.2	55	2	AAR43310	Aar43310 Human eps
392	5	6.2	45	8	ADH56328	Adh56328 Human S30	465	5	6.2	55	2	AAR60228	Aar60228 Human IGE
393	5	6.2	45	8	ADH505162	Adh505162 Staphyloc	466	5	6.2	55	2	AAR90134	Aar90134 Human IGE
394	5	6.2	45	8	ADR84017	Adr84017 S. pyogen	467	5	6.2	55	4	AAM20074	Aam20074 Peptide #
395	5	6.2	46	2	AAW12809	Aaw12809 Hepatitis	468	5	6.2	55	4	ABB40231	Abb40231 Peptide #
396	5	6.2	46	4	AAW83497	Aam83497 Human imm	469	5	6.2	55	4	AAW33891	Aam33891 Peptide #
397	5	6.2	46	6	ABU06983	Abu06983 Maize Sta	470	5	6.2	55	4	AAW87877	Aam87877 Human imm
398	5	6.2	46	8	ADU14874	Adu14874 Pseudomon	471	5	6.2	55	4	AAW81203	Aam81203 Human hae
399	5	6.2	47	2	AAW54445	Aaw54445 Amb a 1.1	472	5	6.2	55	4	ABB24663	Abb24663 Protein #
400	5	6.2	47	2	AAW02500	Aaw02500 Peptide c	473	5	6.2	55	4	AAW73705	Aam73705 Human bon
401	5	6.2	47	2	AAW77585	Aaw77585 Staphyloc	474	5	6.2	55	4	AAU67645	Aau67645 Propionib
402	5	6.2	47	3	AAV91367	Aay91367 Human sec	475	5	6.2	55	4	AAU61010	Aau61010 Human bra
403	5	6.2	47	4	AAW91285	Aam91285 Human imm	476	5	6.2	55	4	ABG55442	Abg55442 Human liv
404	5	6.2	47	4	AAW04542	Aao04542 Human pol	477	5	6.2	55	5	ABG43580	Abg43580 Human pep
405	5	6.2	47	5	ABU10245	Abu10245 Human lun	478	5	6.2	55	6	ABM64164	Abm64164 Propionib
406	5	6.2	47	5	AAW47160	Aam47160 Modular e	479	5	6.2	56	9	ADY65290	Ady65290 S. mansoni
407	5	6.2	47	6	ABW99527	Abw99527 Amino aci	480	5	6.2	58	2	ADH11263	Adh11263 Vertebrat
408	5	6.2	47	8	ADT40570	Adt40570 hSARS vir	481	5	6.2	58	4	AAW14808	Aam14808 Peptide #
409	5	6.2	47	8	ADW79987	Adw79987 SARS viru	482	5	6.2	58	4	AAW16867	Aam16867 Peptide #
410	5	6.2	47	8	ADT38100	Adt38100 hSARS vir	483	5	6.2	58	4	ABB33775	Abb33775 Peptide #
411	5	6.2	48	2	AAW19273	Aaw19273 Lactobin	484	5	6.2	58	4	ABB33775	Abb33775 Peptide #
412	5	6.2	48	4	ABG16211	Abg16211 Novel hum	485	5	6.2	58	4	AAW29352	Aam29352 Peptide #
413	5	6.2	48	5	ABW79289	Abw79289 Human pro	486	5	6.2	58	4	AAW27235	Aam27235 Peptide #
414	5	6.2	49	3	AAV97055	Aay97055 T helper	487	5	6.2	58	4	ABB28592	Abb28592 Peptide #
415	5	6.2	49	4	AAW18760	Aam18760 Peptide #	488	5	6.2	58	4	ABB21265	Abb21265 Protein #
416	5	6.2	49	4	ABB37858	Abb37858 Peptide #	489	5	6.2	58	4	ABB19219	Abb19219 Protein #
417	5	6.2	49	4	AAW31265	Aam31265 Peptide #	490	5	6.2	58	4	AAW69033	Aam69033 Human bon
418	5	6.2	49	4	ABB23118	Abb23118 Protein #	491	5	6.2	58	4	AAU56898	Aau56898 Propionib
419	5	6.2	49	4	AAW70989	Aam70989 Human bon	492	5	6.2	58	4	AAU56898	Aau56898 Propionib
420	5	6.2	49	4	AAW58489	Aam58489 Human bra	493	5	6.2	58	4	AAW54542	Aam54542 Human bra
421	5	6.2	49	4	ABG52706	Abg52706 Human liv	494	5	6.2	58	4	AAW56657	Aam56657 Human bra
422	5	6.2	49	5	ABG40508	Abg40508 Human pep	495	5	6.2	58	4	ABG50703	Abg50703 Human liv
423	5	6.2	49	5	ABG32776	Abg32776 Clone 161	496	5	6.2	58	4	ABG48612	Abg48612 Human liv
424	5	6.2	49	6	ABG73715	Abg73715 Murine TH	497	5	6.2	58	4	AAW02533	Aam02533 Peptide #
425	5	6.2	49	6	ABO01284	Abu01284 Growth de	498	5	6.2	58	5	ABP05921	Abp05921 Human ORF
426	5	6.2	49	8	ABH97009	Abh97009 S. pneumo	499	5	6.2	58	5	ABG36605	Abg36605 Human pep
427	5	6.2	49	9	ABG13364	Abg13364 Streptoco	500	5	6.2	58	5	ABG38630	Abg38630 Human pep
428	5	6.2	50	3	AGI51593	Agi51593 Arabidops	501	5	6.2	58	6	ABM53417	Abm53417 Propionib
429	5	6.2	50	4	AAW90864	Aam90864 Human imm	502	5	6.2	59	4	AAW99721	Aam99721 Human exc
430	5	6.2	50	4	AAW83061	Aam83061 Human imm	503	5	6.2	59	4	AAW84823	Aam84823 Human imm
431	5	6.2	50	4	AAU43635	Aau43635 Propionib	504	5	6.2	59	4	AAW42536	Aam42536 Human kid
432	5	6.2	50	6	ABW40154	Abw40154 Propionib	505	5	6.2	59	5	ABP32508	Abp32508 Human ORF
433	5	6.2	50	9	ADY17142	Ady17142 PRO polyt	506	5	6.2	59	8	ADU65699	Adu65699 S. agalact
434	5	6.2	50	9	AUZ98559	Auz98559 Human ami	507	5	6.2	60	4	ABH16085	Abh16085 Human ner
435	5	6.2	51	4	ABB38618	Abb38618 Peptide #	508	5	6.2	61	2	AAW58746	Aaw58746 Ragweed a
436	5	6.2	51	4	AAW32076	Aam32076 Peptide #	509	5	6.2	61	2	AAW58746	Aaw58746 Ragweed a
437	5	6.2	51	4	ABB23717	Abb23717 Protein #	510	5	6.2	61	2	AAW58752	Aaw58752 Ragweed a
438	5	6.2	51	4	AAW71787	Aam71787 Human bon	511	5	6.2	61	4	AAU47457	Aau47457 Propionib
439	5	6.2	51	4	AAW45988	Aau45988 Propionib	512	5	6.2	61	5	ABP04969	Abp04969 Human ORF
440	5	6.2	51	4	AAU64750	Aau64750 Propionib	513	5	6.2	61	5	ABH05858	Abh05858 UNC Clone
441	5	6.2	51	4	AAU49813	Aau49813 Propionib	514	5	6.2	61	5	ABH05856	Abh05856 UNC Clone
442	5	6.2	51	4	AAW59247	Aam59247 Human bra	515	5	6.2	61	5	ABH05930	Abh05930 UNC Clone
443	5	6.2	51	4	ABG53471	Abg53471 Human liv	516	5	6.2	61	5	ABH05928	Abh05928 UNC Clone
444	5	6.2	51	4	ABH15219	Abh15219 Human ner	517	5	6.2	61	6	ABM43976	Abm43976 Propionib
445	5	6.2	51	5	ABG41601	Abg41601 Human pep	518	5	6.2	62	4	AAU45594	Aau45594 Propionib
446	5	6.2	51	6	ABW46332	Abw46332 Propionib	519	5	6.2	62	5	ABP01694	Abp01694 Human ORF
447	5	6.2	51	6	ABM61269	Abm61269 Propionib	520	5	6.2	62	5	ABP30611	Abp30611 Streptoco
448	5	6.2	51	6	ABW42507	Abw42507 Propionib	521	5	6.2	62	5	ABG99606	Abg99606 Conus sp
449	5	6.2	52	2	AAW27803	Aaw27803 Amino aci	522	5	6.2	62	5	ABG99557	Abg99557 Conus sp
450	5	6.2	52	2	AAW93061	Aaw93061 Human Tan	523	5	6.2	62	5	ABG99589	Abg99589 Conus sp
451	5	6.2	52	4	AAO13321	Aao13321 Human pol	524	5	6.2	62	5	ABG99517	Abg99517 Conus sp
452	5	6.2	52	5	ABP02807	Abp02807 Human ORF	525	5	6.2	62	5	ABG99591	Abg99591 Conus sp
453	5	6.2	52	5	ABP34149	Abp34149 Human kin	526	5	6.2	62	5	ABG99604	Abg99604 Conus sp
454	5	6.2	53	2	AAW95647	Aaw95647 Klebsiell	527	5	6.2	62	5	ABG99600	Abg99600 Conus sp
455	5	6.2	53	3	AAW12366	Aag12366 Zea mays	528	5	6.2	62	6	ABM42113	Abm42113 Propionib
456	5	6.2	53	4	ABG74472	Aag74472 Human col	529	5	6.2	62	6	ABU00317	Abu00317 Human roy
457	5	6.2	53	5	ABP06547	Abp06547 Human ORF	530	5	6.2	62	8	ADR50887	Adr50887 C. textil
458	5	6.2	53	3	ABG02662	Abg02662 Human sec	531	5	6.2	62	9	ABM90902	Abm90902 M. xanthu
459	5	6.2	54	5	ABP06309	Abp06309 Human ORF	532	5	6.2	62	9	ABE17626	Aeb17626 Conus ban
460	5	6.2	54	8	ABO58532	Abu58532 Human gen	533	5	6.2	63	2	AAW55312	Aaw55312 H. pylori
461	5	6.2	54	8	ADW88816	Adw88816 Streptoco	534	5	6.2	63	2	AAW93058	Aaw93058 Human Tan
462	5	6.2	54	8	ADW80069	Adw80069 Streptoco	535	5	6.2	63	3	AAW97128	Aay97128 Tau conot



536	5	6.2	63	4	AAU46485	Aau46485 Propionib	609	69	2	AAV39396	Aav39396 Mutant Sh
537	5	6.2	63	6	ABM43004	Abm43004 Propionib	610	69	2	AAV43010	Aav43010 Mutant Sh
538	5	6.2	63	6	ABU61516	Abu61516 Novel fru	611	69	2	AAV43012	Aav43012 Mutant Sh
539	5	6.2	63	6	ABU30394	Abu30394 Protein e	612	69	2	AAV43015	Aav43015 Mutant Sh
540	5	6.2	63	8	ADK02076	Adk02076 Hepatitis	613	69	3	AAV68360	Aav68360 Verotoxin
541	5	6.2	63	8	ADK01365	Adk01365 Hepatitis	614	69	3	AAV66234	Aav66234 E coli he
542	5	6.2	64	3	AG26501	Aag26501 Arabidops	615	69	8	ADF39753	E. coli O
543	5	6.2	64	6	ABU00159	Abu00159 Human nov	616	69	8	ADK88488	Adk88488 Plant ful
544	5	6.2	64	7	ADC00242	Adc00242 Enterohae	617	69	9	ADV34850	Adv34850 Shiga tox
545	5	6.2	64	7	ADC00547	Adc00547 Enterohae	618	69	9	ADH11261	Adh11261 Vertebrat
546	5	6.2	65	2	AAV59677	Aay59677 Secreted	619	70	3	ABM54182	Abm54182 Human pan
547	5	6.2	65	3	AAV95754	Aay95754 Bacillus m	620	70	3	AAV6511	Aav6511 Arabidops
548	5	6.2	65	4	AAW84262	Aaw84262 Human imm	621	70	4	AAW25321	Aaw25321 Human pro
549	5	6.2	65	4	AG90494	Aag90494 C glutami	622	70	4	AAU67594	Aau67594 Propionib
550	5	6.2	65	4	ABG08549	Abg08549 Novel hum	623	70	6	ABM64113	Abm64113 Propionib
551	5	6.2	65	5	ABP27246	Abp27246 Streptoco	624	70	6	ADA34659	Ada34659 Acinetoba
552	5	6.2	65	5	ABP27247	Abp27247 Streptoco	625	70	6	ADF04299	Adf04299 Bacterial
553	5	6.2	65	5	AAO22515	Aao22515 Small aci	626	70	7	ADW28832	Adw28832 Human nep
554	5	6.2	65	6	ABU46560	Abu46560 Protein e	627	70	9	ADK97445	Adk97445 Human nep
555	5	6.2	65	7	ABU63673	Abu63673 Bacillus	628	71	2	AAW27924	Aaw27924 Staphyloc
556	5	6.2	65	7	ADM77827	Adm77827 Human pro	629	71	4	AAW83013	Aaw83013 Human imm
557	5	6.2	65	8	ADP19508	Adp19508 Human sec	630	71	4	ABM15829	Abm15829 Human ner
558	5	6.2	65	8	ADV88463	Adv88463 Streptoco	631	71	6	ABM64957	Abm64957 Propionib
559	5	6.2	65	8	ADV79716	Adv79716 Streptoco	632	71	6	ABM73105	Abm73105 Staphyloc
560	5	6.2	65	8	ADW81874	Adw81874 Streptoco	633	72	2	AAW95646	Aaw95646 Klebsiell
561	5	6.2	65	9	ADW86763	Adw86763 Alpha/bet	634	72	2	ABG21281	Abg21281 Novel hum
562	5	6.2	65	9	ADZ89287	Adz89287 Secreted	635	72	2	AAV60495	Aav60495 Human nor
563	5	6.2	66	2	AAV60391	Aay60391 Human nor	636	73	2	AAU86882	Aau86882 Novel hum
564	5	6.2	66	4	AAW15462	Aaw15462 Peptide #	637	73	4	ABM35015	Abm35015 Peptide #
565	5	6.2	66	4	ABM34471	Abm34471 Peptide #	638	73	4	AAW28524	Aaw28524 Peptide #
566	5	6.2	66	4	ABM33533	Abm33533 Peptide #	639	73	4	ABM20429	Abm20429 Protein #
567	5	6.2	66	4	AAW26993	Aaw26993 Peptide #	640	73	4	AAW68203	Aaw68203 Human bon
568	5	6.2	66	4	AAW27949	Aaw27949 Peptide #	641	73	4	AAO12698	Aao12698 Human pol
569	5	6.2	66	4	ABM29299	Abm29299 Peptide #	642	73	4	AAU42806	Aau42806 Propionib
570	5	6.2	66	4	ABM28354	Abm28354 Peptide #	643	73	4	AAU61390	Aau61390 Propionib
571	5	6.2	66	4	ABM19881	Abm19881 Protein #	644	73	4	AAU67213	Aau67213 Propionib
572	5	6.2	66	4	AAW67653	Aaw67653 Human bon	645	73	4	AAW55830	Aaw55830 Human bra
573	5	6.2	66	4	AAW66707	Aaw66707 Human bon	646	73	4	ABG59908	Abg59908 Human liv
574	5	6.2	66	4	AAW55257	Aaw55257 Human bra	647	73	4	ABG49850	Abg49850 Human liv
575	5	6.2	66	4	ABG49288	Abg49288 Human liv	648	73	4	AAW06830	Aaw06830 Human foe
576	5	6.2	66	4	AAW03218	Aaw03218 Peptide #	649	73	5	ABG37730	Abg37730 Human pep
577	5	6.2	66	5	ABP05347	Abp05347 Human ORF	650	73	5	ABM80911	Abm80911 Murine eo
578	5	6.2	66	5	ABP29448	Abp29448 Streptoco	651	73	6	ABM57909	Abm57909 Propionib
579	5	6.2	66	5	ABG37226	Abg37226 Human pep	652	73	6	ABM39325	Abm39325 Propionib
580	5	6.2	66	6	ABP78532	Abp78532 N. gonorr	653	73	6	ABM63732	Abm63732 Propionib
581	5	6.2	66	6	ABP79953	Abp79953 N. gonorr	654	73	6	ADB60216	Adb60216 Connectiv
582	5	6.2	66	6	ABF80949	Abf80949 N. gonorr	655	73	8	ADR40245	Adr40245 Mouse mat
583	5	6.2	66	7	ABW02072	Abw02072 Soybean d	656	74	3	AAW60119	Aaw60119 Arabidops
584	5	6.2	66	8	ADL05295	Adl05295 M. catar	657	74	3	AAW37366	Aaw37366 Arabidops
585	5	6.2	67	4	AAU23433	Aau23433 Novel hum	658	74	4	AAW83973	Aaw83973 Human imm
586	5	6.2	67	5	ABM80522	Abm80522 Apple MAD	659	74	4	AAW49265	Aaw49265 Propionib
587	5	6.2	67	7	ADH63019	Adh63019 Soybean d	660	74	4	ABM29302	Abm29302 Novel hum
588	5	6.2	67	7	ADH63019	Adh63019 Soybean d	661	74	6	ABM45784	Abm45784 Propionib
589	5	6.2	68	2	AAW07642	Aaw07642 Shiga-lik	662	74	6	ADH87278	Adh87278 Enterococ
590	5	6.2	68	2	AAW55549	Aaw55549 H. pylori	663	74	8	ADJ66992	Adj66992 Human sec
591	5	6.2	68	4	AAU44740	Aau44740 Propionib	664	75	3	AAW01046	Aaw01046 Human sec
592	5	6.2	68	4	AG70788	Aag70788 S cerevis	665	75	4	AAU60166	Aau60166 Propionib
593	5	6.2	68	5	ABP05100	Abp05100 Human ORF	666	75	5	ABP32201	Abp32201 Human ORF
594	5	6.2	68	5	ABG69861	Abg69861 Human sec	667	75	6	ABM56685	Abm56685 Propionib
595	5	6.2	68	6	ABM41259	Abm41259 Propionib	668	75	8	ADL06051	Adl06051 M. catar
596	5	6.2	68	8	ADN19245	Adn19245 Bacterial	669	75	9	ADY25893	Ady25893 NOV prote
597	5	6.2	69	1	AAW81053	Aaw81053 Sequence	670	76	3	AAW61538	Aaw61538 Arabidops
598	5	6.2	69	1	AAW81052	Aaw81052 Sequence	671	76	3	AAW28084	Aaw28084 Arabidops
599	5	6.2	69	2	AAW72540	Aaw72540 ADP-ribos	672	76	3	AAW95697	Aaw95697 Human exc
600	5	6.2	69	2	AAW41811	Aaw41811 Escherich	673	76	4	AAW42512	Aaw42512 Human kid
601	5	6.2	69	2	AAW95221	Aaw95221 Verotoxin	674	76	5	ADK35335	Adk35335 Novel hum
602	5	6.2	69	2	AAW43008	Aaw43008 Mutant Sh	675	76	5	ABO83410	Ab083410 Pseudomon
603	5	6.2	69	2	AAW43001	Aaw43001 Mutant Sh	676	76	8	ADK46904	Adk46904 Streptoco
604	5	6.2	69	2	AAW43003	Aaw43003 Mutant Sh	677	76	8	ADO60367	Ado60367 Oryza sat
605	5	6.2	69	2	AAW43024	Aaw43024 Mutant Sh	678	76	8	ADX90379	Adx90379 Plant ful
606	5	6.2	69	2	AAW43005	Aaw43005 Mutant Sh	679	77	2	AAW38489	Aaw38489 S. pneumo
607	5	6.2	69	2	AAW39394	Aaw39394 Shiga-lik	680	77	4	ABG20402	Abg20402 Novel hum
608	5	6.2	69	2	AAW43007	Aaw43007 Mutant Sh	681	77	4	AAU21269	Aau21269 Human nov

682	5	6.2	77	5	ABP38541	Abp38541	Staphyloc	755	4	5.0	5	9	ADx19158	Human PSC
683	5	6.2	77	8	ADs06192	AdS06192	Staphyloc	756	4	5.0	5	9	AEb87868	L. starke
684	5	6.2	77	9	ADz64429	ADz64429	Human can	757	4	5.0	5	9	AEb87888	Lipomyces
685	5	6.2	78	3	AGS1222	AGS1222	Arabidops	758	4	5.0	6	1	AAP40807	Sequence
686	5	6.2	78	4	AM13898	Am13898	Peptide #	759	4	5.0	6	2	AAR53677	Fragment
687	5	6.2	78	4	ABB32843	Abb32843	Peptide #	760	4	5.0	6	2	AAR86350	Cyclic HI
688	5	6.2	78	4	AM26304	Aam26304	Peptide #	761	4	5.0	6	2	AAR91817	Mab-425-C
689	5	6.2	78	4	ABB27673	Abb27673	Human pep	762	4	5.0	6	2	AAR97589	Mab PK39H
690	5	6.2	78	4	ABB18325	Abb18325	Protein #	763	4	5.0	6	2	AAR97581	Mab PK39H
691	5	6.2	78	4	AM66029	Am66029	Human bon	764	4	5.0	6	2	AAR97576	Mab PK39H
692	5	6.2	78	4	AAU57775	Aau57775	Propionib	765	4	5.0	6	2	AAR97588	Mab PK39H
693	5	6.2	78	4	AM53648	Aam53648	Human bra	766	4	5.0	6	2	AAW45020	Immunomod
694	5	6.2	78	4	ABG47695	Abg47695	Human liv	767	4	5.0	6	2	AAW45020	Immunomod
695	5	6.2	78	4	AM01641	Aam01641	Peptide #	768	4	5.0	6	2	AAW17510	Protein k
696	5	6.2	78	4	AAU33101	Aau33101	Novel hum	769	4	5.0	6	2	AAW51172	Cysteine
697	5	6.2	78	5	ABB94260	Abb94260	Chlamydia	770	4	5.0	6	2	AAW87273	Peptide d
698	5	6.2	78	5	ABG35677	Abg35677	Human pep	771	4	5.0	6	2	AAW87357	Peptide d
699	5	6.2	78	6	ABM54294	Abm54294	Propionib	772	4	5.0	6	2	AAW87290	Peptide d
700	5	6.2	78	6	ABR38910	AbR38910	pBAL ORF	773	4	5.0	6	2	AAW87266	Peptide d
701	5	6.2	78	6	ABR24462	Abu24462	Protein e	774	4	5.0	6	2	AAy23488	V beta 6
702	5	6.2	78	6	ABU26766	Abu26766	Protein e	775	4	5.0	6	2	AAW93518	Bacterial
703	5	6.2	78	8	ADR99395	AdR99395	Chlamydia	776	4	5.0	6	2	AAy09434	Immunosact
704	5	6.2	79	3	AAQ29579	Aeg29579	Arabidops	777	4	5.0	6	2	AAy28776	Human hep
705	5	6.2	79	3	AAQ28083	Aeg28083	Arabidops	778	4	5.0	6	2	AAy49058	Membrane
706	5	6.2	79	4	AM87265	Aam87265	Human imm	779	4	5.0	6	3	AAy99849	Human t-p
707	5	6.2	79	4	AAU52736	Aau52736	Propionib	780	4	5.0	6	3	AAy97482	Hepaticis
708	5	6.2	79	4	AAU18598	Aau18598	Human lun	781	4	5.0	6	3	AAy12856	STAT3 DNA
709	5	6.2	79	5	ABP06081	Abp06081	Human ORF	782	4	5.0	6	3	AAy12857	STAT3 DNA
710	5	6.2	79	5	ABP04941	Abp04941	Human ORF	783	4	5.0	6	3	AAy12857	STAT3 DNA
711	5	6.2	79	5	ABP64060	Abp64060	Human ORF	784	4	5.0	6	3	AAy01556	Collagena
712	5	6.2	79	5	ABB48090	Abb48090	Listeria	785	4	5.0	6	4	AAy01559	Collagena
713	5	6.2	79	6	ABM49255	Abm49255	Propionib	786	4	5.0	6	4	AAy49843	Human end
714	5	6.2	79	7	ABB33222	Abb33222	Human nov	787	4	5.0	6	5	AAy75031	Desmoglei
715	5	6.2	79	7	ADf59578	Adf59578	Human pol	788	4	5.0	6	5	AAU85688	Collagena
716	5	6.2	79	8	ADT56514	Adt56514	Plant pol	789	4	5.0	6	5	AAU85685	Collagena
717	5	6.2	80	2	AAW74978	Aaw74978	Human sec	790	4	5.0	6	5	AAU81468	VapA prot
718	5	6.2	80	3	AAW44577	Aaw44577	Virulence	791	4	5.0	6	5	AAU81467	VapA prot
719	5	6.2	80	4	AAE01366	Aae01366	Human gen	792	4	5.0	6	6	ABP95894	Microtetr
720	5	6.2	80	4	AAQ01628	Aao01628	Human pol	793	4	5.0	6	7	ADG17720	Human pro
721	5	6.2	80	4	AAU64258	Aau64258	Propionib	794	4	5.0	6	8	ADH78397	JNK/SAPK-
722	5	6.2	80	5	ABP54529	Abp54529	Actinobac	795	4	5.0	6	8	ADO37784	Binding p
723	5	6.2	80	5	ABG64098	Abg64098	Human alb	796	4	5.0	6	8	ADO28306	Capture s
724	5	6.2	80	5	ABP33468	Abp33468	Human ORF	797	4	5.0	6	8	ADQ94498	Novel dru
725	5	6.2	80	5	ABG95438	Abg95438	Human nov	798	4	5.0	6	8	ADR50483	6-mer pep
726	5	6.2	80	6	ABM60777	Abm60777	Propionib	799	4	5.0	6	8	ADR50483	Peptide o
727	5	6.2	80	6	ABO34632	AbO34632	Region of	800	4	5.0	6	8	ADR87143	Anti-Stat
728	5	6.2	80	7	ADI23293	Adi23293	Novel hum	801	4	5.0	6	8	ADR87144	Stat3 con
729	5	6.2	80	7	ABO76130	AbO76130	Pseudomon	802	4	5.0	6	8	ADs96129	Tagged po
730	5	6.2	80	8	ADH74295	Adh74295	Human sec	803	4	5.0	6	9	ADM86814	Protein l
731	5	6.2	80	8	ADL77363	Adl77363	Albumin f	804	4	5.0	6	9	ADx39149	STAT3ip p
732	4	5.0	4	2	AAE53727	Aar53727	Tetrapept	805	4	5.0	6	9	ADZ46489	Antigenic
733	4	5.0	4	4	AAE02264	Aae02264	Human 36P	806	4	5.0	6	9	AEA01814	Cleavable
734	4	5.0	4	4	AAE51331	Aab51331	Angiotens	807	4	5.0	6	9	AEA41781	GAG-bindi
735	4	5.0	4	6	ABU10294	Abu10294	Undaria p	808	4	5.0	6	9	AEA41260	GAG-bindi
736	4	5.0	4	9	AEA13862	Aea13862	VEGF rela	809	4	5.0	6	9	AEA41258	GAG-bindi
737	4	5.0	4	9	AEA39593	Aea39593	Caspase s	810	4	5.0	6	9	AEA41774	GAG-bindi
738	4	5.0	5	2	AAy23469	Aay23469	V beta 6	811	4	5.0	6	9	ABE30599	Therapeut
739	4	5.0	5	2	AAy01537	Aay01537	Peptide d	812	4	5.0	7	2	AAAR24662	Immunomod
740	4	5.0	5	5	AAJ11489	Abj11489	Human 125	813	4	5.0	7	2	AAAR60922	Enterotox
741	4	5.0	5	5	AAU81483	Aau81483	VapA prot	814	4	5.0	7	2	AAAR60923	Enterotox
742	4	5.0	5	5	AAU81482	Aau81482	VapA prot	815	4	5.0	7	2	AAAR64889	C7 peptid
743	4	5.0	5	6	ABU72728	Abu72728	Novel pro	816	4	5.0	7	2	AAAR83024	Calcium-i
744	4	5.0	5	6	ABU12234	Abu12234	Streptoco	817	4	5.0	7	2	AAW01485	Calcium-i
745	4	5.0	5	6	ABU12233	Abu12233	Streptoco	818	4	5.0	7	2	AAAR86702	Pilin der
746	4	5.0	5	6	ABP75024	Abp75024	Proteome	819	4	5.0	7	2	AAW13169	Ca-indepc
747	4	5.0	5	6	ABJ57034	Abj57034	184P1E2-r	820	4	5.0	7	2	AAW17840	Cytosolic
748	4	5.0	5	7	ADC17578	Adc17578	Type IV c	821	4	5.0	7	2	ABB76924	Cyclodext
749	4	5.0	5	7	ADL17474	Adl17474	Type IV c	822	4	5.0	7	2	AAy23406	V beta 6
750	4	5.0	5	8	ADG63973	AdG63973	Human 213	823	4	5.0	7	2	AAW93504	Bacterial
751	4	5.0	5	8	ADR19100	Adr19100	Type IV c	824	4	5.0	7	2	AAy17020	Heat choc
752	4	5.0	5	8	ADR18996	Adr18996	Human typ	825	4	5.0	7	2	AAy49020	Membrane
753	4	5.0	5	8	ADR90638	Adr90638	Human mon	826	4	5.0	7	2	AAy49015	Membrane
754	4	5.0	5	8	ADU73684	Adu73684	Control c	827	4	5.0	7	2	AAy48624	Membrane

828	4	5.0	7	2	AAW81831	AAW81831 Phospholi	901	4	5.0	7	9	AEA27966	Aea27966 Transform
829	4	5.0	7	3	AAW78302	AAW78302 ProMMP-9	902	4	5.0	7	9	AEb11125	Aeb11125 Neurotrop
830	4	5.0	7	3	AAy84969	AAy84969 Amino aci	903	4	5.0	7	9	AEb52362	AEb52362 Chymosin
831	4	5.0	7	3	AAy52584	AAy52584 Amaranthu	904	4	5.0	7	9	AEb52363	AEb52363 AtIantic
832	4	5.0	7	3	AAy61862	AAy61862 Cadherin-	905	4	5.0	7	9	AEb52364	AEb52364 Human pep
833	4	5.0	7	4	AAU04419	AAU04419 Neisseria	906	4	5.0	7	9	AEb52365	AEb52365 Porcine p
834	4	5.0	7	4	AAU72162	AAU72162 Melanoma	907	4	5.0	8	2	AAr43485	AAr43485 Ro/SSA ep
835	4	5.0	7	4	AAAB49848	AAAB49848 Human end	908	4	5.0	8	2	AAr43460	AAr43460 Ro/SSA ep
836	4	5.0	7	4	AAAB49847	AAAB49847 Human end	909	4	5.0	8	2	AAr60632	AAr60632 Human PC
837	4	5.0	7	5	AAE21386	AAE21386 Neurospor	910	4	5.0	8	2	AAr66349	AAr66349 Cyclic HI
838	4	5.0	7	5	AAU80712	AAU80712 Javelin p	911	4	5.0	8	2	AAr67973	AAr67973 EII loop
839	4	5.0	7	5	ABb46180	ABb46180 Desmoglei	912	4	5.0	8	2	AAr95061	AAr95061 Multidoma
840	4	5.0	7	5	AAU81557	AAU81557 Enterokin	913	4	5.0	8	2	AAW17688	AAW17688 Substrate
841	4	5.0	7	5	ABg96779	ABg96779 Human leu	914	4	5.0	8	2	AAy21397	AAy21397 Human HUP
842	4	5.0	7	5	ABP49525	ABP49525 Zinc fing	915	4	5.0	8	2	AAy23401	AAy23401 V beta 6
843	4	5.0	7	5	ABJ11431	ABJ11431 Human 125	916	4	5.0	8	2	AAy10407	AAy10407 T cell ep
844	4	5.0	7	5	ABJ11433	ABJ11433 Human 125	917	4	5.0	8	2	AAy16849	AAy16849 Heat shoc
845	4	5.0	7	5	ABb80641	ABb80641 Clostridi	918	4	5.0	8	2	AAW86117	AAW86117 Streptoki
846	4	5.0	7	5	AAU81453	AAU81453 Vapa prot	919	4	5.0	8	3	AAb01334	AAb01334 MHC Class
847	4	5.0	7	5	AAU81455	AAU81455 Vapa prot	920	4	5.0	8	3	AAb12056	AAb12056 GI GTPase
848	4	5.0	7	5	AAU81454	AAU81454 Vapa prot	921	4	5.0	8	3	AAy61863	AAy61863 Cadherin-
849	4	5.0	7	5	AAU81456	AAU81456 Vapa prot	922	4	5.0	8	4	AAm98727	AAm98727 Human pep
850	4	5.0	7	5	ABP52983	ABP52983 Cellular	923	4	5.0	8	4	AAU04422	AAU04422 Neisseria
851	4	5.0	7	5	AAE28528	AAE28528 Pseudomon	924	4	5.0	8	4	AAU04422	AAU04422 Neisseria
852	4	5.0	7	5	ABg77640	ABg77640 Targettin	925	4	5.0	8	4	AAg36934	AAg36934 Tenascin-
853	4	5.0	7	5	ABg77666	ABg77666 Targettin	926	4	5.0	8	4	AAg79237	AAg79237 Peptide o
854	4	5.0	7	5	ABg77639	ABg77639 Targettin	927	4	5.0	8	4	ABP24008	ABP24008 HIV A11 m
855	4	5.0	7	5	ABg77627	ABg77627 Targettin	928	4	5.0	8	4	ABP22232	ABP22232 HIV A03 m
856	4	5.0	7	5	ABg77631	ABg77631 Targettin	929	4	5.0	8	4	AAJ02617	AAJ02617 Hepatitis
857	4	5.0	7	5	ABg68028	ABg68028 Human ADP	930	4	5.0	8	4	AAJ02930	AAJ02930 Hepatitis
858	4	5.0	7	5	AAE20564	AAE20564 Soybean d	931	4	5.0	8	4	AAJ00830	AAJ00830 Hepatitis
859	4	5.0	7	5	ABb82221	ABb82221 Calcium i	932	4	5.0	8	5	AAE08157	AAE08157 Peptide #
860	4	5.0	7	6	ABU72676	ABU72676 Novel pro	933	4	5.0	8	5	ABb78120	ABb78120 Amino aci
861	4	5.0	7	6	ABU72664	ABU72664 Novel pro	934	4	5.0	8	5	ABb78121	ABb78121 Amino aci
862	4	5.0	7	6	ABU79839	ABU79839 Enterokin	935	4	5.0	8	5	ABb46465	ABb46465 Desmoglei
863	4	5.0	7	6	ABJ39341	ABJ39341 Human leu	936	4	5.0	8	5	ABb46187	ABb46187 Desmoglei
864	4	5.0	7	6	ABJ39334	ABJ39334 Human leu	937	4	5.0	8	5	ABb46194	ABb46194 Desmoglei
865	4	5.0	7	6	ABU61532	ABU61532 Botulinum	938	4	5.0	8	5	ABG69774	ABG69774 Polyptei
866	4	5.0	7	6	AAO19862	AAO19862 B licheni	939	4	5.0	8	5	AAU11508	AAU11508 PADV-5 pV
867	4	5.0	7	6	ABP75033	ABP75033 Proteome	940	4	5.0	8	5	AAU11507	AAU11507 PADV-5 pV
868	4	5.0	7	6	ABP75098	ABP75098 Proteome	941	4	5.0	8	5	AAU73285	AAU73285 Human pro
869	4	5.0	7	6	ABP75148	ABP75148 Proteome	942	4	5.0	8	5	ABb83320	ABb83320 Ras prote
870	4	5.0	7	6	ABU61908	ABU61908 Mouse gly	943	4	5.0	8	5	ABP62250	ABP62250 Human inm
871	4	5.0	7	6	ADA24183	ADA24183 Alzheimer	944	4	5.0	8	5	ABP62249	ABP62249 Human inm
872	4	5.0	7	7	ADA63881	ADA63881 Zinc fing	945	4	5.0	8	5	AAU81439	AAU81439 Vapa prot
873	4	5.0	7	7	ADb79619	ADb79619 Parapoxvi	946	4	5.0	8	5	AAU81442	AAU81442 Vapa prot
874	4	5.0	7	7	ADC44273	ADC44273 Endotheli	947	4	5.0	8	5	AAU81440	AAU81440 Vapa prot
875	4	5.0	7	7	ADD69528	ADD69528 Food enri	948	4	5.0	8	5	AAU81443	AAU81443 Vapa prot
876	4	5.0	7	7	ADF70698	ADF70698 Kluyverom	949	4	5.0	8	5	ABP52982	ABP52982 Cellular
877	4	5.0	7	7	ADG72830	ADG72830 Heat shoc	950	4	5.0	8	5	AAU97758	AAU97758 Mycobacte
878	4	5.0	7	7	ADG72676	ADG72676 Heat shoc	951	4	5.0	8	5	AAU98641	AAU98641 Mycobacte
879	4	5.0	7	7	ADW21836	ADW21836 Synthetic	952	4	5.0	8	5	ABG80089	ABG80089 MHC class
880	4	5.0	7	7	ADJ98596	ADJ98596 Human leu	953	4	5.0	8	5	AAU80832	AAU80832 Rat Rb-in
881	4	5.0	7	8	ADH73690	ADH73690 Botulinum	954	4	5.0	8	6	ABJ19914	ABJ19914 MHC bindi
882	4	5.0	7	8	ADL66495	ADL66495 Human col	955	4	5.0	8	6	ABP72180	ABP72180 Carcinoma
883	4	5.0	7	8	ADL95887	ADL95887 Human pro	956	4	5.0	8	6	ABR64102	ABR64102 E. coli g
884	4	5.0	7	8	ADL95874	ADL95874 Human pro	957	4	5.0	8	7	ADA07599	ADA07599 Human sec
885	4	5.0	7	8	ADL95878	ADL95878 Human pro	958	4	5.0	8	7	ADC98779	ADC98779 Staphyloc
886	4	5.0	7	8	ADJ95886	ADJ95886 Human pro	959	4	5.0	8	7	ADb84707	ADb84707 Mammalian
887	4	5.0	7	8	ADO63915	ADO63915 Human 213	960	4	5.0	8	7	ADG72954	ADG72954 Heat shoc
888	4	5.0	7	8	ADO63928	ADO63928 Human 213	961	4	5.0	8	7	ADL17630	ADL17630 Human AP6
889	4	5.0	7	8	ADN08577	ADN08577 Ceramic t	962	4	5.0	8	7	ADW31889	ADW31889 HLA bindi
890	4	5.0	7	8	ADN08697	ADN08697 Cotton wi	963	4	5.0	8	7	ADW31888	ADW31888 HLA bindi
891	4	5.0	7	8	ADP75021	ADP75021 Parapoxvi	964	4	5.0	8	8	ADG94462	ADG94462 Human JAM
892	4	5.0	7	8	ADQ94503	ADQ94503 Novel dru	965	4	5.0	8	8	ADG94466	ADG94466 Human JAM
893	4	5.0	7	8	ADU08796	ADU08796 Heat shoc	966	4	5.0	8	8	ADG94489	ADG94489 Human JAM
894	4	5.0	7	8	ADT78253	ADT78253 C. botuli	967	4	5.0	8	8	ADG94621	ADG94621 Human JAM
895	4	5.0	7	8	ADU64144	ADU64144 Murine he	968	4	5.0	8	8	ADH89860	ADH89860 Cell pene
896	4	5.0	7	9	ADW86454	ADW86454 Peptide #	969	4	5.0	8	8	ADK63028	ADK63028 Epitope 1
897	4	5.0	7	9	ADW39229	ADW39229 Antibacte	970	4	5.0	8	8	ADI46865	ADI46865 Permeabil
898	4	5.0	7	9	ADY59630	ADY59630 Candida u	971	4	5.0	8	8	ADI46860	ADI46860 Permeabil
899	4	5.0	7	9	ADZ17658	ADZ17658 Heptapept	972	4	5.0	8	8	ADI46887	ADI46887 Permeabil
900	4	5.0	7	9	ADZ04432	ADZ04432 VL derive	973	4	5.0	8	8	ADI47020	ADI47020 Permeabil

```
974 4 5.0 8 8 ADK03836 Hepatitis
975 4 5.0 8 8 ADK03826 Hepatitis
976 4 5.0 8 8 ADK03835 Hepatitis
977 4 5.0 8 8 ADM06911 Matrix me
978 4 5.0 8 8 ADK00432 avrPtoB (
979 4 5.0 8 8 ADN41525 Novel hum
980 4 5.0 8 8 ADP87064 Junctiona
981 4 5.0 8 8 ADP87196 Human cla
982 4 5.0 8 8 ADP87041 Junctiona
983 4 5.0 8 8 ADP87037 Junctiona
984 4 5.0 8 8 ADQ10826 Polioviru
985 4 5.0 8 8 ADR69417 Novel hyb
986 4 5.0 8 8 ADR69710 Novel hyb
987 4 5.0 8 8 ADR40256 Malaria p
988 4 5.0 8 8 ADS81306 Tumour-as
989 4 5.0 8 8 ADU07953 Viral der
990 4 5.0 8 8 ADU08402 Heat shoc
991 4 5.0 8 8 ADU08633 Heat shoc
992 4 5.0 8 9 ADV13875 Yeast N-t
993 4 5.0 8 9 ADV13894 Yeast N-t
994 4 5.0 8 9 ADW95770 Anti-hil-
995 4 5.0 8 9 ADX15775 Mouse ant
996 4 5.0 8 9 ADY38294 Human Cpp
997 4 5.0 8 9 AEA90015 Phage dis
998 4 5.0 9 1 AAP80837 Sequence
999 4 5.0 9 2 AAR59226 Peptide f
1000 4 5.0 9 2 AAR60633 Human Pc
```

## ALIGNMENTS

```
RESULT 1
ID AAW35851 standard; protein; 79 AA.
XX
AC AAW35851;
XX
DT 27-APR-1998 (first entry)
XX
DE Human CD9 for use in T lymphocyte veto molecule.
XX
KW Human; CD9; T lymphocyte veto molecule; chimeric molecule;
KW targeting polypeptide; suppression; immune response; treatment;
KW autoimmune disease; allergy; immunological disorder;
KW transplant rejection.
XX
OS Homo sapiens.
XX
PN WO9737687-A1.
XX
PD 16-OCT-1997.
XX
PF 10-APR-1997; 97WO-US005943.
XX
PR 10-APR-1996; 96US-00630172.
XX
PA (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
XX
PI Staerz UD;
XX
DR WPI; 1997-512419/47.
XX
PT T lymphocyte veto molecule comprising response cell activating protein -
PT linked to molecule that targets stimulator cell marker, used for
PT selective suppression of immune response, e.g. prevention of graft
PT rejection or treatment of auto-immune disease.
XX
PS Claim 37; Page 61; 309pp; English.
XX
CC A novel T lymphocyte veto molecule is a chimeric molecule comprising a
CC protein, e.g. the present sequence, linked to a targeting polypeptide
CC that binds a molecule, which differentiates a host cell from a tissue
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CC graft cell, or selectively targets a stimulator cell involved in the
CC autoimmune response. A veto molecule, in which the protein binds a
CC molecule that targets stimulator cells, can be used to suppress an immune
CC response and therefore treat autoimmune diseases, e.g. systemic lupus
CC erythematosus, myasthenia gravis, rheumatoid arthritis, insulin dependent
CC diabetes mellitus, multiple sclerosis, coeliac disease, autoimmune
CC thyroiditis, Addison's or Grave's diseases and rheumatoid carditis,
CC allergies and other immunological disorders. Where the protein binds a
CC molecule that differentiates graft and host cells, the veto molecule can
CC be used to reduce transplant rejection. The veto molecule provides
CC specific regulation of particular stimulator cells that can kill graft
CC cells or respond to autoantigens, but leave other stimulator cells
CC unaffected, e.g. CD4 or CD8 positive cells can be regulated without one
CC affecting the other. The veto molecule can be administered locally to
CC minimise generalised immunosuppression
XX
SQ Sequence 79 AA;
```

```
Query Match 58.8%; Score 47; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 3.1e-40;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 HKDEVIKEVQSFYKDTYNKLTKDPSQRETLKAIHYALNCCGLAGGV 47
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 HKDEVIKEVQSFYKDTYNKLTKDPSQRETLKAIHYALNCCGLAGGV 47
```

```
RESULT 2
ID ABU05058 standard; protein; 79 AA.
XX
AC ABU05058;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1724.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicx RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1724; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
```

CC transporter, cytoskeletal protein, receptor or transcription factor. The  
 CC polypeptide is useful as an immunogenic composition for eliciting in a  
 CC mammal an immunogenic response directed against any of the purified  
 CC polypeptide. The purified polypeptide, or the antibody that binds to this  
 CC polypeptide, is useful for treating cancer. The polypeptide is also  
 CC useful for identifying compounds that binds to a naturally processed  
 CC class I or class II MHC-binding polypeptide. The polypeptides and  
 CC polynucleotides are particularly useful for treating or preventing  
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
 CC lymphoma or leukaemia. These are also useful for screening agents for  
 CC treating the above mentioned diseases. This sequence represents an  
 CC expressed protein tag (EPT) isolated from human tissue for translational  
 CC profiling. Note: This sequence does not appear in the printed  
 CC specification but was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 79 AA;

Query Match 58.8%; Score 47; DB 6; Length 79;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-40;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVKEVOEYKQYTNKLTQKDEPQRETLKAIHYALNCCGLAGV 47  
 DB 1 HKDEVKEVOEYKQYTNKLTQKDEPQRETLKAIHYALNCCGLAGV 47

## RESULT 3

ADJ57561  
 ID ADJ57561 standard; protein; 38 AA.

AC ADJ57561;

XX 06-MAY-2004 (first entry)

XX Human CD9 fibronectin-binding domain polypeptide fragment.

KW Human; CD9; antithrombotic; antiarteriosclerotic; vasotropic;  
 KW haemostatic; antiangiogenic; cytostatic.

XX Homo sapiens.

XX WO2004007685-A2.

XX 22-JAN-2004.

PF 14-JUL-2003; 2003WO-US022050.

XX 12-JUL-2002; 2002US-0395864P.

XX (UYTE-) UNIV TENNESSEE RES FOUND.

XX Jennings LK, Longhurst CM, Cook GA, Bao J, Zhang C, White MW;  
 PI Crossno JT, Lu Y;

DR WPI; 2004-122924/12.

PT Interfering with CD9 binding to fibronectin by binding a fibronectin-  
 PT binding domain of the CD9 protein or polypeptide, useful in treating  
 PT thrombosis, atherosclerosis, restenosis, bleeding disorders, angiogenesis  
 PT and cancers.

XX Claim 7; SEQ ID NO 4; 126pp; English.

XX The present sequence is that of a polypeptide fragment from the  
 CC fibronectin-binding domain of human CD9 ADJ57558. The peptide, or an  
 CC antibody that binds to it, is used in claimed methods for: interfering  
 CC with CD9 binding to fibronectin; modifying adhesion, motility or  
 CC spreading of a CD9-expressing cell on fibronectin; inhibiting  
 CC proliferation or survival of CD9-expressing cells; modifying pericellular  
 CC fibronectin matrix assembly; modifying invasiveness of a cell through a  
 CC collagen and/or laminin matrix; and modifying cell-to-cell interaction.  
 CC The methods are based on the finding that increased CD9 expression is

CC implicated in (i) decreased adhesiveness of cells to extracellular matrix  
 CC (via alpha-beta-1 integrin) and/or decreased cell invasiveness and/or  
 CC decreased pericellular fibronectin matrix assembly, and/or (ii) increased  
 CC cell motility, spreading, proliferation, cell survival against apoptosis,  
 CC and/or cell-to-cell contacts. Conditions or disease states involving  
 CC proliferation or survival of CD9-expressing cells can be treated, e.g.  
 CC thrombosis, atherosclerosis, vein graft failure, restenosis, transplanted  
 CC arteriopathy, bleeding disorders, angiogenesis, and primary and  
 CC metastatic cancers including breast cancer, prostate cancer, colon  
 CC cancer, melanoma, ovarian cancer, neuroblastoma, glioma and glioblastoma.

XX Sequence 38 AA;

Query Match 47.5%; Score 38; DB 8; Length 38;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-31;  
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 KDEPQRETLKAIHYALNCCGLAGVGEQFISDICPKKV 60  
 DB 1 KDEPQRETLKAIHYALNCCGLAGVGEQFISDICPKKV 38

## RESULT 4

ABP76310

ID ABP76310 standard; protein; 80 AA.

XX AC ABP76310;

XX 21-FEB-2003 (first entry)

XX Human GENSET protein SEQ ID 860.

KW Cytostatic; antiinflammatory; nootropic; neuroprotective; cardiant;  
 KW gastrointestinal; gene therapy; GENSET; heavy metal toxicity; cancer;  
 KW inflammatory disease; immune disorder; neuromuscular; toxicity;  
 KW central nervous system; cardiovascular; gastrointestinal.

XX Homo sapiens.

XX WO200283898-A1.

XX 24-OCT-2002.

XX 18-APR-2001; 2001WO-IB000914.

XX 18-APR-2001; 2001WO-IB000914.

XX (GEST ) GENSET.

XX Bejanin S, Tanaka H, Dumas Milne Edwards J, Jobert S, Giordano J;

XX WPI; 2003-075548/07.

XX New GENSET polynucleotides and polypeptides, useful for treating heavy  
 PT metal toxicity, cancer, inflammatory diseases, immune disorders, and the  
 PT neuromuscular, CNS, cardiovascular or gastrointestinal effects of the  
 PT toxicity.

XX Claim 14; Page 710; 735pp; English.

XX The present invention relates to novel GENSET polynucleotides (AB236404-  
 CC AB236911) encoding polypeptides (ABP75963-ABP76368). The polynucleotides  
 CC and polypeptides are useful in screening and diagnostic assays for  
 CC abnormal GENSET expression and/or biological activity. They are also  
 CC useful for screening of compounds for treating or preventing GENSET-  
 CC related disorders, such as heavy metal toxicity, cancer, inflammatory  
 CC diseases, immune disorders, and the neuromuscular, central nervous system  
 CC (CNS), cardiovascular or gastrointestinal effects of the toxicity

XX Sequence 80 AA;

Query Match 40.0%; Score 32; DB 6; Length 80;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-25;

```
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKDEVIKVQVRYKDYNYKLTKDKPQRETLK 32
Db 44 HKDEVIKVQVRYKDYNYKLTKDKPQRETLK 75

RESULT 5
ABU05051
ID ABU05051 standard; protein; 30 AA.
XX
AC ABU05051;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (BPT) #1717.
XX
KW Translational profiling; expressed protein tag; BPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCO INC.
XX
PI Chicx RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1717; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, or transcription inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (BPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 30 AA;

Query Match 37.5%; Score 30; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.8e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 PKDVLFTFTVKSCFDAIKEYFDNK 80
Db 1 PKDVLFTFTVKSCFDAIKEYFDNK 25

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 LNCGLAGGVQFISDIPCCKDVLFTFTVK 67
Db 1 LNCGLAGGVQFISDIPCCKDVLFTFTVK 30

RESULT 6
ADJ57562
ID ADJ57562 standard; peptide; 25 AA.
XX
AC ADJ57562;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human CD9 fibronectin-binding domain peptide fragment.
XX
KW Human; CD9; antithrombotic; antiarteriosclerotic; vasotrophic;
KW haemostatic; antiangiogenic; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2004007685-A2.
XX
PD 22-JAN-2004.
XX
PF 14-JUL-2003; 2003WO-US022050.
XX
PR 12-JUL-2002; 2002US-0395864P.
XX
PA (UYTE-) UNIV TENNESSEE RES FOUND.
XX
PI Jennings LK, Longhurst CM, Cook GA, Bao J, Zhang C, White MM;
PI Croesno JT, Lu Y;
XX
DR WPI; 2004-122924/12.
XX
PT Interfering with CD9 binding to fibronectin by binding a fibronectin-
PT binding domain of the CD9 protein or polypeptide, useful in treating
PT thrombosis, atherosclerosis, restenosis, bleeding disorders, angiogenesis
PT and cancers.
XX
PS Claim 7; SEQ ID NO 5; 126pp; English.
XX
CC The present sequence is that of a peptide fragment from the fibronectin-
CC binding domain of human CD9 ADJ57558. The peptide, or an antibody that
CC binds to it, is used in claimed methods for: interfering with CD9 binding
CC to fibronectin; modifying adhesion, motility or spreading of a CD9-
CC expressing cell on fibronectin; inhibiting proliferation or survival of
CC CD9-expressing cells; modifying pericellular fibronectin matrix assembly;
CC modifying invasiveness of a cell through a collagen and/or laminin matrix
CC ; and modifying cell-to-cell interaction. The methods are based on the
CC finding that increased CD9 expression is implicated in (i) decreased
CC adhesiveness of cells to extracellular matrix (via alpha5-beta-1
CC integrin) and/or decreased cell invasiveness and/or decreased
CC pericellular fibronectin matrix assembly, and/or (ii) increased cell
CC motility, spreading, proliferation, cell survival against apoptosis,
CC and/or cell-to-cell contacts. Conditions or disease states involving
CC proliferation or survival of CD9-expressing cells can be treated, e.g.
CC thrombosis, atherosclerosis, vein graft failure, restenosis, transplant
CC arteriopathy, bleeding disorders, angiogenesis, and primary and
CC metastatic cancers including breast cancer, prostate cancer, colon
CC cancer, melanoma, ovarian cancer, neuroblastoma, glioma and glioblastoma.
XX
SQ Sequence 25 AA;

Query Match 31.2%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.4e-18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

RESULT 7	
ADJ57564	
ID	ADJ57564 standard; peptide; 22 AA.
XX AC	ADJ57564;
XX XX	
DT DT	06-MAY-2004 (first entry)
XX XX	
DE DE	Human CD9 fibronectin-binding domain peptide fragment.
XX XX	
KW KW	Human; CD9; antithrombotic; antiarteriosclerotic; vasotropic;
KW KW	haemostatic; angiogenic; cytotstatic.
OS OS	Homo sapiens.
XX XX	
PX PX	WO2004007685-A2.
NN NN	
PD PD	22-JAN-2004.
XX XX	
XX XX	14-JUL-2003; 2003WO-US022050.
PR PR	
XX XX	12-JUL-2002; 2002US-0395864P.
PA PA	(UYTB-) UNIV TENNESSEE RES FOUND.
XX XX	
PI PI	Jennings LK, Longhurst CM, Cook GA, Bao J, Zhang C, White MM;
PI PI	Crossno JT, Lu Y;
DR DR	WPI; 2004-122924/12.
XX XX	
PT PT	Interfering with CD9 binding to fibronectin by binding a fibronectin-
PT PT	binding domain of the CD9 protein or polypeptide, useful in treating
PT PT	thrombosis, atherosclerosis, restenosis, bleeding disorders, angiogenesis
PT PT	and cancers.
XX XX	
PS PS	Example 1; SEQ ID NO 7; 126pp; English.
XX XX	
CC CC	The present sequence is that of a peptide fragment from the extracellular
CC CC	domain (amino acids 125-146) of human CD9 ADJ57558. The peptide was used
CC CC	in an example from the invention to investigate the interaction between
CC CC	CD9 and fibronectin. Peptide fragments ADJ57560-ADJ57563 of human CD9 are
CC CC	used in claimed methods for: interfering with CD9 binding to fibronectin;
CC CC	modifying adhesion, motility or spreading of a CD9-expressing cell on
CC CC	fibronectin; inhibiting proliferation or survival of CD9-expressing cells
CC CC	; modifying pericellular fibronectin matrix assembly; modifying
CC CC	invasiveness of a cell through a collagen and/or laminin matrix; and
CC CC	modifying cell-to-cell interaction. The methods are based on the finding
CC CC	that increased CD9 expression is implicated in (i) decreased adhesiveness
CC CC	of cells to extracellular matrix (via alpha5-beta-1 integrin) and/or
CC CC	decreased cell invasiveness and/or decreased pericellular fibronectin
CC CC	matrix assembly, and/or (ii) increased cell motility, spreading,
CC CC	proliferation, cell survival against apoptosis, and/or cell-to-cell
CC CC	contacts. Conditions or disease states involving proliferation or
CC CC	survival of CD9-expressing cells can be treated, e.g. thrombosis,
CC CC	atherosclerosis, vein graft failure, restenosis, transplant arteriopathy,
CC CC	bleeding disorders, angiogenesis, and primary and metastatic cancers
CC CC	including breast cancer, prostate cancer, colon cancer, melanoma, ovarian
CC CC	cancer, neuroblastoma, glioma and glioblastoma.
XX XX	
SQ SQ	Sequence 22 AA;
	Query Match 27.5%; Score 22; DB 8; Length 22;
	Best Local Similarity 100.0%; Pred.No. 4.8e-15;
	Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY QY	13 YKDYNKLTKDPEQRETILKAI 34
Dd Dd	
	1 YKDYNKLTKDPEQRETILKAI 22
RESULT 8	



XX AC ADJ57563;  
XX 06-MAY-2004 (first entry)  
XX Human CD9 fibronectin-binding domain peptide fragment.  
XX Human; CD9; antithrombotic; antiarteriosclerotic; vasotropic;  
KW haemostatic; antiangiogenic; cytostatic.  
XX Homo sapiens.  
XX WO2004007685-A2.  
XX PD 22-JAN-2004.  
XX PF 14-JUL-2003; 2003WO-US022050.  
XX PR 12-JUL-2002; 2002US-0395864P.  
XX (UYTE-) UNIV TENNESSEE RES FOUND.  
XX PA Jennings LK, Longhurst CM, Cook GA, Bao J, Zhang C, White MM;  
PI Crossno JT, Lu Y;  
XX WPI; 2004-122924/12.  
XX Interfering with CD9 binding to fibronectin by binding a fibronectin-  
PT binding domain of the CD9 protein or polypeptide, useful in treating  
PT thrombosis, atherosclerosis, restenosis, bleeding disorders, angiogenesis  
PT and cancers.  
XX Claim 7; SEQ ID NO 6; 126pp; English.  
XX The present sequence is that of a peptide fragment from the fibronectin-  
CC binding domain of human CD9 ADJ57563. The peptide, or an antibody that  
CC binds to it, is used in claimed methods for: interfering with CD9 binding  
CC to fibronectin; modifying adhesion, motility or spreading of a CD9-  
CC expressing cell on fibronectin; inhibiting proliferation or survival of  
CC CD9-expressing cells; modifying pericellular fibronectin matrix assembly;  
CC modifying invasiveness of a cell through a collagen and/or laminin matrix  
CC ; and modifying cell-to-cell interaction. The methods are based on the  
CC finding that increased CD9 expression is implicated in (i) decreased  
CC adhesiveness of cells to extracellular matrix (via alpha5-beta1  
CC integrin) and/or decreased cell invasiveness and/or decreased  
CC pericellular fibronectin matrix assembly, and/or (ii) increased cell  
CC motility, spreading, proliferation, cell survival against apoptosis,  
CC and/or cell-to-cell contacts. Conditions or disease states involving  
CC proliferation or survival of CD9-expressing cells can be treated, e.g.  
CC thrombosis, atherosclerosis, vein graft failure, restenosis, transplant  
CC arteriopathy, bleeding disorders, angiogenesis, and primary and  
CC metastatic cancers including breast cancer, prostate cancer, colon  
CC cancer, melanoma, ovarian cancer, neuroblastoma, glioma and glioblastoma.  
XX SQ Sequence 18 AA;  
Query Match 22.5%; Score 18; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.1e-11;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 56 PKQDVLEFTVKSCPDAI 73  
DB 1 PKQDVLEFTVKSCPDAI 18  
RESULT 10  
ABU03385  
ID ABU03385 standard; protein; 10 AA.  
XX AC ABU03385;  
XX DT 29-JAN-2003 (first entry)  
XX

DE Human expressed protein tag (EPT) #165.  
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
XX Homo sapiens.  
XX WO200278524-A2.  
XX PD 10-OCT-2002.  
XX PF 28-MAR-2002; 2002WO-US009671.  
XX PR 28-MAR-2001; 2001US-0279495P.  
XX PR 21-MAY-2001; 2001US-0292544P.  
XX PR 08-AUG-2001; 2001US-0310801P.  
XX PR 01-OCT-2001; 2001US-0326370P.  
XX PR 04-DEC-2001; 2001US-0336780P.  
XX PR 20-FEB-2002; 2002US-0358985P.  
XX PA (ZYCO-) ZYCO INC.  
XX PI Chicx RM, Tomlinson AJ, Urban RG;  
XX WPI; 2003-040607/03.  
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.  
XX Claim 10; SEQ ID NO 165; 134pp; English.  
XX The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 10 AA;  
Query Match 12.5%; Score 10; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.005;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 58 KDVLFTFTVK 67  
DB 1 KDVLFTFTVK 10  
RESULT 11  
ABP43064  
ID ABP43064 standard; protein; 33 AA.  
XX AC ABP43064;  
XX DT 22-AUG-2002 (first entry)  
XX



DE Human ovarian antigen HVCAC42, SEQ ID NO:4196.  
XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;  
KW ovarian cancer; breast cancer; tumour; reproductive system disorder;  
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;  
KW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;  
KW inflammatory condition; immune disorder; blood disorder;  
KW cardiovascular disorder; respiratory disorder; neurological disorder;  
KW gastrointestinal disorder; urinary system disorder; drug screening;  
KW gene therapy; chromosome mapping; forensic analysis;  
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;  
KW antiinflammatory; gynaecological; reproductive.  
XX  
OS Homo sapiens.  
XX  
PN WO200200677-A1.  
XX  
PD 03-JAN-2002.  
XX  
PF 07-JUN-2001; 2001WO-US018569.  
XX  
PR 07-JUN-2000; 2000US-0209467P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Birse CE, Rosen CA;  
XX  
DR WPI: 2002-147878/19.  
DR N-PSDB; ABQ56141.  
XX  
PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,  
PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian  
PT cancer), immune disorders, cardiovascular disorders and neurological  
PT diseases.  
XX  
PS Claim 11; SEQ ID NO 4196; 2922pp; English.  
XX  
CC The invention relates to 2175 novel human ovarian antigens (ABP41054-  
CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also  
CC encompasses polypeptides 90% identical and polynucleotides 95% identical  
CC to the sequences of the invention. The invention additionally relates to  
CC recombinant vectors and host cells comprising human ovarian antigen  
CC polynucleotides, antibodies against human ovarian antigens, and the use  
CC of ovarian antigen polynucleotides and polypeptides in diagnosing,  
CC treating, prognosing or preventing various ovary and/or breast-related  
CC disorders. Such conditions include ovarian cancer and breast cancer, and  
CC metastatic tumours of ovarian or breast origin, reproductive system  
CC disorders (e.g., infertility, disorders of pregnancy, anovulation,  
CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine  
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic  
CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and  
CC vaginitis), immune disorders (e.g., congenital and acquired  
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),  
CC blood-related disorders (e.g., anaemia), cardiovascular disorders,  
CC respiratory disorders, neurological disorders, gastrointestinal disorders  
CC and urinary system disorders. Ovarian antigen polypeptides and  
CC polynucleotides may also be used in screening for compounds which  
CC modulate ovarian antigen expression or activity. The polynucleotides may  
CC further be used for gene therapy, chromosome mapping, in the  
CC identification of individuals and in forensic analysis, and the  
CC polypeptides may be used as food additives or to prepare antibodies  
CC useful in disease diagnosis, drug targeting and phenotyping. The present  
CC sequence represents a human ovarian antigen of the invention. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 33 AA;

Query Match 10.0%; Score 8; DB 5; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 YKDTYNKL 20  
Db 22 YKDTYNKL 29  
|||||  
RESULT 12  
ABU51670  
ID ABU51670 standard; protein; 58 AA.  
XX  
AC ABU51670;  
XX  
DT 07-MAY-2003 (first entry)  
XX  
DE Helicobacter pylori selected interacting domain (SID) protein #1014.  
XX  
KW Protein-protein interaction; ulcer; selected interacting domain; SID.  
XX  
OS Helicobacter pylori.  
XX  
PN WO200266501-A2.  
XX  
PD 29-AUG-2002.  
XX  
PF 28-DEC-2001; 2001WO-EP015428.  
XX  
PR 02-JAN-2001; 2001US-0259302P.  
XX  
PA (HYBR-) HYBRIGENICS.  
PA (INSP) INST PASTEUR.  
XX  
PI Legrain P, Rain J, Colland F, De Reuse H, Labigne A;  
XX  
DR WPI: 2002-674910/72.  
DR N-PSDB; ABX66415.  
XX  
PT New complexes of protein-protein interactions in Helicobacter pylori,  
PT useful for identifying modulating compounds for treating or preventing  
PT ulcers in mammals.  
XX  
PS Claim 6; Page 334; 642pp; English.  
XX  
CC The invention describes a complex of protein-protein interactions in  
CC Helicobacter pylori selected from 421 complexes given in the  
CC specification. The complex of protein-protein interactions are useful for  
CC screening for agents which modulate the interaction of proteins.  
CC Modulating compounds which binds to a targeted bacterial protein may be  
CC used for treating or preventing ulcers in a human or animal. This is the  
CC amino acid sequence of a selected interacting domain (SID), identified  
CC via protein-protein interactions. Note: Where the patent number printed  
CC at the top of the pages in the specification has obscured areas of  
CC protein sequence, the indexer has replaced the residue with an X to  
CC represent an illegible residue  
XX  
SQ Sequence 58 AA;

Query Match 8.8%; Score 7; DB 5; Length 58;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 IKEVFDN 79  
Db 38 IKEVFDN 44  
|||||

RESULT 13  
ABR67406  
ID ABR67406 standard; peptide; 9 AA.  
XX  
AC ABR67406;  
XX

DT 07-AUG-2003 (first entry)  
XX  
DE Human protein disulfide isomerase peptide residues 539-547.

XX human; human leukocyte antigen-E; HLA-E; CD94/NGK2 cell receptor;  
KW cycostatic; antirheumatic; antiarthritic; antitumor; antineoplastic;  
KW neuroprotective; antidiabetic; dermatological; immunosuppressive;  
KW thymimetic; antianaemic; antiatherosclerotic; hypotensive; virucide;  
tumour.  
XX Homo sapiens.  
OS WO2003011895-A2.  
XX PN 13-FEB-2003.  
XX PD 31-JUL-2002; 2002WO-US024311.  
XX PF 31-JUL-2001; 2001US-0308598P.  
XX PR (SOED/) SOEDERSTROEM K P.  
XX PA Soederstroem KP;  
PI WPI; 2003-256432/25.  
XX DR Novel human leukocyte antigen-E binding peptide, useful in medicine for  
XX modulating the effect of CD94/NGK2 cell receptors and in tumor treatment.  
PT Disclosure; Page 26; 140pp; English.  
XX PS The invention relates to a novel human leukocyte antigen (HLA)-E binding  
XX peptide that modulates the effect of CD94/NGK2 cell receptors. A peptide  
CC of the invention has cytostatic, antirheumatic, antiarthritic, antitumor,  
CC antineoplastic, neuroprotective, antidiabetic, dermatological,  
CC immunosuppressive, thymimetic, antianaemic, antiatherosclerotic,  
CC hypotensive, and virucide activity. A peptide of the invention is useful  
CC in medicine and for modulating the effect of CD94/NGK2 cell receptors.  
CC The peptide is also useful in tumor treatment. The peptides shown in  
CC ABR67357-ABR67464, and also in ABR67466-ABR67467 represent peptides of  
CC the invention  
XX  
XX Sequence 9 AA;  
SQ  
Query Match 7.5%; Score 6; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 56 PKKQVL 61  
Db 4 PKKQVL 9  
RESULT 14  
AAW31082  
ID AAW31082 standard; peptide; 16 AA.  
XX AC AAW31082;  
XX DT 09-JAN-1998 (first entry)  
DE Mugwort pollen allergen T cell epitope.  
XX DE  
XX Cofactor-independent phosphoglycerate mutase; PGM-i; E.C. 5.4.21;  
KW Timothy grass; pollen; allergy; plant allergen; panallergen; B cell;  
KW T cell; epitope; immunotherapy; detection; diagnosis; hay fever;  
conserved.  
XX Artemisia vulgaris.  
OS WO9705258-A2.  
XX PN 13-FEB-1997.  
XX PD 02-AUG-1996; 96WO-AT000141.  
XX PF  
XX

PR 02-AUG-1995; 95AT-00001320.  
XX (BIOM-) BIOMAY PRODN & HANDELS GMBH.  
XX Ferreira F, Richter K, Engel E, Ebner C, Jilek A, Rheinberger H;  
PI Kraft D, Breitenbach M;  
XX WPI; 1997-145695/13.  
XX New recombinant DNA encoding plant phosphoglycerate mutase or its  
PT antigenic epitope(s) - useful for diagnosis or treatment of allergies to  
PT pollen and plant-derived foods.  
XX Disclosure; Fig 12a; 160pp; German.  
XX AAW31041-W31050 are T cell epitopes of mugwort pollen co-factor-  
CC independent phosphoglycerate mutase (PGM-i) isoform Art6. PGM-i is a  
CC highly conserved plant allergen (panallergen) which can cause cross-  
CC reactivity in patients allergic to pollen and plant-derived foods. PGM-i  
CC and it's B cell and T cell epitopes can be used for the in vitro  
CC detection of allergy against PGM-i, by measuring serum IgE or a cellular  
CC reaction. They can also be used in immunotherapy and will not cause an  
CC autoimmune response because PGM-i is significantly different from the  
CC human enzyme, which is co-factor dependent  
XX Sequence 16 AA;  
SQ  
Query Match 7.5%; Score 6; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 99;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 71 DAIKEV 76  
Db 9 DAIKEV 14  
RESULT 15  
ADV67376  
ID ADV67376 standard; peptide; 18 AA.  
XX AC ADV67376;  
XX DT 10-MAR-2005 (first entry)  
XX DE Amino acid sequence of antimicrobial peptide Gen2 variant #9.  
KW antimicrobial; microbial infection; bacterial infection;  
KW fungal infection; lung disease; sexually transmitted disease;  
KW food additive; cosmetics; preservation; cleaning; disinfection; paint;  
KW water line; water; Gen2.  
XX Synthetic.  
OS WO2004108757-A2.  
XX PN 16-DEC-2004.  
XX PD 10-JUN-2004; 2004WO-DK000399.  
XX PF 11-JUN-2003; 2003DK-00000865.  
XX PR 20-JUN-2003; 2003DK-00000924.  
XX PA (NOVO ) NOVOZYMES AS.  
XX (UVTB-) UNIV TRIESTE.  
XX PI Segura DR, Mygind PH, Hoegenhaug HK, Tossi A;  
XX WPI; 2005-031659/03.  
XX Novel antimicrobial polypeptide, useful for killing or inhibiting growth  
PT of microbial cells and as medicament, antimicrobial veterinarian or human  
PT therapeutic or prophylactic agent.  
XX

PS Claim 3; SEQ ID NO 11; 62pp; English.  
XX  
CC ADV67367-ADV67411 represent synthetic antimicrobial peptides, based on a  
CC formula given in the specification. Antimicrobial peptides of the  
CC invention are useful for killing, or inhibiting the growth of, microbial  
CC cells. They are useful as a medicament, antimicrobial veterinarian or  
CC human therapeutic or prophylactic agent, and for preparing veterinarian  
CC or human therapeutic agents for treating microbial infections, such as  
CC bacterial or fungal infections, preferably gram positive bacterial  
CC infections (the infections may be associated with lung diseases and  
CC sexually transmitted diseases). Antimicrobial peptides of the invention  
CC are for preserving foods, beverages and cosmetics. They are also useful  
CC for cleaning surfaces and cooking utensils in food processing plants and  
CC in any area in which food is prepared or served such as hospitals,  
CC nursing homes, restaurants, especially fast food restaurants etc. . The  
CC antimicrobial peptides are useful as a preservation agent or disinfection  
CC agent in water based paints, and for microbial control of water lines,  
CC for disinfection of water.  
XX  
SQ Sequence 18 AA;

Query Match 7.5%; Score 6; DB 9; Length 18;  
Best Local Similarity 100.0%; Fred. NO. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 18 NKLKTK 23  
|||  
Db 4 NKLKTK 9

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## SUMMARIES

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1	47	58.8	79	2	US-08-630-172-8	Sequence 8, Appli
2	47	58.8	79	2	US-09-375-419-8	Sequence 8, Appli
3	30	37.5	30	1	US-08-254-493-4	Sequence 4, Appli
4	20	37.5	30	1	US-08-408-222B-4	Sequence 4, Appli
5	29	36.2	29	1	US-08-254-493-5	Sequence 5, Appli
6	29	36.2	29	1	US-08-254-493-6	Sequence 6, Appli
7	29	36.2	29	1	US-08-408-222B-5	Sequence 5, Appli
8	29	36.2	29	1	US-08-408-222B-6	Sequence 6, Appli
9	6	7.5	62	2	US-09-621-976-5649	Sequence 5649, Ap
10	6	7.5	62	2	US-09-489-039A-12814	Sequence 12814, A
11	6	7.5	76	2	US-09-107-532A-4420	Sequence 4420, Ap
12	5	6.2	6	2	US-09-136-251-9	Sequence 9, Appli
13	5	6.2	6	2	US-09-634-496-9	Sequence 9, Appli
14	5	6.2	6	2	US-09-635-145A-9	Sequence 9, Appli
15	5	6.2	8	2	US-09-200-757-1	Sequence 1, Appli
16	5	6.2	8	2	US-09-200-757-2	Sequence 2, Appli
17	5	6.2	10	2	US-09-200-757-3	Sequence 3, Appli
18	5	6.2	10	2	US-09-200-757-4	Sequence 4, Appli
19	5	6.2	10	2	US-09-926-163B-18	Sequence 18, Appl
20	5	6.2	10	2	US-10-394-980-398	Sequence 398, App
21	5	6.2	10	2	US-10-394-980-452	Sequence 452, App
22	5	6.2	11	6	5204097-5	Patent No. 5204097
23	5	6.2	13	1	US-08-305-871A-28	Sequence 28, Appl
24	5	6.2	14	6	5204097-4	Patent No. 5204097
25	5	6.2	15	2	US-09-490-702B-15	Sequence 15, Appl
26	5	6.2	15	2	US-09-767-460-15	Sequence 15, Appl
27	5	6.2	16	2	US-08-602-999A-384	Sequence 384, App

101	5	6.2	51	6	5274075-11	Patent No. 5274075	174	5	6.2	80	2	US-09-149-476-578	Sequence 578, App
102	5	6.2	52	2	US-09-128-155-8	Sequence 8, Appli	175	5	6.2	80	2	US-09-252-991A-24876	Sequence 24876, A
103	5	6.2	53	2	US-08-836-500A-8	Sequence 8, Appli	176	5	6.2	80	2	US-09-270-767-44007	Sequence 44007, A
104	5	6.2	54	2	US-09-679-750-8	Sequence 8, Appli	177	5	6.2	80	2	US-09-270-767-59415	Sequence 59415, A
105	5	6.2	55	2	US-09-270-767-36652	Sequence 36652, A	178	5	6.2	80	2	US-09-809-665A-129	Sequence 129, App
106	5	6.2	56	2	US-09-270-767-51869	Sequence 51869, A	179	4	5.0	4	1	US-08-456-424-138	Sequence 138, App
107	5	6.2	57	1	US-09-513-999C-6743	Sequence 6743, Ap	180	4	5.0	4	2	US-09-258-754-430	Sequence 430, App
108	5	6.2	58	1	US-08-290-448A-57	Sequence 57, Appl	181	4	5.0	4	2	US-09-042-107-430	Sequence 430, App
109	5	6.2	59	1	US-08-290-448A-51	Sequence 61, Appl	182	4	5.0	4	2	US-09-722-250D-430	Sequence 430, App
110	5	6.2	60	1	US-08-290-448A-57	Sequence 57, Appl	183	4	5.0	4	2	US-09-676-475A-430	Sequence 430, App
111	5	6.2	61	1	US-08-290-448A-61	Sequence 61, Appl	184	4	5.0	4	2	US-09-698-781-10	Sequence 10, Appl
112	5	6.2	62	1	US-08-175-069A-57	Sequence 57, Appl	185	4	5.0	4	2	US-10-607-595-430	Sequence 430, App
113	5	6.2	63	1	US-08-175-069A-61	Sequence 61, Appl	186	4	5.0	5	1	US-07-778-156-11	Sequence 11, Appl
114	5	6.2	64	1	US-08-446-137B-12	Sequence 12, Appl	187	4	5.0	5	1	US-08-335-138-41	Sequence 41, Appl
115	5	6.2	65	1	US-08-461-939B-57	Sequence 57, Appl	188	4	5.0	5	1	US-08-422-166-11	Sequence 11, Appl
116	5	6.2	66	1	US-08-461-939B-61	Sequence 61, Appl	189	4	5.0	5	2	US-09-012-669F-52	Sequence 52, Appl
117	5	6.2	67	1	US-08-464-000-57	Sequence 57, Appl	190	4	5.0	5	2	US-09-133-521-10	Sequence 10, Appl
118	5	6.2	68	1	US-08-464-000-61	Sequence 61, Appl	191	4	5.0	5	2	US-09-621-377B-30	Sequence 30, Appl
119	5	6.2	69	1	US-09-248-796A-21602	Sequence 21602, A	192	4	5.0	5	2	US-10-031-893-30	Sequence 30, Appl
120	5	6.2	70	2	US-09-580-201A-16	Sequence 16, Appl	193	4	5.0	5	2	US-09-788-006-106	Sequence 106, App
121	5	6.2	71	2	US-09-580-201A-16	Sequence 16, Appl	194	4	5.0	5	2	US-09-788-006-107	Sequence 107, App
122	5	6.2	72	2	US-09-902-540-10101	Sequence 10101, A	195	4	5.0	5	2	US-10-353-174-30	Sequence 30, Appl
123	5	6.2	73	2	US-09-128-155-4	Sequence 4, Appli	196	4	5.0	5	2	US-10-394-980-307	Sequence 307, App
124	5	6.2	74	2	US-09-497-491-47	Sequence 47, Appl	197	4	5.0	6	1	US-08-180-209B-52	Sequence 52, Appl
125	5	6.2	75	2	US-09-248-796A-21203	Sequence 21203, A	198	4	5.0	6	1	US-08-180-209B-52	Sequence 52, Appl
126	5	6.2	76	2	US-09-248-796A-21203	Sequence 21203, A	199	4	5.0	6	1	US-08-260-199A-3	Sequence 3, Appli
127	5	6.2	77	2	US-09-248-796A-25412	Sequence 25412, A	200	4	5.0	6	1	US-08-260-199A-8	Sequence 8, Appli
128	5	6.2	78	2	US-09-898-659-38	Sequence 38, Appl	201	4	5.0	6	1	US-08-260-199A-13	Sequence 13, Appl
129	5	6.2	79	2	US-09-248-796A-24891	Sequence 24891, A	202	4	5.0	6	1	US-08-260-199A-24	Sequence 24, Appl
130	5	6.2	80	1	US-08-981-012A-11	Sequence 11, Appl	203	4	5.0	6	1	US-08-260-199A-25	Sequence 25, Appl
131	5	6.2	81	2	US-09-247-155-108	Sequence 108, App	204	4	5.0	6	1	US-08-594-447-69	Sequence 69, Appl
132	5	6.2	82	2	US-09-337-501-10	Sequence 10, Appl	205	4	5.0	6	1	US-08-541-964-68	Sequence 68, Appl
133	5	6.2	83	2	US-09-621-976-4513	Sequence 4513, Ap	206	4	5.0	6	1	US-08-528-523-4	Sequence 4, Appli
134	5	6.2	84	2	US-09-479-040-29	Sequence 29, Appl	207	4	5.0	6	1	US-08-665-647-83	Sequence 83, Appl
135	5	6.2	85	2	US-09-903-190-108	Sequence 108, App	208	4	5.0	6	2	US-08-474-853-52	Sequence 52, Appl
136	5	6.2	86	1	US-08-437-607A-44	Sequence 44, Appl	209	4	5.0	6	2	US-09-166-205B-52	Sequence 52, Appl
137	5	6.2	87	2	US-08-446-137B-10	Sequence 10, Appl	210	4	5.0	6	2	US-08-877-605-166	Sequence 166, App
138	5	6.2	88	2	US-09-540-236-2981	Sequence 2981, Ap	211	4	5.0	6	2	US-08-877-605-173	Sequence 173, App
139	5	6.2	89	2	US-09-621-976-3994	Sequence 3994, Ap	212	4	5.0	6	2	US-08-877-605-190	Sequence 190, App
140	5	6.2	90	2	US-09-463-559-22	Sequence 22, Appl	213	4	5.0	6	2	US-08-877-605-257	Sequence 257, App
141	5	6.2	91	2	US-09-248-796A-22622	Sequence 22622, A	214	4	5.0	6	2	US-09-535-852-917	Sequence 917, App
142	5	6.2	92	1	US-08-180-761B-3	Sequence 3, Appli	215	4	5.0	6	2	US-09-881-572A-6	Sequence 6, Appli
143	5	6.2	93	1	US-09-248-796A-26169	Sequence 26169, A	216	4	5.0	6	2	US-09-586-937-31	Sequence 31, Appl
144	5	6.2	94	1	US-08-292-968-21	Sequence 21, Appl	217	4	5.0	6	4	PCT-US94-02629-52	Sequence 52, Appl
145	5	6.2	95	1	US-08-467-974-21	Sequence 21, Appl	218	4	5.0	7	1	US-08-281-133-8	Sequence 8, Appli
146	5	6.2	96	2	US-08-467-974-21	Sequence 21, Appl	219	4	5.0	7	1	US-08-084-739-4	Sequence 4, Appli
147	5	6.2	97	2	US-09-082-514-21	Sequence 21, Appl	220	4	5.0	7	1	US-07-638-492-11	Sequence 11, Appl
148	5	6.2	98	2	US-09-270-767-41728	Sequence 41728, A	221	4	5.0	7	1	US-08-422-106-8	Sequence 8, Appli
149	5	6.2	99	2	US-09-328-352-5946	Sequence 5946, Ap	222	4	5.0	7	1	US-08-260-199A-2	Sequence 2, Appli
150	5	6.2	100	2	US-09-543-681A-4584	Sequence 4584, Ap	223	4	5.0	7	1	US-08-735-716-8	Sequence 8, Appli
151	5	6.2	101	6	5204097-1	Patent No. 5204097	224	4	5.0	7	1	US-08-555-568B-8	Sequence 8, Appli
152	5	6.2	102	2	US-09-621-976-4752	Sequence 4752, Ap	225	4	5.0	7	2	US-08-916-443A-8	Sequence 8, Appli
153	5	6.2	103	2	US-08-836-500A-6	Sequence 6, Appli	226	4	5.0	7	2	US-09-258-754-389	Sequence 389, App
154	5	6.2	104	2	US-09-679-750-6	Sequence 6, Appli	227	4	5.0	7	2	US-09-258-754-404	Sequence 404, App
155	5	6.2	105	2	US-09-366-887A-24	Sequence 24, Appl	228	4	5.0	7	2	US-09-042-107-389	Sequence 389, App
156	5	6.2	106	2	US-09-248-796A-24220	Sequence 24220, A	229	4	5.0	7	2	US-03-042-127-404	Sequence 404, App
157	5	6.2	107	2	US-09-517-204-24	Sequence 24, Appl	230	4	5.0	7	2	US-09-519-223-8	Sequence 8, Appli
158	5	6.2	108	2	US-09-134-000C-5163	Sequence 5163, Ap	231	4	5.0	7	2	US-09-187-859-1700	Sequence 1700, Ap
159	5	6.2	109	2	US-09-540-236-3737	Sequence 3737, Ap	232	4	5.0	7	2	US-08-897-843A-8	Sequence 8, Appli
160	5	6.2	110	2	US-09-248-796A-25808	Sequence 25808, A	233	4	5.0	7	2	US-09-839-542B-1700	Sequence 1700, Ap
161	5	6.2	111	2	US-09-513-999C-5127	Sequence 5127, Ap	234	4	5.0	7	2	US-08-753-750B-16	Sequence 16, Appl
162	5	6.2	112	2	US-09-180-827-3	Sequence 3, Appli	235	4	5.0	7	2	US-09-722-250D-389	Sequence 389, App
163	5	6.2	113	2	US-09-252-991A-32156	Sequence 32156, A	236	4	5.0	7	2	US-09-722-250D-404	Sequence 404, App
164	5	6.2	114	2	US-09-583-110-3419	Sequence 3419, Ap	237	4	5.0	7	2	US-09-535-852-924	Sequence 924, App
165	5	6.2	115	2	US-09-248-796A-24296	Sequence 24296, A	238	4	5.0	7	2	US-09-927-180-8	Sequence 8, Appli
166	5	6.2	116	2	US-08-858-207A-285	Sequence 285, App	239	4	5.0	7	2	US-09-676-475A-389	Sequence 389, App
167	5	6.2	117	2	US-09-134-001C-3386	Sequence 3386, Ap	240	4	5.0	7	2	US-09-676-475A-404	Sequence 404, App
168	5	6.2	118	2	US-09-248-796A-23767	Sequence 23767, A	241	4	5.0	7	2	US-09-620-840C-7	Sequence 7, Appli
169	5	6.2	119	2	US-09-248-796A-23996	Sequence 23996, A	242	4	5.0	7	2	US-09-884-767A-24	Sequence 24, Appl
170	5	6.2	120	2	US-09-248-796A-27345	Sequence 27345, A	243	4	5.0	7	2	US-10-394-980-316	Sequence 316, App
171	5	6.2	121	2	US-09-621-976-4746	Sequence 4746, Ap	244	4	5.0	7	2	US-10-394-980-331	Sequence 331, App
172	5	6.2	122	2	US-09-270-767-44291	Sequence 44291, A	245	4	5.0	7	2	US-10-394-980-431	Sequence 431, App
173	5	6.2	123	2	US-09-248-796A-24174	Sequence 24174, A	246	4	5.0	7	2	US-10-607-595-389	Sequence 389, App

247	4	5.0	7	2	US-10-607-595-404	Sequence 404, App	320	4	5.0	10	2	US-08-475-955-69	Sequence 69, Appl
248	4	5.0	7	2	US-10-006-869-1700	Sequence 1700, Ap	321	4	5.0	10	2	US-09-504-262D-15	Sequence 15, Appl
249	4	5.0	7	4	PCT-US95-08069-8	Sequence 8, Appli	322	4	5.0	10	2	US-09-620-091-17	Sequence 17, Appl
250	4	5.0	7	6	5169835-27	Patent No. 5169835	323	4	5.0	10	2	US-09-211-715-202	Sequence 202, App
251	4	5.0	8	1	US-08-213-897A-2	Sequence 2, Appli	324	4	5.0	10	2	US-09-935-430-94	Sequence 94, Appl
252	4	5.0	8	1	US-08-032-846-36	Sequence 36, Appl	325	4	5.0	10	2	US-09-935-430-632	Sequence 632, App
253	4	5.0	8	1	US-08-024-253-13	Sequence 13, Appl	326	4	5.0	10	2	US-09-767-460-45	Sequence 45, Appl
254	4	5.0	8	1	US-08-459-568-42	Sequence 42, Appl	327	4	5.0	10	2	US-10-102-283-189	Sequence 189, App
255	4	5.0	8	1	US-08-399-411-42	Sequence 42, Appl	328	4	5.0	10	2	US-07-867-819D-18	Sequence 18, Appl
256	4	5.0	8	2	US-08-516-859A-42	Sequence 42, Appl	329	4	5.0	10	2	US-07-867-819D-69	Sequence 69, Appl
257	4	5.0	8	2	US-08-160-604-61	Sequence 61, Appl	330	4	5.0	11	1	US-08-424-957-40	Sequence 40, Appl
258	4	5.0	8	2	US-08-584-008A-6	Sequence 6, Appli	331	4	5.0	11	1	US-08-746-283-21	Sequence 21, Appl
259	4	5.0	8	2	US-08-474-636-36	Sequence 36, Appl	332	4	5.0	11	1	US-08-746-257A-19	Sequence 19, Appl
260	4	5.0	8	2	US-09-586-472-420	Sequence 42, Appl	333	4	5.0	11	2	US-08-916-443A-1	Sequence 1, Appli
261	4	5.0	8	2	US-09-227-357-420	Sequence 420, App	334	4	5.0	11	2	US-09-215-966-5	Sequence 5, Appli
262	4	5.0	8	2	US-09-187-859-1701	Sequence 1701, Ap	335	4	5.0	11	2	US-09-215-966-20	Sequence 20, Appl
263	4	5.0	8	2	US-09-528-706-42	Sequence 42, Appl	336	4	5.0	11	2	US-09-035-686-40	Sequence 40, Appl
264	4	5.0	8	2	US-09-839-542B-1701	Sequence 1701, Ap	337	4	5.0	11	2	US-08-160-604-57	Sequence 57, Appl
265	4	5.0	8	2	US-09-535-852-931	Sequence 931, App	338	4	5.0	11	2	US-09-133-521-20	Sequence 20, Appl
266	4	5.0	8	2	US-09-535-852-938	Sequence 938, App	339	4	5.0	11	2	US-09-268-347-14	Sequence 14, Appl
267	4	5.0	8	2	US-09-535-852-1209	Sequence 1209, Ap	340	4	5.0	11	2	US-09-576-824A-490	Sequence 490, App
268	4	5.0	8	2	US-08-475-955-156	Sequence 156, App	341	4	5.0	11	2	US-09-756-983-7	Sequence 7, Appli
269	4	5.0	8	2	US-08-475-955-166	Sequence 166, App	342	4	5.0	11	2	US-09-419-788-129	Sequence 129, App
270	4	5.0	8	2	US-09-865-548A-79	Sequence 79, Appl	343	4	5.0	11	2	US-09-419-788-155	Sequence 155, App
271	4	5.0	8	2	US-09-973-278-647	Sequence 647, App	344	4	5.0	11	2	US-09-555-115A-20	Sequence 20, Appl
272	4	5.0	8	2	US-09-756-283A-30	Sequence 30, Appl	345	4	5.0	11	2	US-09-555-115A-21	Sequence 21, Appl
273	4	5.0	8	2	US-10-006-869-1701	Sequence 1701, Ap	346	4	5.0	11	2	US-09-555-115A-22	Sequence 22, Appl
274	4	5.0	9	1	US-08-215-805A-39	Sequence 39, Appl	347	4	5.0	11	6	5187155-25	Patent No. 5187155
275	4	5.0	9	1	US-08-032-846-11	Sequence 11, Appl	348	4	5.0	12	1	US-08-212-433A-10	Sequence 10, Appl
276	4	5.0	9	1	US-08-292-968-18	Sequence 18, Appl	349	4	5.0	12	1	US-08-166-930-5	Sequence 5, Appli
277	4	5.0	9	1	US-08-637-899-8	Sequence 8, Appli	350	4	5.0	12	1	US-08-190-788A-158	Sequence 158, App
278	4	5.0	9	1	US-08-467-974-18	Sequence 18, Appl	351	4	5.0	12	1	US-08-383-474B-161	Sequence 161, App
279	4	5.0	9	1	US-08-467-536-18	Sequence 18, Appl	352	4	5.0	12	1	US-08-465-391A-158	Sequence 158, App
280	4	5.0	9	1	US-08-467-976-18	Sequence 18, Appl	353	4	5.0	12	1	US-08-406-330-34	Sequence 34, Appl
281	4	5.0	9	2	US-09-082-514-18	Sequence 18, Appl	354	4	5.0	12	1	US-08-464-538B-158	Sequence 158, App
282	4	5.0	9	2	US-08-474-636-11	Sequence 11, Appl	355	4	5.0	12	1	US-08-463-076E-210	Sequence 210, App
283	4	5.0	9	2	US-09-187-859-1702	Sequence 1702, Ap	356	4	5.0	12	1	US-08-874-678-7	Sequence 7, Appli
284	4	5.0	9	2	US-09-297-269-38	Sequence 26, Appl	357	4	5.0	12	1	US-08-993-581B-33	Sequence 33, Appl
285	4	5.0	9	2	US-09-297-269-38	Sequence 38, Appl	358	4	5.0	12	1	US-08-727-045A-5	Sequence 5, Appli
286	4	5.0	9	2	US-09-244-583-16	Sequence 16, Appl	359	4	5.0	12	1	US-08-716-256-10	Sequence 10, Appl
287	4	5.0	9	2	US-09-481-620A-117	Sequence 117, App	360	4	5.0	12	2	US-08-742-243-65	Sequence 65, Appl
288	4	5.0	9	2	US-09-341-982-73	Sequence 73, Appl	361	4	5.0	12	2	US-08-742-243-67	Sequence 67, Appl
289	4	5.0	9	2	US-09-839-542B-1702	Sequence 1702, Ap	362	4	5.0	12	2	US-08-742-243-66	Sequence 66, Appl
290	4	5.0	9	2	US-09-535-852-1216	Sequence 1216, Ap	363	4	5.0	12	2	US-08-742-243-67	Sequence 67, Appl
291	4	5.0	9	2	US-08-765-837-6	Sequence 6, Appli	364	4	5.0	12	2	US-08-643-839-7	Sequence 68, Appl
292	4	5.0	9	2	US-09-865-548A-56	Sequence 56, Appl	365	4	5.0	12	2	US-09-238-448-2	Sequence 2, Appli
293	4	5.0	9	2	US-09-865-548A-176	Sequence 176, App	366	4	5.0	12	2	US-09-133-521-22	Sequence 22, Appl
294	4	5.0	9	2	US-09-680-514-26	Sequence 17, Appl	367	4	5.0	12	2	US-09-308-175A-20	Sequence 20, Appl
295	4	5.0	9	2	US-09-065-903-17	Sequence 17, Appl	368	4	5.0	12	2	US-09-348-886-7	Sequence 7, Appli
296	4	5.0	9	2	US-10-006-869-1702	Sequence 1702, Ap	369	4	5.0	12	2	US-09-408-172-5	Sequence 5, Appli
297	4	5.0	10	1	US-08-424-682A-2	Sequence 2, Appli	370	4	5.0	12	2	US-08-999-689A-12	Sequence 12, Appl
298	4	5.0	10	1	US-08-214-650-36	Sequence 36, Appl	371	4	5.0	12	2	US-09-341-982-79	Sequence 79, Appl
299	4	5.0	10	1	US-08-468-543-21	Sequence 21, Appl	372	4	5.0	12	2	US-10-053-485-22	Sequence 22, Appl
300	4	5.0	10	1	US-08-469-692-21	Sequence 21, Appl	373	4	5.0	12	2	US-09-403-752A-111	Sequence 111, App
301	4	5.0	10	1	US-08-482-228-121	Sequence 121, App	374	4	5.0	12	2	US-09-748-578-1	Sequence 1, Appli
302	4	5.0	10	1	US-08-398-046-21	Sequence 21, Appl	375	4	5.0	12	2	US-09-385-219A-82	Sequence 82, Appl
303	4	5.0	10	2	US-09-139-762A-45	Sequence 45, Appl	376	4	5.0	12	2	US-09-381-903-56	Sequence 56, Appl
304	4	5.0	10	2	US-09-139-762A-89	Sequence 89, Appl	377	4	5.0	12	2	US-09-381-903-57	Sequence 57, Appl
305	4	5.0	10	2	US-09-139-762A-105	Sequence 105, App	378	4	5.0	12	2	US-09-381-903-58	Sequence 58, Appl
306	4	5.0	10	2	US-08-482-528-121	Sequence 121, App	379	4	5.0	12	2	PCT-US94-02191-5	Sequence 5, Appli
307	4	5.0	10	2	US-09-184-658-15	Sequence 15, App	380	4	5.0	12	4	PCT-US94-02191-8	Sequence 8, Appli
308	4	5.0	10	2	US-08-159-339A-487	Sequence 487, App	381	4	5.0	12	2	PCT-US95-03239-10	Sequence 10, Appl
309	4	5.0	10	2	US-08-159-339A-500	Sequence 500, App	382	4	5.0	12	2	5252328-15	Patent No. 5252328
310	4	5.0	10	2	US-08-159-339A-627	Sequence 627, App	383	4	5.0	12	2		
311	4	5.0	10	2	US-08-159-339A-834	Sequence 834, App	384	4	5.0	12	2		
312	4	5.0	10	2	US-08-159-339A-836	Sequence 836, App	385	4	5.0	12	2		
313	4	5.0	10	2	US-09-042-353-364	Sequence 364, App	386	4	5.0	12	2		
314	4	5.0	10	2	US-08-758-417A-212	Sequence 212, App	387	4	5.0	12	2		
315	4	5.0	10	2	US-09-311-784A-269	Sequence 269, App	388	4	5.0	12	2		
316	4	5.0	10	2	US-09-311-784A-288	Sequence 288, App	389	4	5.0	12	4		
317	4	5.0	10	2	US-09-490-702B-45	Sequence 45, Appl	390	4	5.0	12	4		
318	4	5.0	10	2	US-09-784-642-11	Sequence 11, Appl	391	4	5.0	12	4		
319	4	5.0	10	2	US-08-475-955-18	Sequence 18, Appl	392	4	5.0	12	6		

393	4	5.0	13	1	US-07-732-114A-4	Sequence 4, Appl	466	4	5.0	13	2	US-10-090-185-35	Sequence 35, Appl
394	4	5.0	13	1	US-08-336-087-5	Sequence 5, Appl	467	4	5.0	13	2	US-10-090-185-39	Sequence 39, Appl
395	4	5.0	13	1	US-08-186-266-10	Sequence 10, Appl	468	4	5.0	13	2	PCT-US95-04121-13	Sequence 13, Appl
396	4	5.0	13	1	US-08-479-400-5	Sequence 5, Appl	469	4	5.0	14	1	US-08-084-739-3	Sequence 3, Appl
397	4	5.0	13	1	US-08-305-871A-19	Sequence 19, Appl	470	4	5.0	14	1	US-07-961-837-7	Sequence 7, Appl
398	4	5.0	13	1	US-08-305-871A-20	Sequence 20, Appl	471	4	5.0	14	1	US-08-325-071-17	Sequence 17, Appl
399	4	5.0	13	1	US-08-305-871A-21	Sequence 21, Appl	472	4	5.0	14	1	US-08-232-453A-68	Sequence 68, Appl
400	4	5.0	13	1	US-08-305-871A-22	Sequence 22, Appl	473	4	5.0	14	1	US-08-463-620-6	Sequence 6, Appl
401	4	5.0	13	1	US-08-305-871A-23	Sequence 23, Appl	474	4	5.0	14	1	US-08-463-620-7	Sequence 7, Appl
402	4	5.0	13	1	US-08-305-871A-24	Sequence 24, Appl	475	4	5.0	14	1	US-08-480-190-189	Sequence 189, App
403	4	5.0	13	1	US-08-305-871A-25	Sequence 25, Appl	476	4	5.0	14	1	US-08-764-640-95	Sequence 95, Appl
404	4	5.0	13	1	US-08-305-871A-26	Sequence 26, Appl	477	4	5.0	14	1	US-08-764-640-96	Sequence 96, Appl
405	4	5.0	13	1	US-08-305-871A-27	Sequence 27, Appl	478	4	5.0	14	1	US-08-488-379-189	Sequence 189, App
406	4	5.0	13	1	US-08-305-871A-29	Sequence 29, Appl	479	4	5.0	14	1	US-08-480-793-1	Sequence 1, Appl
407	4	5.0	13	1	US-08-170-114A-4	Sequence 4, Appl	480	4	5.0	14	1	US-08-224-917-6	Sequence 6, Appl
408	4	5.0	13	1	US-08-188-583-33	Sequence 33, Appl	481	4	5.0	14	1	US-08-224-917-7	Sequence 7, Appl
409	4	5.0	13	1	US-08-397-286-3	Sequence 3, Appl	482	4	5.0	14	1	US-08-484-905-56	Sequence 56, Appl
410	4	5.0	13	1	US-08-395-204-5	Sequence 5, Appl	483	4	5.0	14	1	US-08-914-853-6	Sequence 6, Appl
411	4	5.0	13	2	US-09-076-646-3	Sequence 3, Appl	484	4	5.0	14	1	US-08-914-853-7	Sequence 7, Appl
412	4	5.0	13	2	US-08-913-805A-13	Sequence 13, Appl	485	4	5.0	14	2	US-08-481-985B-56	Sequence 56, Appl
413	4	5.0	13	2	US-08-526-136-23	Sequence 23, Appl	486	4	5.0	14	2	US-08-807-952B-9	Sequence 9, Appl
414	4	5.0	13	2	US-08-751-359-20	Sequence 20, Appl	487	4	5.0	14	2	US-08-807-952B-12	Sequence 12, Appl
415	4	5.0	13	2	US-09-442-629-13	Sequence 13, Appl	488	4	5.0	14	2	US-08-973-225-95	Sequence 95, Appl
416	4	5.0	13	2	US-08-907-146-20	Sequence 20, Appl	489	4	5.0	14	2	US-08-973-225-96	Sequence 96, Appl
417	4	5.0	13	2	US-09-387-418A-35	Sequence 35, Appl	490	4	5.0	14	2	US-08-973-225-218	Sequence 218, App
418	4	5.0	13	2	US-09-387-418A-39	Sequence 39, Appl	491	4	5.0	14	2	US-09-244-238A-95	Sequence 95, Appl
419	4	5.0	13	2	US-08-788-822A-23	Sequence 23, Appl	492	4	5.0	14	2	US-08-244-238A-96	Sequence 96, Appl
420	4	5.0	13	2	US-08-788-822A-24	Sequence 24, Appl	493	4	5.0	14	2	US-08-370-476-56	Sequence 56, Appl
421	4	5.0	13	2	US-08-788-822A-25	Sequence 25, Appl	494	4	5.0	14	2	US-09-385-442-31	Sequence 31, Appl
422	4	5.0	13	2	US-08-788-822A-26	Sequence 26, Appl	495	4	5.0	14	2	US-08-461-004A-17	Sequence 17, Appl
423	4	5.0	13	2	US-08-788-822A-27	Sequence 27, Appl	496	4	5.0	14	2	US-09-516-704-95	Sequence 95, Appl
424	4	5.0	13	2	US-08-469-260A-445	Sequence 445, App	497	4	5.0	14	2	US-09-516-704-96	Sequence 96, Appl
425	4	5.0	13	2	US-08-488-446-445	Sequence 445, App	498	4	5.0	14	2	US-09-025-596-100	Sequence 100, App
426	4	5.0	13	2	US-09-692-170C-29	Sequence 29, Appl	499	4	5.0	14	2	US-09-549-090-95	Sequence 95, Appl
427	4	5.0	13	2	US-08-467-344A-445	Sequence 445, App	500	4	5.0	14	2	US-09-549-090-96	Sequence 96, Appl
428	4	5.0	13	2	US-09-543-608A-26	Sequence 26, Appl	501	4	5.0	14	2	US-09-549-090-218	Sequence 218, App
429	4	5.0	13	2	US-09-543-608A-27	Sequence 27, Appl	502	4	5.0	14	2	US-09-675-922-12	Sequence 12, Appl
430	4	5.0	13	2	US-09-543-608A-28	Sequence 28, Appl	503	4	5.0	14	2	US-09-832-230A-95	Sequence 95, Appl
431	4	5.0	13	2	US-09-543-608A-29	Sequence 29, Appl	504	4	5.0	14	2	US-09-832-230A-96	Sequence 96, Appl
432	4	5.0	13	2	US-09-543-608A-30	Sequence 30, Appl	505	4	5.0	14	2	US-08-475-399A-189	Sequence 30, Appl
433	4	5.0	13	2	US-09-543-608A-31	Sequence 31, Appl	506	4	5.0	14	2	US-09-394-455-30	Sequence 14, Appl
434	4	5.0	13	2	US-09-543-608A-32	Sequence 32, Appl	507	4	5.0	14	2	US-09-202-077-14	Sequence 14, Appl
435	4	5.0	13	2	US-09-543-608A-33	Sequence 33, Appl	508	4	5.0	14	2	US-09-073-661-100	Sequence 100, App
436	4	5.0	13	2	US-09-543-608A-34	Sequence 34, Appl	509	4	5.0	14	2	US-09-428-082B-52	Sequence 52, Appl
437	4	5.0	13	2	US-09-543-608A-35	Sequence 35, Appl	510	4	5.0	14	2	US-10-100-785-100	Sequence 100, App
438	4	5.0	13	2	US-09-543-608A-36	Sequence 36, Appl	511	4	5.0	14	2	US-09-443-199C-1239	Sequence 1239, Ap
439	4	5.0	13	2	US-09-543-608A-37	Sequence 37, Appl	512	4	5.0	14	2	US-09-405-986A-21	Sequence 21, Appl
440	4	5.0	13	2	US-08-475-955-54	Sequence 54, Appl	513	4	5.0	14	2	US-08-077-255A-189	Sequence 189, App
441	4	5.0	13	2	US-09-060-450-8	Sequence 8, Appl	514	4	5.0	14	2	US-10-101-279-100	Sequence 3, Appl
442	4	5.0	13	2	US-09-405-986A-4	Sequence 4, Appl	515	4	5.0	14	2	US-09-388-316C-30	Sequence 100, App
443	4	5.0	13	2	US-09-405-986A-6	Sequence 6, Appl	516	4	5.0	14	2	US-09-709-201B-100	Sequence 30, Appl
444	4	5.0	13	2	US-09-233-043D-2575	Sequence 2575, App	517	4	5.0	14	2	US-09-623-548A-1410	Sequence 1410, Ap
445	4	5.0	13	2	US-08-424-550B-445	Sequence 445, App	518	4	5.0	14	2	US-10-100-759-100	Sequence 100, App
446	4	5.0	13	2	US-10-405-231A-29	Sequence 29, Appl	519	4	5.0	14	2	US-09-657-276-1410	Sequence 1410, Ap
447	4	5.0	13	2	US-10-238-607-29	Sequence 29, Appl	520	4	5.0	14	2	US-09-563-760A-12	Sequence 12, Appl
448	4	5.0	13	2	US-09-984-365-29	Sequence 29, Appl	521	4	5.0	14	2	US-09-586-937-56	Sequence 56, Appl
449	4	5.0	13	2	US-09-935-430-654	Sequence 654, App	522	4	5.0	14	2	US-09-798-338B-3	Sequence 3, Appl
450	4	5.0	13	2	US-09-724-953-2	Sequence 2, Appl	523	4	5.0	14	2	PCT-US92-05825A-1	Sequence 1, Appl
451	4	5.0	13	2	US-09-724-953-2	Sequence 2, Appl	524	4	5.0	14	4	PCT-US93-07545-189	Sequence 189, App
452	4	5.0	13	2	US-09-556-818-65	Sequence 65, Appl	525	4	5.0	14	4	PCT-US95-03934A-6	Sequence 6, Appl
453	4	5.0	13	2	US-09-580-018-44	Sequence 44, Appl	526	4	5.0	14	4	PCT-US95-03934A-7	Sequence 7, Appl
454	4	5.0	13	2	US-09-724-940-44	Sequence 44, Appl	527	4	5.0	14	4	PCT-US95-03934A-7	Sequence 7, Appl
455	4	5.0	13	2	US-10-697-055-29	Sequence 29, Appl	528	4	5.0	14	4	PCT-US95-11127-20	Sequence 20, Appl
456	4	5.0	13	2	US-09-935-430-654	Sequence 654, App	529	4	5.0	14	6	5178861-2	Patent No. 5178861
457	4	5.0	13	2	US-09-724-953-2	Sequence 2, Appl	530	4	5.0	14	6	5178861-11	Patent No. 5178861
458	4	5.0	13	2	US-07-867-819D-54	Sequence 54, Appl	531	4	5.0	14	6	5405952-6	Patent No. 5405952
459	4	5.0	13	2	US-09-724-940-44	Sequence 44, Appl	532	4	5.0	14	6	5445818-2	Patent No. 5445818
460	4	5.0	13	2	US-09-979-952-2	Sequence 2, Appl	533	4	5.0	15	1	US-07-859-291C-27	Sequence 27, Appl
461	4	5.0	13	2	US-09-585-817-2	Sequence 2, Appl	534	4	5.0	15	1	US-07-768-286B-16	Sequence 16, Appl
462	4	5.0	13	2	US-10-153-469A-41	Sequence 41, Appl	535	4	5.0	15	1	US-07-768-286B-18	Sequence 18, Appl
463	4	5.0	13	2	US-10-153-469A-42	Sequence 42, Appl	536	4	5.0	15	1	US-08-127-351-26	Sequence 26, Appl
464	4	5.0	13	2	US-10-104-889-41	Sequence 41, Appl	537	4	5.0	15	1	US-08-030-077-9	Sequence 9, Appl
465	4	5.0	13	2	US-10-104-889-42	Sequence 42, Appl	538	4	5.0	15	1	US-08-245-853-2	Sequence 2, Appl



539	4	5.0	15	1	US-08-480-367B-26	Sequence 26, Appl	612	4	5.0	16	2	US-08-959-206A-23	Sequence 23, Appl
540	4	5.0	15	1	US-08-487-221A-26	Sequence 26, Appl	613	4	5.0	16	2	US-09-315-304B-1192	Sequence 1192, Ap
541	4	5.0	15	1	US-08-480-370-26	Sequence 26, Appl	614	4	5.0	16	2	US-09-598-784-5	Sequence 5, Appl
542	4	5.0	15	1	US-08-299-636-5	Sequence 5, Appl	615	4	5.0	16	2	US-08-788-822A-10	Sequence 10, Appl
543	4	5.0	15	1	US-08-279-155-6	Sequence 5, Appl	616	4	5.0	16	2	US-08-413-233-3	Sequence 3, Appl
544	4	5.0	15	1	US-08-464-456-5	Sequence 5, Appl	617	4	5.0	16	2	US-09-834-784-1192	Sequence 1192, Ap
545	4	5.0	15	1	US-08-573-675-2	Sequence 2, Appl	618	4	5.0	16	2	US-09-515-965A-1192	Sequence 1192, Ap
546	4	5.0	15	1	US-08-703-988A-6	Sequence 6, Appl	619	4	5.0	16	2	US-09-532-709G-6	Sequence 6, Appl
547	4	5.0	15	1	US-08-463-052-5	Sequence 5, Appl	620	4	5.0	16	2	US-09-350-641C-1192	Sequence 1192, Ap
548	4	5.0	15	1	US-08-477-108A-11	Sequence 11, Appl	621	4	5.0	16	2	US-09-405-986A-22	Sequence 22, Appl
549	4	5.0	15	1	US-08-480-551-5	Sequence 5, Appl	622	4	5.0	16	2	US-09-405-986A-23	Sequence 23, Appl
550	4	5.0	15	1	US-08-195-874-2	Sequence 2, Appl	623	4	5.0	16	2	US-09-925-715-23	Sequence 23, Appl
551	4	5.0	15	1	US-08-616-844-51	Sequence 51, Appl	624	4	5.0	16	2	US-09-910-009A-27	Sequence 27, Appl
552	4	5.0	15	1	US-08-750-856A-8	Sequence 8, Appl	625	4	5.0	16	2	US-09-910-009A-388	Sequence 388, Appl
553	4	5.0	15	1	US-08-400-796-9	Sequence 9, Appl	626	4	5.0	16	2	US-09-709-103-62	Sequence 62, Appl
554	4	5.0	15	1	US-08-637-759B-239	Sequence 239, Appl	627	4	5.0	16	2	US-09-439-410A-62	Sequence 62, Appl
555	4	5.0	15	1	US-08-599-654-51	Sequence 51, Appl	628	4	5.0	16	2	US-09-350-841A-1192	Sequence 1192, Ap
556	4	5.0	15	1	US-08-612-842-6	Sequence 6, Appl	629	4	5.0	16	2	US-09-674-973A-35	Sequence 35, Appl
557	4	5.0	15	1	US-08-484-905B-26	Sequence 26, Appl	630	4	5.0	16	2	US-09-541-345-67	Sequence 67, Appl
558	4	5.0	15	2	US-08-481-985B-26	Sequence 26, Appl	631	4	5.0	16	2	US-09-541-345-93	Sequence 93, Appl
559	4	5.0	15	2	US-08-871-355A-239	Sequence 239, Appl	632	4	5.0	16	2	US-09-908-322-32	Sequence 32, Appl
560	4	5.0	15	2	US-08-944-868A-51	Sequence 51, Appl	633	4	5.0	16	2	US-09-208-658-231	Sequence 231, Appl
561	4	5.0	15	2	US-08-944-423A-51	Sequence 51, Appl	634	4	5.0	16	2	US-10-226-877A-51	Sequence 51, Appl
562	4	5.0	15	2	US-08-946-026-45	Sequence 45, Appl	635	4	5.0	16	2	US-09-836-770A-4	Sequence 4, Appl
563	4	5.0	15	2	US-08-834-314-3	Sequence 3, Appl	636	4	5.0	16	2	US-09-825-517A-93	Sequence 93, Appl
564	4	5.0	15	2	US-08-944-496-51	Sequence 51, Appl	637	4	5.0	16	2	US-10-680-670-6	Sequence 6, Appl
565	4	5.0	15	2	US-08-370-476-26	Sequence 26, Appl	638	4	5.0	16	2	PCT-US96-01314-28	Sequence 28, Appl
566	4	5.0	15	2	US-09-201-945-239	Sequence 239, Appl	639	4	5.0	16	4	5445818-10	Patent No. 5445818
567	4	5.0	15	2	US-09-310-187A-3	Sequence 3, Appl	640	4	5.0	16	6	5445818-10	Patent No. 5445818
568	4	5.0	15	2	US-08-475-955-5	Sequence 5, Appl	641	4	5.0	17	1	US-08-084-739-5	Sequence 5, Appl
569	4	5.0	15	2	US-09-671-089-50	Sequence 50, Appl	642	4	5.0	17	1	US-07-638-492-1	Sequence 1, Appl
570	4	5.0	15	2	US-09-160-076-2	Sequence 2, Appl	643	4	5.0	17	1	US-07-638-492-2	Sequence 2, Appl
571	4	5.0	15	2	US-09-819-308-17	Sequence 17, Appl	644	4	5.0	17	1	US-08-194-290-8	Sequence 8, Appl
572	4	5.0	15	2	US-07-867-819D-5	Sequence 5, Appl	645	4	5.0	17	1	US-08-325-553-38	Sequence 38, Appl
573	4	5.0	15	4	PCT-US93-08659-1	Sequence 1, Appl	646	4	5.0	17	1	US-08-318-200-22	Sequence 22, Appl
574	4	5.0	15	4	PCT-US95-01671-2	Sequence 2, Appl	647	4	5.0	17	1	US-08-388-756-5	Sequence 5, Appl
575	4	5.0	15	6	PCT-US95-11127-21	Sequence 21, Appl	648	4	5.0	17	1	US-08-015-770B-1	Sequence 1, Appl
576	4	5.0	15	6	517843-11	Patent No. 517843	649	4	5.0	17	1	US-08-486-135-11	Sequence 11, Appl
577	4	5.0	15	6	5443956-1	Patent No. 5443956	650	4	5.0	17	1	US-08-260-199A-1	Sequence 1, Appl
578	4	5.0	15	6	5470825-2	Patent No. 5470825	651	4	5.0	17	1	US-08-468-975-8	Sequence 8, Appl
579	4	5.0	16	1	US-08-127-351-25	Sequence 25, Appl	652	4	5.0	17	1	US-08-470-152-11	Sequence 11, Appl
580	4	5.0	16	1	US-08-480-367B-25	Sequence 25, Appl	653	4	5.0	17	1	US-08-460-502-6	Sequence 6, Appl
581	4	5.0	16	1	US-08-107-235-5	Sequence 5, Appl	654	4	5.0	17	1	US-08-748-428-5	Sequence 5, Appl
582	4	5.0	16	1	US-08-487-221A-25	Sequence 25, Appl	655	4	5.0	17	1	US-08-500-860A-25	Sequence 25, Appl
583	4	5.0	16	1	US-08-480-370-25	Sequence 25, Appl	656	4	5.0	17	1	US-08-468-964B-9	Sequence 9, Appl
584	4	5.0	16	1	US-08-299-636-4	Sequence 4, Appl	657	4	5.0	17	1	US-08-394-152A-38	Sequence 38, Appl
585	4	5.0	16	1	US-08-279-153-5	Sequence 5, Appl	658	4	5.0	17	1	US-08-475-634D-1	Sequence 1, Appl
586	4	5.0	16	1	US-08-464-456-4	Sequence 4, Appl	659	4	5.0	17	1	US-07-871-282A-9	Sequence 9, Appl
587	4	5.0	16	1	US-08-468-543-6	Sequence 6, Appl	660	4	5.0	17	1	US-08-363-276B-9	Sequence 9, Appl
588	4	5.0	16	1	US-08-305-871A-9	Sequence 9, Appl	661	4	5.0	17	1	US-08-614-377A-8	Sequence 8, Appl
589	4	5.0	16	1	US-08-703-988A-5	Sequence 5, Appl	662	4	5.0	17	1	US-08-253-678A-9	Sequence 9, Appl
590	4	5.0	16	1	US-08-463-052-4	Sequence 4, Appl	663	4	5.0	17	2	US-08-785-247-10	Sequence 10, Appl
591	4	5.0	16	1	US-08-178-268-39	Sequence 39, Appl	664	4	5.0	17	2	US-08-582-134B-9	Sequence 9, Appl
592	4	5.0	16	1	US-08-631-427A-5	Sequence 5, Appl	665	4	5.0	17	2	US-08-722-240-19	Sequence 19, Appl
593	4	5.0	16	1	US-08-480-551-4	Sequence 4, Appl	666	4	5.0	17	2	US-08-170-299-9	Sequence 9, Appl
594	4	5.0	16	1	US-08-476-062A-28	Sequence 28, Appl	667	4	5.0	17	2	US-08-467-791-8	Sequence 8, Appl
595	4	5.0	16	1	US-08-469-692-6	Sequence 6, Appl	668	4	5.0	17	2	US-09-215-966-4	Sequence 4, Appl
596	4	5.0	16	1	US-08-433-133-1	Sequence 1, Appl	669	4	5.0	17	2	US-08-974-549A-100	Sequence 100, Appl
597	4	5.0	16	1	US-09-133-774-4	Sequence 4, Appl	670	4	5.0	17	2	US-08-996-679-63	Sequence 63, Appl
598	4	5.0	16	1	US-09-133-774-5	Sequence 5, Appl	671	4	5.0	17	2	US-08-061-376-8	Sequence 8, Appl
599	4	5.0	16	1	US-09-133-774-6	Sequence 6, Appl	672	4	5.0	17	2	US-08-939-853A-14	Sequence 14, Appl
600	4	5.0	16	1	US-08-398-046-6	Sequence 6, Appl	673	4	5.0	17	2	US-08-755-034-9	Sequence 9, Appl
601	4	5.0	16	1	US-08-612-842-5	Sequence 5, Appl	674	4	5.0	17	2	US-09-115-395-23	Sequence 23, Appl
602	4	5.0	16	2	US-09-303-862-4	Sequence 4, Appl	675	4	5.0	17	2	US-09-142-648B-8	Sequence 8, Appl
603	4	5.0	16	2	US-09-303-862-5	Sequence 5, Appl	676	4	5.0	17	2	US-08-990-823-86	Sequence 86, Appl
604	4	5.0	16	2	US-09-303-862-6	Sequence 6, Appl	677	4	5.0	17	2	US-08-990-823-88	Sequence 88, Appl
605	4	5.0	16	2	US-08-714-960B-5	Sequence 5, Appl	678	4	5.0	17	2	US-09-113-977C-68	Sequence 68, Appl
606	4	5.0	16	2	US-09-284-625-25	Sequence 25, Appl	679	4	5.0	17	2	US-08-860-904-11	Sequence 11, Appl
607	4	5.0	16	2	US-09-975-040-11	Sequence 11, Appl	680	4	5.0	17	2	US-09-055-075C-10	Sequence 10, Appl
608	4	5.0	16	2	US-09-082-279B-1192	Sequence 1192, Ap	681	4	5.0	17	2	US-09-055-075C-12	Sequence 12, Appl
609	4	5.0	16	2	US-08-960-054A-27	Sequence 27, Appl	682	4	5.0	17	2	US-09-250-059-54	Sequence 54, Appl
610	4	5.0	16	2	US-08-981-392-32	Sequence 32, Appl	683	4	5.0	17	2	US-09-248-074-54	Sequence 54, Appl
611	4	5.0	16	2	US-08-958-993A-27	Sequence 27, Appl	684	4	5.0	17	2		

685	4	5.0	17	2	US-09-187-859-50	Sequence 50, Appl	758	4	5.0	18	2	US-10-283-599-196	Sequence 196, App
686	4	5.0	17	2	US-09-148-711A-6	Sequence 6, Appli	759	4	5.0	18	2	US-09-465-718-196	Sequence 196, App
687	4	5.0	17	2	US-09-458-870-54	Sequence 54, Appl	760	4	5.0	18	2	US-10-615-959-32	Sequence 32, Appl
688	4	5.0	17	2	US-09-351-048A-68	Sequence 68, Appl	761	4	5.0	18	2	US-09-973-278-658	Sequence 658, App
689	4	5.0	17	2	US-08-913-951-100	Sequence 100, App	762	4	5.0	18	6	5459046-9	Patent No. 5459046
690	4	5.0	17	2	US-09-345-624A-1	Sequence 1, Appli	763	4	5.0	18	6	5523089-34	Patent No. 5523089
691	4	5.0	17	2	US-09-919-124-10	Sequence 10, Appl	764	4	5.0	19	1	US-08-101-041A-5	Sequence 5, Appli
692	4	5.0	17	2	US-09-919-124-12	Sequence 12, Appl	765	4	5.0	19	1	US-08-392-646-18	Sequence 18, Appl
693	4	5.0	17	2	US-08-705-477E-38	Sequence 38, Appl	766	4	5.0	19	1	US-08-503-062-1	Sequence 1, Appli
694	4	5.0	17	2	US-09-839-542B-50	Sequence 50, Appl	767	4	5.0	19	1	US-08-503-062-21	Sequence 21, Appl
695	4	5.0	17	2	US-09-477-135A-86	Sequence 86, Appl	768	4	5.0	19	2	US-09-010-999-8	Sequence 8, Appli
696	4	5.0	17	2	US-09-477-135A-87	Sequence 87, Appl	769	4	5.0	19	2	US-08-604-365-11	Sequence 11, Appl
697	4	5.0	17	2	US-09-477-135A-88	Sequence 88, Appl	770	4	5.0	19	2	US-08-975-040-2	Sequence 2, Appli
698	4	5.0	17	2	US-09-402-181B-100	Sequence 100, App	771	4	5.0	19	2	US-08-975-040-8	Sequence 8, Appli
699	4	5.0	17	2	US-09-721-456-100	Sequence 100, App	772	4	5.0	19	2	US-08-975-040-19	Sequence 19, Appl
700	4	5.0	17	2	US-09-567-003C-3	Sequence 3, Appli	773	4	5.0	19	2	US-09-082-279B-1190	Sequence 1190, Ap
701	4	5.0	17	2	US-09-535-852-1935	Sequence 1935, Ap	774	4	5.0	19	2	US-09-027-998A-34	Sequence 34, Appl
702	4	5.0	17	2	US-09-662-052-7	Sequence 7, Appli	775	4	5.0	19	2	US-09-101-927-17	Sequence 17, Appl
703	4	5.0	17	2	US-09-383-062-47	Sequence 47, Appl	776	4	5.0	19	2	US-09-101-927-19	Sequence 19, Appl
704	4	5.0	17	2	US-09-674-973A-36	Sequence 36, Appl	777	4	5.0	19	2	US-09-315-304B-1190	Sequence 1190, Ap
705	4	5.0	17	2	US-10-193-653-68	Sequence 68, Appl	778	4	5.0	19	2	US-09-149-476-569	Sequence 569, App
706	4	5.0	17	2	US-09-839-884-47	Sequence 47, Appl	779	4	5.0	19	2	US-09-082-358B-75	Sequence 75, Appl
707	4	5.0	17	2	US-09-937-126-20	Sequence 20, Appl	780	4	5.0	19	2	US-09-486-072-18	Sequence 18, Appl
708	4	5.0	17	2	US-08-466-381C-38	Sequence 38, Appl	781	4	5.0	19	2	US-09-834-784-1190	Sequence 1190, Ap
709	4	5.0	17	2	US-10-006-869-50	Sequence 50, Appl	782	4	5.0	19	2	US-09-689-678-11	Sequence 11, Appl
710	4	5.0	17	4	PCT-US95-16718-9	Sequence 9, Appli	783	4	5.0	19	2	US-09-829-855-214	Sequence 214, App
711	4	5.0	17	4	PCT-US96-08995-9	Sequence 9, Appli	784	4	5.0	19	2	US-09-515-965A-1190	Sequence 1190, Ap
712	4	5.0	18	1	US-07-928-930A-2	Sequence 2, Appli	785	4	5.0	19	2	US-09-350-641C-1190	Sequence 1190, Ap
713	4	5.0	18	1	US-07-920-597-7	Sequence 7, Appli	786	4	5.0	19	2	US-09-302-626B-153	Sequence 153, App
714	4	5.0	18	1	US-08-288-568-2	Sequence 2, Appli	787	4	5.0	19	2	US-09-302-626B-154	Sequence 154, App
715	4	5.0	18	1	US-08-487-461-2	Sequence 2, Appli	788	4	5.0	19	2	US-09-302-626B-155	Sequence 155, App
716	4	5.0	18	1	US-08-432-691-2	Sequence 2, Appli	789	4	5.0	19	2	US-10-038-612-33	Sequence 33, Appl
717	4	5.0	18	1	US-08-327-709-2	Sequence 2, Appli	790	4	5.0	19	2	US-10-038-612-34	Sequence 34, Appl
718	4	5.0	18	1	US-08-423-399B-15	Sequence 15, Appl	791	4	5.0	19	2	US-09-525-269A-22	Sequence 22, Appl
719	4	5.0	18	1	US-08-487-459-2	Sequence 2, Appli	792	4	5.0	19	2	US-09-350-841A-1190	Sequence 1190, Ap
720	4	5.0	18	1	US-08-190-687B-26	Sequence 26, Appl	793	4	5.0	19	2	US-09-471-276-1251	Sequence 1251, Ap
721	4	5.0	18	1	US-08-652-369A-1	Sequence 1, Appli	794	4	5.0	19	2	US-09-762-767B-13	Sequence 13, Appl
722	4	5.0	18	1	US-08-464-956-2	Sequence 2, Appli	795	4	5.0	19	2	US-09-962-756-1197	Sequence 1197, Ap
723	4	5.0	18	1	US-07-876-941A-29	Sequence 29, Appl	796	4	5.0	19	2	US-09-962-756-1552	Sequence 1552, Ap
724	4	5.0	18	1	US-08-031-538-37	Sequence 37, Appl	797	4	5.0	19	2	US-09-943-692-34	Sequence 34, Appl
725	4	5.0	18	2	US-08-940-095-196	Sequence 196, App	798	4	5.0	19	4	PCT-US96-11495-1	Sequence 1, Appli
726	4	5.0	18	2	US-08-807-992B-6	Sequence 6, Appli	799	4	5.0	19	4	PCT-US96-11495-21	Sequence 21, Appl
727	4	5.0	18	2	US-08-807-992B-15	Sequence 15, Appl	800	4	5.0	20	1	US-07-851-976B-2	Sequence 2, Appli
728	4	5.0	18	2	US-08-807-992B-19	Sequence 19, Appl	801	4	5.0	20	1	US-08-082-844-1	Sequence 1, Appli
729	4	5.0	18	2	US-08-807-992B-26	Sequence 26, Appl	802	4	5.0	20	1	US-07-864-475A-5	Sequence 5, Appli
730	4	5.0	18	2	US-08-940-093-196	Sequence 196, App	803	4	5.0	20	1	US-08-442-884-4	Sequence 4, Appli
731	4	5.0	18	2	US-08-940-096-196	Sequence 196, App	804	4	5.0	20	1	US-08-291-609-2	Sequence 2, Appli
732	4	5.0	18	2	US-09-109-957-10	Sequence 10, Appl	805	4	5.0	20	1	US-08-401-136-7	Sequence 7, Appli
733	4	5.0	18	2	US-07-861-458C-119	Sequence 119, App	806	4	5.0	20	1	US-08-416-950-7	Sequence 7, Appli
734	4	5.0	18	2	US-09-465-719-196	Sequence 196, App	807	4	5.0	20	1	US-08-464-235-18	Sequence 18, Appl
735	4	5.0	18	2	US-09-453-605-196	Sequence 196, App	808	4	5.0	20	1	US-08-480-190-190	Sequence 190, App
736	4	5.0	18	2	US-09-227-357-431	Sequence 431, App	809	4	5.0	20	1	US-08-468-279-35	Sequence 35, Appl
737	4	5.0	18	2	US-09-453-838-196	Sequence 196, App	810	4	5.0	20	1	US-08-564-972-16	Sequence 16, Appl
738	4	5.0	18	2	US-08-469-260A-571	Sequence 571, App	811	4	5.0	20	1	US-08-564-972-17	Sequence 17, Appl
739	4	5.0	18	2	US-09-140-749-60	Sequence 60, Appl	812	4	5.0	20	1	US-08-394-600B-19	Sequence 19, Appl
740	4	5.0	18	2	US-09-840-009-22	Sequence 22, Appl	813	4	5.0	20	1	US-08-657-884-2	Sequence 2, Appli
741	4	5.0	18	2	US-08-940-136-196	Sequence 196, App	814	4	5.0	20	1	US-08-714-677-17	Sequence 17, Appl
742	4	5.0	18	2	US-08-488-446-571	Sequence 571, App	815	4	5.0	20	1	US-08-393-540-17	Sequence 17, Appl
743	4	5.0	18	2	US-09-453-841-196	Sequence 196, App	816	4	5.0	20	1	US-08-714-537-17	Sequence 17, Appl
744	4	5.0	18	2	US-10-053-485-62	Sequence 62, Appl	817	4	5.0	20	1	US-08-637-759B-395	Sequence 395, App
745	4	5.0	18	2	US-08-467-344A-571	Sequence 571, App	818	4	5.0	20	1	US-08-637-759B-458	Sequence 458, App
746	4	5.0	18	2	US-08-442-001C-83	Sequence 83, Appl	819	4	5.0	20	1	US-08-488-379-190	Sequence 190, App
747	4	5.0	18	2	US-09-453-833-196	Sequence 196, App	820	4	5.0	20	1	US-08-468-249A-5	Sequence 5, Appli
748	4	5.0	18	2	US-10-009-999A-32	Sequence 32, Appl	821	4	5.0	20	1	US-08-469-830-7	Sequence 7, Appli
749	4	5.0	18	2	US-09-453-826-196	Sequence 196, App	822	4	5.0	20	1	US-08-385-540A-4	Sequence 4, Appli
750	4	5.0	18	2	US-09-453-840-196	Sequence 196, App	823	4	5.0	20	1	US-08-600-273A-4	Sequence 4, Appli
751	4	5.0	18	2	US-08-424-550B-571	Sequence 571, App	824	4	5.0	20	1	US-08-726-306A-31	Sequence 31, Appl
752	4	5.0	18	2	US-09-865-989-196	Sequence 196, App	825	4	5.0	20	2	US-08-850-554-2	Sequence 2, Appli
753	4	5.0	18	2	US-09-525-269A-10	Sequence 10, Appl	826	4	5.0	20	2	US-08-871-355A-395	Sequence 395, App
754	4	5.0	18	2	US-09-453-834-196	Sequence 196, App	827	4	5.0	20	2	US-08-871-355A-458	Sequence 458, App
755	4	5.0	18	2	US-10-079-478-32	Sequence 32, Appl	828	4	5.0	20	2	US-08-115-753-12	Sequence 12, Appl
756	4	5.0	18	2	US-10-079-478-33	Sequence 33, Appl	829	4	5.0	20	2	US-08-486-820-4	Sequence 4, Appli
757	4	5.0	18	2	US-09-763-397A-17	Sequence 17, Appl	830	4	5.0	20	2	US-08-908-643C-69	Sequence 69, Appl

831	4	5.0	20	2	US-08-612-973-89	Sequence 89, Appl	904	4	5.0	20	4	PCT-US94-07040-1	Sequence 1, Appl
832	4	5.0	20	2	US-08-612-973-90	Sequence 90, Appl	905	4	5.0	20	4	PCT-US95-02121-101	Sequence 101, Appl
833	4	5.0	20	2	US-08-861-338-4	Sequence 4, Appl	906	4	5.0	20	4	PCT-US95-02513-19	Sequence 19, Appl
834	4	5.0	20	2	US-08-505-250-16	Sequence 16, Appl	907	4	5.0	21	1	US-08-655-086-4	Sequence 4, Appl
835	4	5.0	20	2	US-09-007-905-59	Sequence 59, Appl	908	4	5.0	21	2	US-08-746-111-6	Sequence 6, Appl
836	4	5.0	20	2	US-09-007-905-64	Sequence 64, Appl	909	4	5.0	21	2	US-08-746-111-8	Sequence 8, Appl
837	4	5.0	20	2	US-09-220-733-4	Sequence 4, Appl	910	4	5.0	21	2	US-08-908-643C-67	Sequence 5, Appl
838	4	5.0	20	2	US-08-463-486-18	Sequence 18, Appl	911	4	5.0	21	2	US-09-313-183A-5	Sequence 5, Appl
839	4	5.0	20	2	US-09-158-980-2	Sequence 2, Appl	912	4	5.0	21	2	US-09-257-179-85	Sequence 85, Appl
840	4	5.0	20	2	US-08-927-597-89	Sequence 89, Appl	913	4	5.0	21	2	US-09-690-454-102	Sequence 102, Appl
841	4	5.0	20	2	US-08-327-597-90	Sequence 90, Appl	914	4	5.0	21	2	US-10-053-485-57	Sequence 57, Appl
842	4	5.0	20	2	US-08-464-496-11	Sequence 11, Appl	915	4	5.0	21	2	US-10-053-485-65	Sequence 65, Appl
843	4	5.0	20	2	US-08-505-250-16	Sequence 16, Appl	916	4	5.0	21	2	US-09-270-767-40466	Sequence 40466, A
844	4	5.0	20	2	US-09-055-075C-8	Sequence 8, Appl	917	4	5.0	21	2	US-09-270-767-55682	Sequence 55682, A
845	4	5.0	20	2	US-09-201-945-395	Sequence 395, Appl	918	4	5.0	21	2	US-09-493-795B-175	Sequence 175, Appl
846	4	5.0	20	2	US-09-201-945-458	Sequence 458, Appl	919	4	5.0	21	2	US-09-493-795B-179	Sequence 179, Appl
847	4	5.0	20	2	US-08-271-539-8	Sequence 8, Appl	920	4	5.0	21	2	US-09-266-543-5	Sequence 5, Appl
848	4	5.0	20	2	US-08-197-484-101	Sequence 101, Appl	921	4	5.0	21	2	US-09-756-247-13	Sequence 13, Appl
849	4	5.0	20	2	US-09-232-074-59	Sequence 59, Appl	922	4	5.0	21	2	US-09-756-247-34	Sequence 34, Appl
850	4	5.0	20	2	US-09-232-074-64	Sequence 64, Appl	923	4	5.0	21	2	US-09-774-639-286	Sequence 286, Appl
851	4	5.0	20	2	US-08-475-399A-190	Sequence 190, Appl	924	4	5.0	21	2	US-10-020-674-4	Sequence 4, Appl
852	4	5.0	20	2	US-08-635-886C-45	Sequence 45, Appl	925	4	5.0	21	2	US-08-167-608-4	Sequence 4, Appl
853	4	5.0	20	2	US-08-635-886C-134	Sequence 134, Appl	926	4	5.0	21	2	US-09-962-756-541	Sequence 541, Appl
854	4	5.0	20	2	US-09-919-124-8	Sequence 8, Appl	927	4	5.0	21	2	US-09-962-756-1739	Sequence 1739, Ap
855	4	5.0	20	2	US-08-395-456C-19	Sequence 19, Appl	928	4	5.0	21	2	US-09-962-756-1744	Sequence 1744, Ap
856	4	5.0	20	2	US-08-487-453A-19	Sequence 19, Appl	929	4	5.0	21	2	US-10-153-469A-4	Sequence 4, Appl
857	4	5.0	20	2	US-08-591-502B-7	Sequence 7, Appl	930	4	5.0	21	2	US-10-104-889-4	Sequence 4, Appl
858	4	5.0	20	2	US-08-974-690C-45	Sequence 45, Appl	931	4	5.0	21	4	PCT-US94-02191-4	Sequence 4, Appl
859	4	5.0	20	2	US-08-974-690C-134	Sequence 134, Appl	932	4	5.0	22	1	US-07-978-892A-3	Sequence 3, Appl
860	4	5.0	20	2	US-09-811-492-2	Sequence 2, Appl	933	4	5.0	22	1	US-08-392-646-19	Sequence 19, Appl
861	4	5.0	20	2	US-08-974-685-45	Sequence 45, Appl	934	4	5.0	22	1	US-08-471-780C-75	Sequence 75, Appl
862	4	5.0	20	2	US-08-974-685-134	Sequence 134, Appl	935	4	5.0	22	1	US-08-543-363-32	Sequence 32, Appl
863	4	5.0	20	2	US-08-077-255A-190	Sequence 190, Appl	936	4	5.0	22	1	US-08-467-282B-75	Sequence 75, Appl
864	4	5.0	20	2	US-09-443-780C-2	Sequence 2, Appl	937	4	5.0	22	1	US-08-471-282A-75	Sequence 75, Appl
865	4	5.0	20	2	US-09-443-780C-6	Sequence 6, Appl	938	4	5.0	22	1	US-08-466-710C-75	Sequence 75, Appl
866	4	5.0	20	2	US-10-038-613-151	Sequence 151, Appl	939	4	5.0	22	2	US-08-940-095-189	Sequence 189, Appl
867	4	5.0	20	2	US-09-724-961-56	Sequence 56, Appl	940	4	5.0	22	2	US-08-468-739C-75	Sequence 75, Appl
868	4	5.0	20	2	US-09-724-961-59	Sequence 59, Appl	941	4	5.0	22	2	US-08-940-096-189	Sequence 189, Appl
869	4	5.0	20	2	US-09-580-018-56	Sequence 56, Appl	942	4	5.0	22	2	US-08-940-096-189	Sequence 189, Appl
870	4	5.0	20	2	US-09-580-018-59	Sequence 59, Appl	943	4	5.0	22	2	US-09-100-089-32	Sequence 32, Appl
871	4	5.0	20	2	US-09-724-551-56	Sequence 56, Appl	944	4	5.0	22	2	US-08-986-837-9	Sequence 9, Appl
872	4	5.0	20	2	US-09-724-551-59	Sequence 59, Appl	945	4	5.0	22	2	US-08-975-040-20	Sequence 20, Appl
873	4	5.0	20	2	US-09-493-795B-193	Sequence 193, Appl	946	4	5.0	22	2	US-09-465-719-189	Sequence 189, Appl
874	4	5.0	20	2	US-09-266-543-4	Sequence 4, Appl	947	4	5.0	22	2	US-08-690-775-2	Sequence 2, Appl
875	4	5.0	20	2	US-09-736-076-4	Sequence 76, Appl	948	4	5.0	22	2	US-09-101-927-18	Sequence 18, Appl
876	4	5.0	20	2	US-09-736-076-4	Sequence 4, Appl	949	4	5.0	22	2	US-09-101-927-20	Sequence 20, Appl
877	4	5.0	20	2	US-09-171-432A-59	Sequence 59, Appl	950	4	5.0	22	2	US-09-453-605-189	Sequence 189, Appl
878	4	5.0	20	2	US-09-171-432A-60	Sequence 60, Appl	951	4	5.0	22	2	US-09-453-838-189	Sequence 189, Appl
879	4	5.0	20	2	US-09-719-646-7	Sequence 7, Appl	952	4	5.0	22	2	US-09-670-827-32	Sequence 32, Appl
880	4	5.0	20	2	US-09-644-022A-3	Sequence 3, Appl	953	4	5.0	22	2	US-08-940-136-189	Sequence 189, Appl
881	4	5.0	20	2	US-09-724-953-14	Sequence 14, Appl	954	4	5.0	22	2	US-09-692-170C-17	Sequence 17, Appl
882	4	5.0	20	2	US-09-724-953-17	Sequence 17, Appl	955	4	5.0	22	2	US-09-692-170C-18	Sequence 18, Appl
883	4	5.0	20	2	US-09-962-756-1129	Sequence 1129, Ap	956	4	5.0	22	2	US-09-692-170C-20	Sequence 20, Appl
884	4	5.0	20	2	US-09-962-756-1137	Sequence 1137, Ap	957	4	5.0	22	2	US-09-692-170C-21	Sequence 21, Appl
885	4	5.0	20	2	US-09-962-756-1141	Sequence 1141, Ap	958	4	5.0	22	2	US-09-692-170C-22	Sequence 22, Appl
886	4	5.0	20	2	US-09-724-567-14	Sequence 14, Appl	959	4	5.0	22	2	US-09-692-170C-23	Sequence 23, Appl
887	4	5.0	20	2	US-09-724-567-17	Sequence 17, Appl	960	4	5.0	22	2	US-09-692-170C-24	Sequence 24, Appl
888	4	5.0	20	2	US-08-928-757-89	Sequence 89, Appl	961	4	5.0	22	2	US-09-453-841-189	Sequence 189, Appl
889	4	5.0	20	2	US-08-928-757-90	Sequence 90, Appl	962	4	5.0	22	2	US-09-809-592-9	Sequence 9, Appl
890	4	5.0	20	2	US-09-724-940-56	Sequence 56, Appl	963	4	5.0	22	2	US-09-453-833-189	Sequence 189, Appl
891	4	5.0	20	2	US-09-724-940-59	Sequence 59, Appl	964	4	5.0	22	2	US-09-453-826-189	Sequence 189, Appl
892	4	5.0	20	2	US-09-979-952-14	Sequence 14, Appl	965	4	5.0	22	2	US-09-405-986A-24	Sequence 24, Appl
893	4	5.0	20	2	US-09-979-952-17	Sequence 17, Appl	966	4	5.0	22	2	US-09-827-949-32	Sequence 32, Appl
894	4	5.0	20	2	US-09-863-054-18	Sequence 18, Appl	967	4	5.0	22	2	US-09-270-767-56923	Sequence 56923, A
895	4	5.0	20	2	US-09-585-817-14	Sequence 14, Appl	968	4	5.0	22	2	US-09-453-840-189	Sequence 189, Appl
896	4	5.0	20	2	US-09-585-817-17	Sequence 17, Appl	969	4	5.0	22	2	US-10-405-231A-17	Sequence 17, Appl
897	4	5.0	20	2	US-10-076-622-614	Sequence 614, Appl	970	4	5.0	22	2	US-10-405-231A-18	Sequence 18, Appl
898	4	5.0	20	2	US-10-007-700-400	Sequence 400, Appl	971	4	5.0	22	2	US-10-405-231A-20	Sequence 20, Appl
899	4	5.0	20	2	US-10-007-700-401	Sequence 401, Appl	972	4	5.0	22	2	US-10-405-231A-21	Sequence 21, Appl
900	4	5.0	20	2	US-10-007-700-457	Sequence 457, Appl	973	4	5.0	22	2	US-10-405-231A-22	Sequence 22, Appl
901	4	5.0	20	4	PCT-US92-07218-11	Sequence 11, Appl	974	4	5.0	22	2	US-10-405-231A-23	Sequence 23, Appl
902	4	5.0	20	4	PCT-US93-07545-190	Sequence 190, Appl	975	4	5.0	22	2	US-10-405-231A-24	Sequence 24, Appl
903	4	5.0	20	4	PCT-US94-02195-18	Sequence 18, Appl	976	4	5.0	22	2	US-10-238-607-17	Sequence 17, Appl

977 4 5.0 22 2 US-10-238-607-18 Sequence 18, Appl  
978 4 5.0 22 2 US-10-238-607-20 Sequence 20, Appl  
979 4 5.0 22 2 US-10-238-607-21 Sequence 21, Appl  
980 4 5.0 22 2 US-10-238-607-22 Sequence 22, Appl  
981 4 5.0 22 2 US-10-238-607-23 Sequence 23, Appl  
982 4 5.0 22 2 US-10-238-607-24 Sequence 24, Appl  
983 4 5.0 22 2 US-09-984-365-17 Sequence 17, Appl  
984 4 5.0 22 2 US-09-984-365-18 Sequence 18, Appl  
985 4 5.0 22 2 US-09-984-365-20 Sequence 20, Appl  
986 4 5.0 22 2 US-09-984-365-21 Sequence 21, Appl  
987 4 5.0 22 2 US-09-984-365-22 Sequence 22, Appl  
988 4 5.0 22 2 US-09-984-365-23 Sequence 23, Appl  
989 4 5.0 22 2 US-09-984-365-24 Sequence 24, Appl  
990 4 5.0 22 2 US-09-865-989-189 Sequence 189, App  
991 4 5.0 22 2 US-09-453-834-189 Sequence 189, App  
992 4 5.0 22 2 US-09-293-769A-75 Sequence 75, Appl  
993 4 5.0 22 2 US-09-093-450-2 Sequence 2, Appl  
994 4 5.0 22 2 US-10-697-055-17 Sequence 17, Appl  
995 4 5.0 22 2 US-10-697-055-18 Sequence 18, Appl  
996 4 5.0 22 2 US-10-697-055-20 Sequence 20, Appl  
997 4 5.0 22 2 US-10-697-055-21 Sequence 21, Appl  
998 4 5.0 22 2 US-10-697-055-22 Sequence 22, Appl  
999 4 5.0 22 2 US-10-697-055-23 Sequence 23, Appl  
1000 4 5.0 22 2 US-10-697-055-24 Sequence 24, Appl

## ALIGNMENTS

RESULT 1  
US-08-630-172-8  
; Sequence 8, Application US/08630172  
; Patent No. 6060054  
; GENERAL INFORMATION:  
; APPLICANT: Staerz, Uwe  
; TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T  
; TITLE OF INVENTION: LYMPHOCYTE VETO  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sheridan Ross & McIntosh  
; STREET: 1700 Lincoln Street, 35th Floor  
; CITY: Denver  
; STATE: Colorado  
; COUNTRY: U.S.  
; ZIP: 80203  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/630,172  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Connell, Gary J.  
; REGISTRATION NUMBER: 32,020  
; REFERENCE/DOCKET NUMBER: 2879-36  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (303) 863-9700  
; TELEFAX: (303) 863-0223  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 79 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-630-172-8

Query Match 58.8%; Score 47; DB 2; Length 79;  
Best Local Similarity 100.0%; Pred. No. 1.9e-43;  
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKDEVKEVQBFYKDTYNKLTKDPEQRETLLKAIHYALNCCGLAGV 47  
Db 1 HKDEVKEVQBFYKDTYNKLTKDPEQRETLLKAIHYALNCCGLAGV 47

## RESULT 2

US-09-375-419-8  
; Sequence 8, Application US/09375419  
; Patent No. 6264950  
; GENERAL INFORMATION:  
; APPLICANT: Staerz, Uwe  
; TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T  
; TITLE OF INVENTION: LYMPHOCYTE VETO  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sheridan Ross & McIntosh  
; STREET: 1700 Lincoln Street, 35th Floor  
; CITY: Denver  
; STATE: Colorado  
; COUNTRY: U.S.  
; ZIP: 80203  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/375,419  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/630,172  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Connell, Gary J.  
; REGISTRATION NUMBER: 32,020  
; REFERENCE/DOCKET NUMBER: 2879-36  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (303) 863-9700  
; TELEFAX: (303) 863-0223  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 79 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-375-419-8

Query Match 58.8%; Score 47; DB 2; Length 79;  
Best Local Similarity 100.0%; Pred. No. 1.9e-43;  
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKDEVKEVQBFYKDTYNKLTKDPEQRETLLKAIHYALNCCGLAGV 47  
Db 1 HKDEVKEVQBFYKDTYNKLTKDPEQRETLLKAIHYALNCCGLAGV 47

## RESULT 3

US-08-254-493-4  
; Sequence 4, Application US/08254493  
; Patent No. 5439886  
; GENERAL INFORMATION:  
; APPLICANT: IKEYAMA, SHUICHI  
; APPLICANT: KOYAMA, MASARU  
; APPLICANT: MIYAKE, MASAYUKI  
; APPLICANT: SENO, MASAHARU  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND  
; TITLE OF INVENTION: PRODUCTION THEREOF  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
; STREET: 130 WATER STREET  
; CITY: BOSTON

Query Match 58.8%; Score 47; DB 2; Length 79;  
Best Local Similarity 100.0%; Pred. No. 1.9e-43;  
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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STATE: MASSACHUSETTS
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/254,493
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/865552
FILING DATE: 09-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 079996-1991
FILING DATE: 12-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 085396-1991
FILING DATE: 17-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 022321-1992
FILING DATE: 07-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 41777
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-254-493-4

Query Match 37.5%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.1e-25;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KDEVIKEVQEFYKDTYNNKLTKEDEPQRETL 31
Db 1 KDEVIKEVQEFYKDTYNNKLTKEDEPQRETL 30

RESULT 4
US-08-408-222B-4
; Sequence 4, Application US/08/08222B
; Patent No. 5776727
; GENERAL INFORMATION:
; APPLICANT: Ikeyama, Shuichi
; APPLICANT: Koyama, Masaru
; APPLICANT: Miyake, Masayuki
; APPLICANT: Senoo, Masaharu
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dike, Bronstein, Roberts & Cushman
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fast-SEQ Version 1.5
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STATE: MASSACHUSETTS
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/254,493
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/865552
FILING DATE: 09-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 079996-1991
FILING DATE: 12-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 085396-1991
FILING DATE: 17-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 022321-1992
FILING DATE: 07-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 41777-DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-408-222B-4

Query Match 37.5%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.1e-25;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KDEVIKEVQEFYKDTYNNKLTKEDEPQRETL 31
Db 1 KDEVIKEVQEFYKDTYNNKLTKEDEPQRETL 30

RESULT 5
US-08-254-493-5
; Sequence 5, Application US/08254493
; Patent No. 5439886
; GENERAL INFORMATION:
; APPLICANT: IKEYAMA, SHUICHI
; APPLICANT: KOYAMA, MASARU
; APPLICANT: MIYAKE, MASAYUKI
; APPLICANT: SENOO, MASAHARU
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/254,493
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/865552
; FILING DATE: 09-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 079996-1991
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;  
; FILING DATE: 12-APR-1991  
; PRIOR APPLICATION DATA: JP 085396-1991  
; FILING DATE: 17-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 022321-1992  
; FILING DATE: 07-FEB-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: RESNICK, DAVID S.  
; REGISTRATION NUMBER: 34235  
; REFERENCE/DOCKET NUMBER: 41777  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 523-3400  
; TELEFAX: (617) 523-6440  
; TELEX: 200291 STRE UR  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 29 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-254-493-5

Query Match 36.2%; Score 29; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 2.5e-24;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 27 QRETLKAIHYALNCCGLAGGVEQFISDIC 55  
Db 1 QRETLKAIHYALNCCGLAGGVEQFISDIC 29

RESULT 6  
US-08-254-493-6  
; Sequence 6, Application US/08254493  
; Patent No. 5439886  
; GENERAL INFORMATION:  
; APPLICANT: IKEYAMA, SHUICHI  
; APPLICANT: KOYAMA, MASARU  
; APPLICANT: MIYAKE, MASAYUKI  
; APPLICANT: SENOO, MASAHARU  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND  
; PRODUCTION THEREOF  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
; STREET: 130 WATER STREET  
; CITY: BOSTON  
; STATE: MASSACHUSETTS  
; COUNTRY: US  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/254,493  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/865552  
; FILING DATE: 09-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 079996-1991  
; FILING DATE: 12-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 085396-1991  
; FILING DATE: 17-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 022321-1992  
; FILING DATE: 07-FEB-1992

;  
; ATTORNEY/AGENT INFORMATION:  
; NAME: RESNICK, DAVID S.  
; REGISTRATION NUMBER: 34235  
; REFERENCE/DOCKET NUMBER: 41777  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 523-3400  
; TELEFAX: (617) 523-6440  
; TELEX: 200291 STRE UR  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 29 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-254-493-6  
Query Match 36.2%; Score 29; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 2.5e-24;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 52 SDICPKDVLFTFTVKSCPDAIKEVFDNK 80  
Db 1 SDICPKDVLFTFTVKSCPDAIKEVFDNK 29  
RESULT 7  
US-08-408-222B-5  
; Sequence 5, Application US/08408222B  
; Patent No. 5776727  
; GENERAL INFORMATION:  
; APPLICANT: Ikeyama, Shuichi  
; APPLICANT: Koyama, Masaru  
; APPLICANT: Miyake, Masauyuki  
; APPLICANT: Senoo, Masaharu  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DIKE, Bronstein, Roberts & Cushman  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/408,222B  
; FILING DATE: 22-MAR-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/254,493  
; FILING DATE: 06-JUN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP-079996-1991  
; FILING DATE: 12-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP-085396-1991  
; FILING DATE: 14-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP-022321-1992  
; FILING DATE: 07-FEB-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Resnick, David S.  
; REGISTRATION NUMBER: 34,235  
; REFERENCE/DOCKET NUMBER: 41777-DIV  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-523-3400  
; TELEFAX: 617-523-6440  
; INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:  
LENGTH: 29 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-408-222B-5

Query Match 36.2%; Score 29; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 2.5e-24;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 QRETLKAIHYALNCCGLAGVQFISDIC 55  
Db 1 QRETLKAIHYALNCCGLAGVQFISDIC 29

RESULT 8  
US-08-408-222B-6  
; Sequence 6, Application US/08408222B  
; Patent No. 5776727  
; GENERAL INFORMATION:  
; APPLICANT: Ikeyama, Shuichi  
; APPLICANT: Koyama, Masaru  
; APPLICANT: Miyake, Masayuki  
; APPLICANT: Senoo, Masaharu  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dike, Bronstein, Roberts & Cushman  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/408,222B  
FILING DATE: 22-MAR-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/254,493  
FILING DATE: 06-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP-079996-1991  
FILING DATE: 12-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP-085396-1991  
FILING DATE: 14-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP-022321-1992  
FILING DATE: 07-FEB-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Resnick, David S.  
REGISTRATION NUMBER: 34,235  
REFERENCE/DOCKET NUMBER: 41777-DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-408-222B-6

Query Match 36.2%; Score 29; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 2.5e-24;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 SDICPKQVLETFIVKSCPDALKEVFDNK 80  
Db 1 SDICPKQVLETFIVKSCPDALKEVFDNK 29

RESULT 9  
US-09-621-976-5649  
; Sequence 5649, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 5649  
; LENGTH: 62  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: -24..-1  
; NAME/KEY: UNSURE  
; LOCATION: -3  
; OTHER INFORMATION: Xaa = Ser,Thr  
US-09-621-976-5649

Query Match 7.5%; Score 6; DB 2; Length 62;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 LAGGVE 48  
Db 15 LAGGVE 20

RESULT 10  
US-09-489-039A-12814  
; Sequence 12814, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 12814  
; LENGTH: 75  
; TYPE: PRT  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-12814

Query Match 7.5%; Score 6; DB 2; Length 75;  
Best Local Similarity 100.0%; Pred. No. 55;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY .66 VKSCPD 71  
Db 6 VKSCPD 11

RESULT 11  
US-09-107-532A-4420  
; Sequence 4420, Application US/09107532A

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; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
;
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
;
; INFORMATION FOR SEQ ID NO: 4420:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 76 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...76
; SEQUENCE DESCRIPTION: SEQ ID NO: 4420:
US-09-107-532A-4420

Query Match 7.5%; Score 6; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 YNKLKT 22
Db 4 YNKLKT 9

RESULT 12
US-09-136-251-9
; Sequence 9, Application US/09136251A
; Patent No. 6127156
; GENERAL INFORMATION:
; APPLICANT: HOSHINO, Tatsuo
; APPLICANT: MIYAZAKI, Taro
; APPLICANT: OJIMA, Setsuko
; APPLICANT: SHINJOH, Masako
; APPLICANT: TOMIYAMA, No. 6127156ibumi
; TITLE OF INVENTION: D-SORBITOL DEHYDROGENASE GENE
; FILE REFERENCE: D-Sorbitol Dehydrogenase Gene
; CURRENT APPLICATION NUMBER: US/09/136,251A
; CURRENT FILING DATE: 1998-08-19
; EARLIER APPLICATION NUMBER: EP 97114432.4
; EARLIER FILING DATE: 1997-08-21

; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
;
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
;
; INFORMATION FOR SEQ ID NO: 4420:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 76 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEtical: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...76
; SEQUENCE DESCRIPTION: SEQ ID NO: 4420:
US-09-107-532A-4420

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Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 PDAIK 74
Db 1 PDAIK 5

RESULT 13
US-09-634-496-9
; Sequence 9, Application US/09634496
; Patent No. 644449
; GENERAL INFORMATION:
; APPLICANT: HOSHINO, Tatsuo
; APPLICANT: MIYAZAKI, Taro
; APPLICANT: OJIMA, Setsuko
; APPLICANT: SHINJOH, Masako
; APPLICANT: TOMIYAMA, No. 644449ibumi
; TITLE OF INVENTION: D-SORBITOL DEHYDROGENASE GENE
; FILE REFERENCE: D-Sorbitol Dehydrogenase Gene
; CURRENT APPLICATION NUMBER: US/09/634,496
; CURRENT FILING DATE: 2000-08-08
; EARLIER APPLICATION NUMBER: US/09/136,251
; EARLIER FILING DATE: 1998-08-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Gluconobacter suboxydans
US-09-634-496-9

Query Match 6.2%; Score 5; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 PDAIK 74
Db 1 PDAIK 5

RESULT 14
US-09-635-145A-9
; Sequence 9, Application US/09635145A
; Patent No. 6653115
; GENERAL INFORMATION:
; APPLICANT: HOSHINO, Tatsuo
; APPLICANT: MIYAZAKI, Taro
; APPLICANT: OJIMA, Setsuko
; APPLICANT: SHINJOH, Masako
; APPLICANT: TOMIYAMA, No. 6653115ibumi
; TITLE OF INVENTION: D-SORBITOL DEHYDROGENASE GENE
; FILE REFERENCE: C38435/118291
; CURRENT APPLICATION NUMBER: US/09/635,145A
; CURRENT FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: EP 97114432.4
; PRIOR FILING DATE: 1997-08-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Gluconobacter suboxydans
US-09-635-145A-9
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Query Match 6.2%; Score 5; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 PDAIK 74  
Db 1 PDAIK 5

## RESULT 15

US-09-200-757-1  
; Sequence 1, Application US/09200757  
; Patent No. 6277958  
; GENERAL INFORMATION:  
; APPLICANT: Aimoto, Saburho  
; TITLE OF INVENTION: METHOD FOR PREPARING PEPTIDE THIOL ESTER  
; FILE REFERENCE: 31763-138092  
; CURRENT APPLICATION NUMBER: US/09/200,757  
; CURRENT FILING DATE: 1998-11-27  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)  
; OTHER INFORMATION: Asp (OBut)  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (2)  
; OTHER INFORMATION: Thr (But)  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (4)  
; OTHER INFORMATION: Thr (But)  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (6)  
; OTHER INFORMATION: Lys (Boc)  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (8)  
; OTHER INFORMATION: Gly (S-CH2CH2-CO)  
; FEATURE:  
; OTHER INFORMATION: this peptide has an amidated C-terminus  
US-09-200-757-1

Query Match 6.2%; Score 5; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 TPTVK 67  
Db 2 TPTVK 6

Search completed: January 20, 2006, 17:51:31  
Job time : 31 secs

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OM protein - protein search, using sw model

Run on: January 20, 2006, 17:45:33 ; Search time 16 Seconds  
(without alignments)  
481.084 Million cell updates/sec

Title: US-10-619-323-1\_COPY\_113\_192

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Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 26016

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Listing first 1000 summaries

Database :

PIR 80:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	7.5	15	S03353	plastocyanin - Mic
2	6	7.5	57	H35057	MHC class II histo
3	6	7.5	60	H82927	hypothetical prote
4	6	7.5	66	PQ0469	cysteine proteinas
5	6	7.5	68	D64538	hypothetical prote
6	5	6.2	33	S42781	relaxin - oranguta
7	5	6.2	39	A61232	pregnancy-associat
8	5	6.2	39	S23804	homeotic protein I
9	5	6.2	39	S23803	homeotic protein I
10	5	6.2	39	C37264	E2 glycoprotein -
11	5	6.2	40	H81591	hypothetical prote
12	5	6.2	41	PQ0560	nonstructural prot
13	5	6.2	41	PQ0563	nonstructural prot
14	5	6.2	41	PQ0564	nonstructural prot
15	5	6.2	41	PQ0562	nonstructural prot
16	5	6.2	41	PQ0565	nonstructural prot
17	5	6.2	46	C83437	hypothetical prote
18	5	6.2	49	T37008	hypothetical prote
19	5	6.2	55	B46485	Ig epsilon chain C
20	5	6.2	56	B89903	hypothetical prote
21	5	6.2	57	C35057	MHC class II histo
22	5	6.2	57	C35058	MHC class II histo
23	5	6.2	58	B43928	probable collagen
24	5	6.2	59	RSBP15	integrase - Staphy
25	5	6.2	60	T34737	probable gas vesic
26	5	6.2	61	D97920	hypothetical prote
27	5	6.2	63	H64095	carbon storage reg
28	5	6.2	63	FECLC	ferredoxin [4Fe-4S
29	5	6.2	63	C59147	conotoxin Gms.1 pr

30	5	6.2	64	2	H91000	hypothetical prote
31	5	6.2	64	2	B90779	hypothetical prote
32	5	6.2	65	2	A22810	small acid-soluble
33	5	6.2	66	2	B87379	ribosomal protein
34	5	6.2	66	2	S14932	homeotic protein H
35	5	6.2	67	2	B71666	ribosomal protein
36	5	6.2	68	1	IABY3	proteinase A inhib
37	5	6.2	68	1	QOHSNB	hypothetical prote
38	5	6.2	68	2	B84267	hypothetical prote
39	5	6.2	68	2	C71970	hypothetical prote
40	5	6.2	69	2	S14074	hypothetical prote
41	5	6.2	69	2	T48461	hypothetical prote
42	5	6.2	70	2	S34217	hypothetical prote
43	5	6.2	71	2	T03353	acclimation protei
44	5	6.2	71	2	D82686	gene e14 protein -
45	5	6.2	73	2	G89307	hypothetical prote
46	5	6.2	75	1	BVECRY	protein T01C3.2 [i
47	5	6.2	75	2	A13305	hypothetical prote
48	5	6.2	76	2	S65527	H+-exporting ATPas
49	5	6.2	76	2	B69472	conserved hypothet
50	5	6.2	76	2	S69162	serine proteinase
51	5	6.2	76	2	S69163	serine proteinase
52	5	6.2	77	2	H96955	hypothetical prote
53	5	6.2	78	2	B86580	CT659 hypothetical
54	5	6.2	78	2	H72043	conserved hypothet
55	5	6.2	78	2	B75193	hypothetical prote
56	5	6.2	78	2	JC7625	proteinase A inhib
57	5	6.2	79	2	AB1238	B. subtilis ynfef p
58	5	6.2	79	2	AG1600	B. subtilis ynfef p
59	5	6.2	79	2	F72354	hypothetical prote
60	5	6.2	79	2	B69874	hypothetical prote
61	5	6.2	79	2	T02461	hypothetical prote
62	5	6.2	79	2	T04983	hypothetical prote
63	5	6.2	80	2	F75598	hypothetical prote
64	4	5.0	9	2	S02617	alcohol dehydrogen
65	4	5.0	9	2	S66636	alpha-2-macroglobu
66	4	5.0	10	2	E49033	T-cell receptor ga
67	4	5.0	10	2	P70213	T-cell receptor al
68	4	5.0	10	2	A61354	T-cell receptor al
69	4	5.0	11	2	S23364	carnitine medium/1
70	4	5.0	12	2	S65626	T-cell receptor al
71	4	5.0	13	2	PC1149	phosphorylase b -
72	4	5.0	14	1	QMVHMM	equinotoxin 1A - s
73	4	5.0	14	2	JN0389	mastoparan M - hor
74	4	5.0	14	2	I56388	histamine-releasein
75	4	5.0	15	2	I52734	Km(r) protein - Es
76	4	5.0	15	2	I29501	gene c-Ki-ras prot
77	4	5.0	16	2	PH1770	fibrinopeptide A -
78	4	5.0	16	2	S51733	T-cell receptor al
79	4	5.0	16	2	PH0791	T-cell receptor al
80	4	5.0	16	2	A42291	T-cell receptor al
81	4	5.0	17	2	PH1789	T-cell receptor al
82	4	5.0	18	2	I73024	T-cell receptor be
83	4	5.0	18	2	A32220	T-cell receptor de
84	4	5.0	18	2	S21669	1H-4-oxoquinoline
85	4	5.0	18	2	B48408	21K high mobility
86	4	5.0	18	2	PH1794	T-cell receptor al
87	4	5.0	18	2	B32220	T-cell receptor de
88	4	5.0	18	2	S27141	hypothetical prote
89	4	5.0	19	2	S38895	KmR protein - Yeas
90	4	5.0	19	2	PH0793	T-cell receptor al
91	4	5.0	19	2	A48408	21K high mobility
92	4	5.0	20	2	B38875	creatine kinase (E
93	4	5.0	20	2	A56900	chymotrypsin I (EC
94	4	5.0	20	2	S71601	recombination prot
95	4	5.0	20	2	A20569	C-reactive protein
96	4	5.0	20	2	F56046	urinary tract ston
97	4	5.0	20	2	A35646	mast cell proteina
98	4	5.0	21	2	D42762	proteasome endopep
99	4	5.0	21	2	A21590	hyaluronidase (EC 3
100	4	5.0	21	2	B33600	glutamate-ammonia
101	4	5.0	22	2	PH1325	Ig heavy chain DJ
102	4	5.0	23	2	C27262	nicotinic acetylch

103	4	5.0	25	2	PC4445	L-ascorbate peroxi	176	4	5.0	40	2	S58853	homeotic protein u
104	4	5.0	26	1	S7EPT4	stp protein - phag	177	4	5.0	41	2	P05611	nonstructural prot
105	4	5.0	26	2	S04376	hypothetical prote	178	4	5.0	41	2	G72312	hypothetical prote
106	4	5.0	26	2	S55799	stp protein - phag	179	4	5.0	41	2	D82130	hypothetical prote
107	4	5.0	26	2	S55798	stp protein - phag	180	4	5.0	41	2	A97948	hypothetical prote
108	4	5.0	26	2	S55797	stp protein - phag	181	4	5.0	41	2	B47752	RNA recognition mo
109	4	5.0	26	2	S55800	stp protein (varia	182	4	5.0	41	2	G1BO	gastric inhibitory
110	4	5.0	26	2	H44589	hypothetical prote	183	4	5.0	42	1	G1PG	gastric inhibitory
111	4	5.0	26	2	S00579	hypothetical prote	184	4	5.0	42	1	G56271	ipfA 5'-region hyp
112	4	5.0	27	2	I40764	hypothetical prote	185	4	5.0	42	2	T07320	hypothetical prote
113	4	5.0	27	2	PC4234	hypothetical prote	186	4	5.0	42	2	T07324	hypothetical prote
114	4	5.0	28	2	A49829	T-cell receptor va	187	4	5.0	42	2	D81730	hypothetical prote
115	4	5.0	28	2	A41476	probable antigen 1	188	4	5.0	42	2	B82657	hypothetical prote
116	4	5.0	29	2	S05032	photosystem II pro	189	4	5.0	43	2	S43195	methionyl aminopep
117	4	5.0	29	2	I49732	NADH2 dehydrogenas	190	4	5.0	43	2	S68006	araalkylamine N-ace
118	4	5.0	30	2	P00723	parvalbumin (limpor	191	4	5.0	43	2	PD0025	28k surface antige
119	4	5.0	30	2	A53415	lectin chain A - I	192	4	5.0	44	2	B38075	N-acetylglactosam
120	4	5.0	30	2	G81031	hypothetical prote	193	4	5.0	44	2	A95166	hypothetical prote
121	4	5.0	30	2	A22498	2-enoate reductase	194	4	5.0	44	2	H90641	hypothetical prote
122	4	5.0	30	2	A34874	transforming prote	195	4	5.0	44	2	G84300	hypothetical prote
123	4	5.0	30	2	B81346	hypothetical prote	196	4	5.0	44	2	T07452	hypothetical prote
124	4	5.0	30	2	A27375	photosystem I iron	197	4	5.0	44	2	A82865	hypothetical prote
125	4	5.0	31	2	S61558	chymotrypsin Fml -	198	4	5.0	44	2	H85492	hypothetical prote
126	4	5.0	31	2	S18356	chymotrypsin (EC 3	199	4	5.0	44	2	D64732	hypothetical prote
127	4	5.0	31	2	A34448	myosin heavy chain	200	4	5.0	44	2	C34327	troponin T, fast 8
128	4	5.0	31	2	S14615	hypothetical prote	201	4	5.0	44	2	INBP10	hypothetical immun
129	4	5.0	31	2	H82241	hypothetical prote	202	4	5.0	45	2	B29548	mast cell proteina
130	4	5.0	32	2	S11610	ribosomal protein	203	4	5.0	45	2	H44530	T-cell receptor al
131	4	5.0	32	2	S01730	hexon protein - hu	204	4	5.0	45	2	S43149	Ig epsilon chain -
132	4	5.0	32	2	A50785	hypothetical prote	205	4	5.0	45	2	B45292	component for volt
133	4	5.0	32	2	D95225	hypothetical prote	206	4	5.0	45	2	S07932	hypothetical prote
134	4	5.0	32	2	C81569	hypothetical prote	207	4	5.0	45	2	F95184	hypothetical prote
135	4	5.0	32	2	S68901	xanthine dehydroge	208	4	5.0	45	2	B85921	hypothetical prote
136	4	5.0	32	2	A53505	pyruvate, phosphat	209	4	5.0	46	1	ACBP74	gene ac protein -
137	4	5.0	33	2	A60601	keratin, 55k, nucl	210	4	5.0	46	2	PT0034	baseplate protein
138	4	5.0	33	2	I46600	myosin - pig (frag	211	4	5.0	46	2	B82371	hypothetical prote
139	4	5.0	33	2	S52151	hypothetical prote	212	4	5.0	46	2	D82363	hypothetical prote
140	4	5.0	34	2	S67972	apolipoprotein AI	213	4	5.0	46	2	D82037	hypothetical prote
141	4	5.0	34	2	G95151	hypothetical prote	214	4	5.0	46	2	C69745	hypothetical prote
142	4	5.0	34	2	D70249	hypothetical prote	215	4	5.0	46	2	G53613	plectoxin IX - spi
143	4	5.0	34	2	S65371	tRNA-guanine trans	216	4	5.0	46	2	B81717	hypothetical prote
144	4	5.0	34	2	I49145	homeobox protein -	217	4	5.0	46	2	A41814	somatotropin recep
145	4	5.0	35	2	B42762	proteasome endopep	218	4	5.0	47	2	A18825	phospholipase A2 (
146	4	5.0	35	2	F87622	hypothetical prote	219	4	5.0	47	2	G13486	transferrin - bovi
147	4	5.0	35	2	B84674	hypothetical prote	220	4	5.0	47	2	G91196	hypothetical prote
148	4	5.0	35	2	C44918	lactococcin G pept	221	4	5.0	47	2	T37086	probable IS elemen
149	4	5.0	35	2	D69330	hypothetical prote	222	4	5.0	48	2	A38882	GRP-binding protei
150	4	5.0	35	2	F85847	unknown protein en	223	4	5.0	48	2	S20779	Ig heavy chain V r
151	4	5.0	35	2	A83041	conserved hypothet	224	4	5.0	48	2	S78287	ribosomal protein
152	4	5.0	36	2	A27682	39K whey protein -	225	4	5.0	48	2	S74261	troponin T3f, fast
153	4	5.0	36	2	S22222	probable lipid tra	226	4	5.0	48	2	T05927	heme A farnesyltra
154	4	5.0	36	2	A59064	egg-laying hormone	227	4	5.0	48	2	T01745	hypothetical prote
155	4	5.0	36	2	A58864	cereolysin O - Bac	228	4	5.0	48	2	T01702	hypothetical prote
156	4	5.0	36	2	S20679	Mx protein - pig (	229	4	5.0	48	2	T22176	hypothetical prote
157	4	5.0	36	2	S16552	hypothetical prote	230	4	5.0	48	2	D82817	hypothetical prote
158	4	5.0	36	2	T30064	hypothetical prote	231	4	5.0	49	2	D70228	hypothetical prote
159	4	5.0	37	2	S70801	probable membrane-	232	4	5.0	49	2	T42123	perD protein - bac
160	4	5.0	37	2	S06217	transforming prote	233	4	5.0	50	2	H90596	hypothetical prote
161	4	5.0	37	2	S17684	thaumatin homolog	234	4	5.0	50	2	S19624	ornatin E - leech
162	4	5.0	37	2	B95121	hypothetical prote	235	4	5.0	50	2	A82772	hypothetical prote
163	4	5.0	38	2	S21710	carbonyl reductase	236	4	5.0	50	2	B82702	hypothetical prote
164	4	5.0	38	2	I66797	troponin T 3f - ra	237	4	5.0	50	2	T50878	hypothetical solub
165	4	5.0	38	2	S71918	myo-inositol 1-pho	238	4	5.0	50	2	D90706	hypothetical prote
166	4	5.0	38	2	S33484	hypothetical prote	239	4	5.0	51	2	S36377	Ig heavy chain V r
167	4	5.0	38	2	B42799	photosystem I iron	240	4	5.0	51	2	I66796	fetal troponin T 3
168	4	5.0	39	2	A05331	colipase - spiny d	241	4	5.0	51	2	T07346	hypothetical prote
169	4	5.0	39	2	A11034	hypothetical prote	242	4	5.0	51	2	C71822	hypothetical prote
170	4	5.0	39	2	H95135	hypothetical prote	243	4	5.0	51	2	G69870	prolactin receptor
171	4	5.0	39	2	S63530	hypothetical prote	244	4	5.0	51	2	I56840	hypothetical prote
172	4	5.0	40	2	S33409	Ig heavy chain V r	245	4	5.0	51	2	F83800	hypothetical prote
173	4	5.0	40	2	C87675	hypothetical prote	246	4	5.0	51	2	AF1456	hypothetical prote
174	4	5.0	40	2	T07560	hypothetical prote	247	4	5.0	51	2	B98174	hypothetical prote
175	4	5.0	40	2	H71330	hypothetical prote	248	4	5.0	51	2	AD1839	hypothetical prote

249	4	5.0	52	2	S52963	probable H+-transp	322	4	5.0	57	2	D96953	hypothetical prote
250	4	5.0	52	2	H27578	T-cell receptor be	323	4	5.0	57	2	D97204	lactoylglutathione
251	4	5.0	52	2	S01945	myosin catalytic 1	324	4	5.0	57	2	C89981	hypothetical prote
252	4	5.0	52	2	T06503	hypothetical prote	325	4	5.0	57	2	AF1381	hypothetical prote
253	4	5.0	52	2	G87562	hypothetical prote	326	4	5.0	57	2	AG1750	hypothetical prote
254	4	5.0	52	2	D81214	hypothetical prote	327	4	5.0	57	2	A56665	solanidine UDP-glu
255	4	5.0	52	2	T32956	hypothetical prote	328	4	5.0	58	2	I53690	cytochrome P450 2B
256	4	5.0	52	2	T33694	hypothetical prote	329	4	5.0	58	2	E36491	phosphoprotein pho
257	4	5.0	52	2	S19623	ornatin C - leech	330	4	5.0	58	2	S46922	lysine-tRNA ligase
258	4	5.0	52	2	H97804	hypothetical prote	331	4	5.0	58	2	PQ0129	34.5K linker prote
259	4	5.0	52	2	A64727	yabQ protein - Esc	332	4	5.0	58	2	A64910	hypothetical prote
260	4	5.0	52	2	AS8935	nitrogenase (EC 1.	333	4	5.0	58	2	S58143	gene 14 protein -
261	4	5.0	53	1	F2BGR	photosystem II pro	334	4	5.0	58	2	G81896	hypothetical prote
262	4	5.0	53	2	S41957	naringenin-chalcon	335	4	5.0	58	2	F69163	hypothetical prote
263	4	5.0	53	2	S56727	calcium-dependent	336	4	5.0	58	2	S73287	hypothetical prote
264	4	5.0	53	2	S56726	calcium-dependent	337	4	5.0	58	2	S58756	hypothetical prote
265	4	5.0	53	2	AG0053	probable exported	338	4	5.0	58	2	B82565	hypothetical prote
266	4	5.0	53	2	F95066	hypothetical prote	339	4	5.0	58	2	T12949	hypothetical prote
267	4	5.0	53	2	D90189	protein translatio	340	4	5.0	58	2	B97333	hypothetical prote
268	4	5.0	53	2	D69103	hypothetical prote	341	4	5.0	58	2	AF0058	ferredoxin [import
269	4	5.0	53	2	H81673	conserved hypothet	342	4	5.0	58	2	AD2390	hypothetical prote
270	4	5.0	53	2	F97104	probable membrane	343	4	5.0	58	2	C56273	hypothetical prote
271	4	5.0	53	2	H98038	degenerate transpo	344	4	5.0	59	1	C56273	sakacin A precurs
272	4	5.0	54	2	S03468	T-cell receptor al	345	4	5.0	59	2	T07976	dihydrokaempferol
273	4	5.0	54	2	FU0022	beta-galactoside-b	346	4	5.0	59	2	A01117	anthranilate synth
274	4	5.0	54	2	S01993	gene 34 protein -	347	4	5.0	59	2	S74260	tropinin Tlf, fast
275	4	5.0	54	2	E95069	hypothetical prote	348	4	5.0	59	2	S11812	opacity protein (c
276	4	5.0	54	2	C90857	hypothetical prote	349	4	5.0	59	2	AF1072	hypothetical prote
277	4	5.0	54	2	T42306	hypothetical prote	350	4	5.0	59	2	F95204	conserved domain p
278	4	5.0	54	2	T42318	hypothetical prote	351	4	5.0	59	2	C72203	hypothetical prote
279	4	5.0	54	2	T45629	hypothetical prote	352	4	5.0	59	2	B70243	hypothetical prote
280	4	5.0	54	2	D82851	hypothetical prote	353	4	5.0	59	2	F70251	hypothetical prote
281	4	5.0	54	2	C97135	hypothetical prote	354	4	5.0	59	2	D81133	hypothetical prote
282	4	5.0	54	2	G85762	probable transposa	355	4	5.0	59	2	C64024	hypothetical prote
283	4	5.0	54	2	B56557	PfEMP2/MESA (clone	356	4	5.0	59	2	D69807	hypothetical prote
284	4	5.0	55	1	BGMS	spermatid transiti	357	4	5.0	59	2	D83672	hypothetical prote
285	4	5.0	55	1	BGRT	protein kinase AK1	358	4	5.0	59	2	B83830	hypothetical prote
286	4	5.0	55	2	S66331	ribosomal protein	359	4	5.0	59	2	G71340	hypothetical prote
287	4	5.0	55	2	E75314	DNA-dependent RNA	360	4	5.0	59	2	D82580	hypothetical prote
288	4	5.0	55	2	A69152	conserved hypothet	361	4	5.0	59	2	S56139	membrane protein n
289	4	5.0	55	2	AC0562	hypothetical prote	362	4	5.0	59	2	E97178	probable transcrip
290	4	5.0	55	2	D81987	hypothetical prote	363	4	5.0	59	2	G97790	lysosome homolog [
291	4	5.0	55	2	C69944	hypothetical prote	364	4	5.0	59	2	C36493	H+-transporting tw
292	4	5.0	55	2	T25692	hypothetical prote	365	4	5.0	59	2	A42461	hypothetical prote
293	4	5.0	55	2	G84007	hypothetical prote	366	4	5.0	60	1	T5EP2J	short toxin 2 homo
294	4	5.0	55	2	C82850	hypothetical prote	367	4	5.0	60	1	T5EP2V	short toxin 2 - we
295	4	5.0	55	2	S53148	H+-transporting tw	368	4	5.0	60	1	LPSE5	lantibiotic Pep5 p
296	4	5.0	55	2	AE2044	hypothetical prote	369	4	5.0	60	2	D70593	probable rubB prot
297	4	5.0	55	2	AH2396	hypothetical prote	370	4	5.0	60	2	S10356	T-cell receptor be
298	4	5.0	56	1	TIPQ	pancreatic secreto	371	4	5.0	60	2	G95026	ribosomal protein
299	4	5.0	56	2	T48952	ribosomal S29-like	372	4	5.0	60	2	G97897	50S ribosomal prot
300	4	5.0	56	2	S74259	tropinin T 3, fast	373	4	5.0	60	2	F83868	small acid-soluble
301	4	5.0	56	2	I53073	fetal tropinin T 2	374	4	5.0	60	2	S62076	M-like protein pre
302	4	5.0	56	2	S10402	finger protein kox	375	4	5.0	60	2	F87332	hypothetical prote
303	4	5.0	56	2	A10756	hypothetical prote	376	4	5.0	60	2	C40128	probable antigen 1
304	4	5.0	56	2	G85054	hypothetical prote	377	4	5.0	60	2	A90942	hypothetical prote
305	4	5.0	56	2	T09177	ydaE protein - Esc	378	4	5.0	60	2	E86867	prophage p83 prote
306	4	5.0	56	2	B71570	hypothetical prote	379	4	5.0	60	2	F84281	hypothetical prote
307	4	5.0	56	2	T35252	small hypothetical	380	4	5.0	60	2	I61886	zinc finger protei
308	4	5.0	56	2	A85956	hypothetical prote	381	4	5.0	60	2	H72785	probable repressor
309	4	5.0	56	2	B90010	hypothetical prote	382	4	5.0	60	2	E85790	hypothetical prote
310	4	5.0	56	2	AB2565	hypothetical prote	383	4	5.0	60	2	A97781	hypothetical prote
311	4	5.0	56	2	C60157	hypothetical prote	384	4	5.0	60	2	B97840	hypothetical prote
312	4	5.0	57	2	S66332	protein kinase AK1	385	4	5.0	60	2	D64940	hypothetical prote
313	4	5.0	57	2	A61479	cytochrome c - try	386	4	5.0	60	2	AH2737	hypothetical prote
314	4	5.0	57	2	E86680	hypothetical prote	387	4	5.0	60	2	F98317	hypothetical prote
315	4	5.0	57	2	C84312	hypothetical prote	388	4	5.0	60	2	A22227	hypothetical prote
316	4	5.0	57	2	T03080	hypothetical prote	389	4	5.0	60	2	AD2522	hypothetical prote
317	4	5.0	57	2	S43810	hypothetical prote	390	4	5.0	60	2	B69376	ferredoxin (fdx-6)
318	4	5.0	57	2	D70255	hypothetical prote	391	4	5.0	60	2	S05708	homeotic protein c
319	4	5.0	57	2	T35655	50S ribosomal prot	392	4	5.0	61	1	A59136	short neurotoxin 1
320	4	5.0	57	2	G64372	hypothetical prote	393	4	5.0	61	1	N1NJ1B	short neurotoxin 1
321	4	5.0	57	2	D82854	hypothetical prote	394	4	5.0	61	1	N1NJ1P	short neurotoxin 1

395	4	5.0	61	1	N1NJ1R	short neurotoxin 1	468	4	5.0	64	2	S52615	hypothetical prote
396	4	5.0	61	1	N1NJ1S	short neurotoxin 1	469	4	5.0	64	2	D81172	hypothetical prote
397	4	5.0	61	1	N1NJ2P	short neurotoxin 1	470	4	5.0	64	2	B70512	hypothetical prote
398	4	5.0	61	1	N1RI1	short neurotoxin 1	471	4	5.0	64	2	T35034	hypothetical prote
399	4	5.0	61	1	RGP22	regulatory protein	472	4	5.0	64	2	F69231	hypothetical prote
400	4	5.0	61	2	G81267	50S ribosomal prot	473	4	5.0	64	2	T13381	hypothetical prote
401	4	5.0	61	2	S11461	annexin, isoform P	474	4	5.0	64	2	A60246	Kinogen, HMW - chi
402	4	5.0	61	2	S60796	M protein precurs	475	4	5.0	64	2	I54385	apartylglucosamin
403	4	5.0	61	2	H5100	hypothetical prote	476	4	5.0	64	2	S22576	hypothetical prote
404	4	5.0	61	2	A69337	conserved hypotet	477	4	5.0	64	2	C82843	hypothetical prote
405	4	5.0	61	2	G95049	hypothetical prote	478	4	5.0	64	2	D82811	hypothetical prote
406	4	5.0	61	2	H90437	hypothetical prote	479	4	5.0	64	2	F82697	hypothetical prote
407	4	5.0	61	2	A81898	hypothetical prote	480	4	5.0	64	2	T12921	hypothetical prote
408	4	5.0	61	2	C75321	preprotein translo	481	4	5.0	64	2	D97165	flagellar protein
409	4	5.0	61	2	H59107	hypothetical prote	482	4	5.0	64	2	D97727	hypothetical prote
410	4	5.0	61	2	F81510	hypothetical prote	483	4	5.0	64	2	AC2544	hypothetical prote
411	4	5.0	61	2	H82853	hypothetical prote	484	4	5.0	64	2	AF2495	hypothetical prote
412	4	5.0	62	1	N1NJ1M	short neurotoxin 1	485	4	5.0	65	1	R5KT35	ribosomal protein
413	4	5.0	62	2	B39327	short neurotoxin 1	486	4	5.0	65	1	E69970	spore coat protein
414	4	5.0	62	2	B35866	short neurotoxin 1	487	4	5.0	65	2	S49486	trichosanthes try
415	4	5.0	62	2	D35866	short neurotoxin d	488	4	5.0	65	2	C72233	ribosomal protein
416	4	5.0	62	2	C35866	short neurotoxin c	489	4	5.0	65	2	S73191	50S ribosomal prot
417	4	5.0	62	2	F25866	short neurotoxin c	490	4	5.0	65	2	AD2234	dnaK-type molecula
418	4	5.0	62	2	E25866	short neurotoxin C	491	4	5.0	65	2	I79540	conserved hypotet
419	4	5.0	62	2	G35866	short neurotoxin b	492	4	5.0	65	2	F69385	hypothetical prote
420	4	5.0	62	2	T13997	aquaporin - common	493	4	5.0	65	2	S16483	hypothetical prote
421	4	5.0	62	2	C90761	probable division	494	4	5.0	65	2	S37026	hypothetical prote
422	4	5.0	62	2	H85624	hypothetical prote	495	4	5.0	65	2	S53704	alpha-2-microglobu
423	4	5.0	62	2	B70245	conserved hypotet	496	4	5.0	65	2	AB0610	hypothetical prote
424	4	5.0	62	2	E70257	conserved hypotet	497	4	5.0	65	2	H95007	hypothetical prote
425	4	5.0	62	2	A98181	hypothetical prote	498	4	5.0	65	2	E86709	hypothetical prote
426	4	5.0	62	2	S25778	hypothetical prote	499	4	5.0	65	2	E86516	hypothetical prote
427	4	5.0	62	2	C84002	alkaliphily relate	500	4	5.0	65	2	T28606	hypothetical prote
428	4	5.0	62	2	T00188	hypothetical prote	501	4	5.0	65	2	S74661	hypothetical prote
429	4	5.0	62	2	D86027	hypothetical prote	502	4	5.0	65	2	G69385	hypothetical prote
430	4	5.0	62	2	S47759	hypothetical prote	503	4	5.0	65	2	T15591	hypothetical prote
431	4	5.0	62	2	AF2059	hypothetical prote	504	4	5.0	65	2	G72172	H8R protein - vari
432	4	5.0	62	2	AG1956	hypothetical prote	505	4	5.0	65	2	F72105	hypothetical prote
433	4	5.0	62	2	AG2432	hypothetical prote	506	4	5.0	65	2	H82524	hypothetical prote
434	4	5.0	62	2	B59147	hypothetical prote	507	4	5.0	65	2	B71158	probable nusa prot
435	4	5.0	62	2	D59147	conotoxin Tx5.1 pr	508	4	5.0	65	2	D71070	probable zinc fing
436	4	5.0	63	2	F82058	conotoxin Gm5.2 pr	509	4	5.0	65	2	B97099	hypothetical prote
437	4	5.0	63	2	AF0984	ribosomal protein	510	4	5.0	65	2	H97193	hypothetical prote
438	4	5.0	63	2	CF07074	probable membrane	511	4	5.0	65	2	F89906	hypothetical prote
439	4	5.0	63	2	H86251	conserved hypotet	512	4	5.0	65	2	AF0303	conserved hypotet
440	4	5.0	63	2	T37351	protein F25C30.5 [	513	4	5.0	65	2	AC2285	hypothetical prote
441	4	5.0	63	2	T28506	RNA polymerase sub	514	4	5.0	65	2	AE1937	hypothetical prote
442	4	5.0	63	2	T28506	hypothetical prote	515	4	5.0	66	1	RCBPL	regulatory protein
443	4	5.0	63	2	F71571	hypothetical prote	516	4	5.0	66	2	I39586	dnaJ protein - Agr
444	4	5.0	63	2	I38244	16R protein - vari	517	4	5.0	66	2	E72222	cold shock protein
445	4	5.0	63	2	G97341	gene SPHAR protein	518	4	5.0	66	2	A86729	mercuric reductase
446	4	5.0	63	2	AH1757	hypothetical prote	519	4	5.0	66	2	C90663	Cro repressor [imp
447	4	5.0	63	2	AC3155	hypothetical prote	520	4	5.0	66	2	C90663	T-cell-stimulating
448	4	5.0	63	2	F98132	non-heme chloroper	521	4	5.0	66	2	A43602	probable membrane
449	4	5.0	63	2	AC2145	hypothetical prote	522	4	5.0	66	2	A99455	hypothetical prote
450	4	5.0	63	2	AD2276	hypothetical prote	523	4	5.0	66	2	T17934	hypothetical prote
451	4	5.0	63	2	AH1856	hypothetical prote	524	4	5.0	66	2	S77592	hypothetical prote
452	4	5.0	63	2	F59147	conotoxin P5.1 pre	525	4	5.0	66	2	T51323	Coot [imported] -
453	4	5.0	64	1	R3EG18	ribosomal protein	526	4	5.0	66	2	PN0644	hypothetical prote
454	4	5.0	64	1	D24546	small acid-soluble	527	4	5.0	66	2	T36227	hypothetical prote
455	4	5.0	64	1	WHIHB2	3b protein - avian	528	4	5.0	66	2	E69464	hypothetical prote
456	4	5.0	64	1	WHIHB5	3b protein - avian	529	4	5.0	66	2	S11155	cold and ABA induc
457	4	5.0	64	1	QABP22	restriction inhibi	530	4	5.0	66	2	B85890	hypothetical prote
458	4	5.0	64	2	S15633	serpin Spi2 (clone	531	4	5.0	66	2	AF3083	hypothetical prote
459	4	5.0	64	2	S15635	serpin Spi2 (clone	532	4	5.0	66	2	S15536	homeoic protein H
460	4	5.0	64	2	JH0338	T-cell receptor al	533	4	5.0	67	2	B56888	ribosomal protein
461	4	5.0	64	2	I77394	Ig heavy chain v r	534	4	5.0	67	2	E37284	alkaline phosphata
462	4	5.0	64	2	S78298	ribosomal protein	535	4	5.0	67	2	S76270	ribosomal protein
463	4	5.0	64	2	E83664	preprotein translo	536	4	5.0	67	2	S48660	troponin T 1, fast
464	4	5.0	64	2	B69384	conserved hypotet	537	4	5.0	67	2	S61817	M-like protein emn
465	4	5.0	64	2	A48411	Myf5 homolog - chi	538	4	5.0	67	2	AC0580	sec-independent pr
466	4	5.0	64	2	B86689	prophage ps2 prote	539	4	5.0	67	2	AB0787	homolog of virulen
467	4	5.0	64	2	T30405	hypothetical prote	540	4	5.0	67	2	H95062	BlpN protein [impo



687	4	5.0	74	2	C64346	hypothetical prote	760	4	5.0	77	2	JC6324	element c protein
688	4	5.0	74	2	B82939	hypothetical prote	761	4	5.0	77	2	B84390	ferredoxin 2[4Fe-4
689	4	5.0	74	2	C82919	hypothetical prote	762	4	5.0	77	2	G95019	ROK family protein
690	4	5.0	74	2	S50923	hypothetical prote	763	4	5.0	77	2	B90885	hypothetical prote
691	4	5.0	74	2	H90973	hypothetical prote	764	4	5.0	77	2	D90127	probable small nuc
692	4	5.0	74	2	B70135	flagellar protein	765	4	5.0	77	2	C84333	hypothetical prote
693	4	5.0	74	2	A81953	SLYX protein homol	766	4	5.0	77	2	C72868	Acorf-145 protein
694	4	5.0	74	2	S23539	hypothetical prote	767	4	5.0	77	2	C42519	Al9L 8.3K protein
695	4	5.0	74	2	A05192	hypothetical prote	768	4	5.0	77	2	H72353	hypothetical prote
696	4	5.0	74	2	D82775	hypothetical prote	769	4	5.0	77	2	F71642	hypothetical prote
697	4	5.0	74	2	AE0227	conserved hypotHet	770	4	5.0	77	2	D69010	hypothetical prote
698	4	5.0	74	2	A69097	ferredoxin - Metha	771	4	5.0	77	2	F84141	hypothetical prote
699	4	5.0	74	2	I41662	hypothetical prote	772	4	5.0	77	2	E82617	hypothetical prote
700	4	5.0	75	1	YBY2	proteinase B inhib	773	4	5.0	77	2	A85882	hypothetical prote
701	4	5.0	75	1	TNLJ51	trans-activating t	774	4	5.0	77	2	A97042	hypothetical prote
702	4	5.0	75	2	G69394	H+-transporting AT	775	4	5.0	77	2	B85733	hypothetical prote
703	4	5.0	75	2	S78159	H+-transporting tw	776	4	5.0	77	2	E97808	hypothetical prote
704	4	5.0	75	2	S58773	H+-transporting tw	777	4	5.0	77	2	A97885	transporter trunc
705	4	5.0	75	2	A81342	30S ribosomal prot	778	4	5.0	77	2	T01738	hypothetical prote
706	4	5.0	75	2	A72355	ribosomal protein	779	4	5.0	77	2	AG3462	hypothetical prote
707	4	5.0	75	2	B97307	acyl carrier prote	780	4	5.0	77	2	A64897	hypothetical prote
708	4	5.0	75	2	F64423	hypothetical prote	781	4	5.0	78	1	B69526	conserved hypotHet
709	4	5.0	75	2	B75106	probable snrnp PAB	782	4	5.0	78	2	B54897	dermaseptin b I pr
710	4	5.0	75	2	T44096	hypothetical prote	783	4	5.0	78	2	JH0344	T-cell receptor al
711	4	5.0	75	2	E91249	C4-type zinc finger	784	4	5.0	78	2	T36595	probable ribosomal
712	4	5.0	75	2	S03594	fil protein - phag	785	4	5.0	78	2	A27683	heat shock 90K pro
713	4	5.0	75	2	T14933	hypothetical prote	786	4	5.0	78	2	B81748	conserved hypotHet
714	4	5.0	75	2	F75345	hypothetical prote	787	4	5.0	78	2	E71487	hypothetical prote
715	4	5.0	75	2	G69544	hypothetical prote	788	4	5.0	78	2	AG0997	conserved hypotHet
716	4	5.0	75	2	T29576	hypothetical prote	789	4	5.0	78	2	B91094	type III secretion
717	4	5.0	75	2	B24853	hypothetical prote	790	4	5.0	78	2	D91160	hypothetical prote
718	4	5.0	75	2	A84068	hypothetical prote	791	4	5.0	78	2	E87088	hypothetical prote
719	4	5.0	75	2	D82616	hypothetical prote	792	4	5.0	78	2	F84461	hypothetical prote
720	4	5.0	75	2	G64755	ykgl protein - Esc	793	4	5.0	78	2	JQ1781	perD protein - Esc
721	4	5.0	75	2	AB1849	hypothetical prote	794	4	5.0	78	2	I69151	hypothetical prote
722	4	5.0	75	2	D71028	probable small nuc	795	4	5.0	78	2	A75442	hypothetical prote
723	4	5.0	75	2	I51341	homeo box protein	796	4	5.0	78	2	F69790	conserved hypotHet
724	4	5.0	76	2	E58933	ATP synthase prote	797	4	5.0	78	2	A70026	hypothetical prote
725	4	5.0	76	2	H83029	30S ribosomal prot	798	4	5.0	78	2	T35207	hypothetical prote
726	4	5.0	76	2	A36104	GTP-binding regula	799	4	5.0	78	2	C64338	hypothetical prote
727	4	5.0	76	2	C82236	cold shock-like pr	800	4	5.0	78	2	T21426	hypothetical prote
728	4	5.0	76	2	S22203	photosystem I chai	801	4	5.0	78	2	T21427	hypothetical prote
729	4	5.0	76	2	S61818	M-like protein enn	802	4	5.0	78	2	C86006	hypothetical prote
730	4	5.0	76	2	E64324	DNA-directed RNA p	803	4	5.0	78	2	D98860	conserved hypotHet
731	4	5.0	76	2	A69391	DNA-directed RNA p	804	4	5.0	78	2	H89853	hypothetical prote
732	4	5.0	76	2	E36966	rfc 3'-region hypo	805	4	5.0	78	2	F85939	type III secretion
733	4	5.0	76	2	T36251	probable lysyl-TRN	806	4	5.0	78	2	A13363	transcription regu
734	4	5.0	76	2	B36850	Al9L protein - var	807	4	5.0	78	2	E65136	hypothetical 8.7 k
735	4	5.0	76	2	T28561	hypothetical prote	808	4	5.0	78	2	AF3003	conserved hypotHet
736	4	5.0	76	2	T17797	hypothetical prote	809	4	5.0	78	2	AG2805	hypothetical prote
737	4	5.0	76	2	F83566	hypothetical prote	810	4	5.0	78	2	C98280	hypothetical prote
738	4	5.0	76	2	E82154	probable transcrip	811	4	5.0	78	2	I51342	homeo box protein
739	4	5.0	76	2	H64393	hypothetical prote	812	4	5.0	79	2	S39850	FKBP immunophilin
740	4	5.0	76	2	T48430	hypothetical prote	813	4	5.0	79	2	B87405	ribosomal protein
741	4	5.0	76	2	T26894	hypothetical prote	814	4	5.0	79	2	B95179	ribosomal protein
742	4	5.0	76	2	T09476	hypothetical prote	815	4	5.0	79	2	A98046	30S ribosomal prot
743	4	5.0	76	2	A39034	neurogranin - bovi	816	4	5.0	79	2	T36351	probable ribosomal
744	4	5.0	76	2	A72166	A20L protein - var	817	4	5.0	79	2	D97286	ribosomal protein
745	4	5.0	76	2	D82787	hypothetical prote	818	4	5.0	79	2	I50549	acetylcholine rece
746	4	5.0	76	2	A01442	gp37-1 (bacterioph	819	4	5.0	79	2	S62078	M-like protein pre
747	4	5.0	76	2	H81272	probable acyl carr	820	4	5.0	79	2	C84077	nitrogen fixation
748	4	5.0	76	2	S82850	NADH2 dehydrogenas	821	4	5.0	79	2	G75155	hypothetical prote
749	4	5.0	76	2	B69110	ferredoxin - Metha	822	4	5.0	79	2	A64334	hypothetical prote
750	4	5.0	76	2	B36359	VSG expression sit	823	4	5.0	79	2	H95035	conserved hypotHet
751	4	5.0	77	1	INSH	insulin precursor	824	4	5.0	79	2	F95210	conserved domain p
752	4	5.0	77	2	A47070	ferredoxin (EC	825	4	5.0	79	2	G86731	exodeoxyribonuclea
753	4	5.0	77	2	JC2189	peptidylprolyl iso	826	4	5.0	79	2	C46026	group I intron end
754	4	5.0	77	2	A01259	complement C3 - pi	827	4	5.0	79	2	D81188	hypothetical prote
755	4	5.0	77	2	A01265	c-H-ras 2 protein	828	4	5.0	79	2	D75326	hypothetical prote
756	4	5.0	77	2	S29229	ubiquitin - Entamo	829	4	5.0	79	2	E69966	hypothetical prote
757	4	5.0	77	2	S29238	chemoreceptor prot	830	4	5.0	79	2	G64375	hypothetical prote
758	4	5.0	77	2	E36943	reverse transcript	831	4	5.0	79	2	F83880	acyl-carrier prote
759	4	5.0	77	2	S63586		832	4	5.0	79	2	F97856	hypothetical prote



833	4	5.0	79	2	B89761	hypothetical prote	3	3.8	10	2	S33844	alpha-2-macroglobu
834	4	5.0	79	2	E97906	conserved hypothet	3	3.8	10	2	B33995	hypotrehaloemic h
835	4	5.0	79	2	AH1418	hypothetical prote	3	3.8	10	2	JC1416	hypertrehaloemic
836	4	5.0	79	2	AB2323	hypothetical prote	3	3.8	10	2	S09138	hypertrehaloemic
837	4	5.0	79	2	AI2512	hypothetical prote	3	3.8	10	2	H28027	protein P11 - curl
838	4	5.0	80	2	PC4098	Ha-ras protein - z	3	3.8	10	2	H61308	hemocyanin subunit
839	4	5.0	80	2	PC4097	Ha-ras protein - E	3	3.8	10	2	A61622	vitellogenin, 190k
840	4	5.0	80	2	A35572	seminalplaemin pre	3	3.8	10	2	A35556	hypothetical prote
841	4	5.0	80	2	S06905	ferritin heavy chu	3	3.8	10	2	PT0212	T-cell receptor al
842	4	5.0	80	2	S61801	M-like protein enu	3	3.8	10	2	C30572	T-cell receptor be
843	4	5.0	80	2	A89860	hypothetical prote	3	3.8	10	2	B61440	polygalacturonase
844	4	5.0	80	2	D69492	conserved hypothet	3	3.8	10	2	D61440	polygalacturonase
845	4	5.0	80	2	S16200	photosystem I iron	3	3.8	10	2	A58365	neuropeptide FFRfa
846	4	5.0	80	2	A32364	photosystem I iron	3	3.8	10	2	S77990	cytochrome-c oxida
847	4	5.0	80	2	S68677	cytochrome c551 -	3	3.8	10	2	T17063	cytochrome-c oxida
848	4	5.0	80	2	A60699	hypothetical prote	3	3.8	10	2	H60787	sperm-activating p
849	4	5.0	80	2	P90782	hypothetical prote	3	3.8	10	2	F60787	sperm-activating p
850	4	5.0	80	2	A90898	probable damage-in	3	3.8	10	2	F60787	sperm-activating p
851	4	5.0	80	2	H91230	hypothetical prote	3	3.8	10	2	D60787	sperm-activating p
852	4	5.0	80	2	B90337	conserved hypothet	3	3.8	10	2	B60787	sperm-activating p
853	4	5.0	80	2	B90368	conserved hypothet	3	3.8	10	2	B60588	sperm-activating p
854	4	5.0	80	2	D96511	hypothetical prote	3	3.8	10	2	B60588	sperm-activating p
855	4	5.0	80	2	H84281	hypothetical prote	3	3.8	10	2	C60588	sperm-activating p
856	4	5.0	80	2	S03225	hypothetical prote	3	3.8	10	2	I60527	sperm-activating p
857	4	5.0	80	2	E72295	conserved hypothet	3	3.8	10	2	D60527	sperm-activating p
858	4	5.0	80	2	A29385	hydrophobic seed p	3	3.8	10	2	C39572	sperm-activating p
859	4	5.0	80	2	T39148	hypothetical prote	3	3.8	10	2	F60527	sperm-activating p
860	4	5.0	80	2	A54059	protein kinase C (	3	3.8	10	2	C60527	sperm-activating p
861	4	5.0	80	2	S03560	transition protein	3	3.8	10	2	E60527	sperm-activating p
862	4	5.0	80	2	G82597	hypothetical prote	3	3.8	10	2	G60527	sperm-activating p
863	4	5.0	80	2	C69317	hypothetical prote	3	3.8	10	2	E39572	sperm-activating p
864	4	5.0	80	2	G86077	hypothetical prote	3	3.8	10	2	D60788	sperm-activating p
865	4	5.0	80	2	E97800	hypothetical prote	3	3.8	10	2	C60788	sperm-activating p
866	4	5.0	80	2	G97805	hypothetical prote	3	3.8	10	2	E60788	sperm-activating p
867	4	5.0	80	2	H89802	30S ribosomal prot	3	3.8	10	2	F60589	sperm-activating p
868	4	5.0	80	2	S40834	hypothetical prote	3	3.8	10	2	C60589	sperm-activating p
869	4	5.0	80	2	E97572	hypothetical prote	3	3.8	10	2	D60589	sperm-activating p
870	4	5.0	80	2	S02067	glycerol kinase (S	3	3.8	10	2	A60527	sperm-activating p
871	3	3.8	5	2	S70615	endo-1,4-beta-xyla	3	3.8	10	2	A60787	sperm-activating p
872	3	3.8	5	2	PT0267	IG heavy chain CRD	3	3.8	10	2	A60588	sperm-activating p
873	3	3.8	5	2	PT0585	T-cell receptor be	3	3.8	10	2	A60788	sperm-activating p
874	3	3.8	6	2	B60110	repetitive protein	3	3.8	11	2	GMR0L	leucosulfakinin -
875	3	3.8	6	2	PT0605	T-cell receptor be	3	3.8	11	2	A38841	rhodopsin homolog
876	3	3.8	6	4	I79564	hypothetical TCL3	3	3.8	11	2	I41946	T-cell receptor ga
877	3	3.8	7	2	PT0666	T-cell receptor be	3	3.8	11	2	S33519	probable secreted
878	3	3.8	7	2	PT0683	T-cell receptor be	3	3.8	11	2	PC3267	ribosomal protein
879	3	3.8	7	2	B35890	RNA-directed DNA p	3	3.8	11	2	S71304	amine oxidase (cop
880	3	3.8	7	4	S15597	orf 4 rara 5'-regl	3	3.8	11	2	A60656	perleukinin - A
881	3	3.8	8	2	A33995	adipokinetic hormo	3	3.8	11	2	A32428	amine oxidase (cop
882	3	3.8	8	2	B49960	neuropeptide Led-C	3	3.8	11	2	S68637	acetylcholinestera
883	3	3.8	8	2	S08996	hypertrehaloemic	3	3.8	11	2	S54347	tubulin beta chain
884	3	3.8	8	2	B49823	adipokinetic hormo	3	3.8	11	2	S23306	substance P - Atla
885	3	3.8	8	2	PT0527	T-cell receptor be	3	3.8	11	2	A28930	ermG leader peptid
886	3	3.8	8	2	PT0509	T-cell receptor be	3	3.8	12	2	S09082	proteasome chain 1
887	3	3.8	8	2	B21440	variant surface gl	3	3.8	12	2	S26552	T-cell receptor be
888	3	3.8	8	2	B24749	neuropeptide B - b	3	3.8	12	2	S26549	T-cell receptor be
889	3	3.8	8	4	I55411	hypothetical histo	3	3.8	12	2	S26553	T-cell receptor be
890	3	3.8	9	2	A28495	conopressin G - co	3	3.8	12	2	S26559	58k bile and gallb
891	3	3.8	9	2	A24244	adipokinetic hormo	3	3.8	12	2	C58502	hypothetical prote
892	3	3.8	9	2	PC2197	zymogen granule me	3	3.8	12	2	D28551	148K exoantigen -
893	3	3.8	9	2	G56978	collagen alpha 1(I	3	3.8	12	2	C33099	T-cell antigen rec
894	3	3.8	9	2	A42266	peptidylglycine mo	3	3.8	12	2	S47360	T-cell receptor al
895	3	3.8	9	2	B30572	T-cell receptor be	3	3.8	12	2	PH1188	T-cell receptor be
896	3	3.8	9	2	S39040	lysine-conopressin	3	3.8	12	2	PH1481	T-cell receptor be
897	3	3.8	9	2	I54379	gene NP2 protein -	3	3.8	12	2	PH1466	T-cell receptor be
898	3	3.8	9	2	A60427	macrophage cytotox	3	3.8	12	2	PH1469	T-cell receptor be
899	3	3.8	9	2	S66635	alpha-2-macroglobu	3	3.8	12	2	E58502	T-cell receptor be
900	3	3.8	9	2	I46016	cytokeratin 4 - bo	3	3.8	12	2	S71034	43.2K bile stone p
901	3	3.8	9	2	PC7074	translation elonga	3	3.8	12	2	S71034	potB protein - Sal
902	3	3.8	9	2	PC7078	unidentified 48.7K	3	3.8	12	2	I40663	bma protein - Clos
903	3	3.8	9	2	QDRB	delta sleep-induci	3	3.8	12	2	PN0162	malate dehydrogena
904	3	3.8	9	2	I73804	hypothetical E2 pr	3	3.8	12	2	S21205	Ig heavy chain V r
905	3	3.8	10	2	S28055	cytochrome b559 co	3	3.8	12	2	S71380	lebetin 1 isoform
												tachykinin - Afric

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979      3   3.8   12   2   S65409      histone H2B - huma
980      3   3.8   13   2   A33208      calreticulin, hepa
981      3   3.8   13   2   E37390      traA protein - Esc
982      3   3.8   13   2   H64124      hypothetical prote
983      3   3.8   13   2   PA0031      protein QA300045 -
984      3   3.8   13   2   B44957      protein L7 - commo
985      3   3.8   13   2   S47362      T-cell antigen rec
986      3   3.8   13   2   S47388      T-cell antigen rec
987      3   3.8   13   2   B61233      conceptus protein
988      3   3.8   13   2   S66235      sperm motility inh
989      3   3.8   13   2   B36042      oxfK protein - Esc
990      3   3.8   13   2   S09733      photosystem I prot
991      3   3.8   13   2   S66558      serine proteinase
992      3   3.8   13   2   S01904      H+-transporting tw
993      3   3.8   14   1   QMVHP2      mastoparan C - Eur
994      3   3.8   14   1   QMWAVV      mastoparan C - Yello
995      3   3.8   14   1   LFECW       trip operon leader
996      3   3.8   14   2   A47421      leukotriene B-4 12
997      3   3.8   14   2   C40944      hypothetical prote
998      3   3.8   14   2   S21247      H+-transporting tw
999      3   3.8   14   2   A60622      somatostatin - spo
1000     3   3.8   14   2   A60840      somatostatin I - E

ALIGNMENTS

RESULT 1
S03353
plastocyanin - Microcystis aeruginosa (fragment)
C:Species: Microcystis aeruginosa
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C:Accession: S03353
R:Tan, S.; Ho, K.K.
Biochim. Biophys. Acta 973, 111-117, 1989
A:Title: Purification of an acidic plastocyanin from Microcystis aeruginosa.
A:Reference number: S03353; MUID:89134784; PMID:2537099
A:Accession: S03353
A:Molecule type: protein
A:Residues: 1-15 <FAN>
A:Cross-references: UNIPROT:P10625; UNIPARC:UPI0000131BAF

Query Match          7.5%; Score 6; DB 2; Length 15;
Best Local Similarity 100.0%; Pred.No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      62 ETFTVK 67
Db      1 ETFTVK 6

RESULT 2
HJ3057
MHC class II histocompatibility antigen DO-B beta chain - rhesus macaque (fragment)
C:Species: Macaca mulatta (rhesus macaque)
C>Date: 03-Aug-1990 #sequence_revision 03-Aug-1990 #text_change 31-Dec-2004
C:Accession: HJ3057
R:Gyllenstein, U.B.; Lashkari, D.; Erlich, H.A.
Proc. Natl. Acad. Sci. U.S.A. 87, 1835-1839, 1990
A:Title: Allelic diversification at the class II DOB locus of the mammalian major histoc
A:Reference number: A35054; MUID:90175391; PMID:2308943
A:Accession: HJ3057
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-57 <GYL>
A:Cross-references: UNIPROT:Q02712; UNIPROT:Q9TPB4; UNIPARC:UPI0000176PDF
C:Superfamily: immunoglobulin homology

Query Match          7.5%; Score 6; DB 2; Length 57;
Best Local Similarity 100.0%; Pred.No. 57;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      58 KDVLFT 63
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Db      45 KDVLFT 50

RESULT 3
HJ2927
hypothetical protein UUI51 [imported] - Ureaplasma urealyticum
C:Species: Ureaplasma urealyticum
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: HJ2927
R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Weiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
A:Reference number: AB2870
A:Accession: HJ2927
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-60 <GLA>
A:Cross-references: UNIPARC:UPI0000139389; GB:AE002115; GB:AF222894; NID:G6899102; PIDN
A:Experimental source: serovar 3; biovar 1
C:Genetics:
A:Gene: UUI51
A:Genetic code: SGC3

Query Match          7.5%; Score 6; DB 2; Length 60;
Best Local Similarity 100.0%; Pred.No. 59;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 DEVIKS 8
Db      50 DEVIKS 55

RESULT 4
PQ0469
cysteine proteinase inhibitor - potato (fragment)
N:Alternate names: wound-induced protein
C:Species: Solanum tuberosum (potato)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: PQ0469; S24768
R:Hildmann, T.; Ebnet, M.; Pena-Cortes, H.; Sanchez-Serrano, J.J.; Willmitzer, L.; Prat
Plant Cell 4, 1157-1170, 1992
A:Title: General roles of abscisic and jasmonic acids in gene activation as a result of
A:Reference number: JQ1692; MUID:93005746; PMID:1392612
A:Accession: PQ0469
A:Molecule type: mRNA
A:Residues: 1-66 <HIL>
A:Cross-references: UNIPROT:Q03196; UNIPARC:UPI0000128D7E; EMBL:X67844; NID:G21440; PIDN
A:Experimental source: strain desiree
C:Keywords: cysteine proteinase inhibitor
F:18-22/Region: inhibitory

Query Match          7.5%; Score 6; DB 2; Length 66;
Best Local Similarity 100.0%; Pred.No. 64;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 KEVQEF 12
Db      53 KEVQEF 58

RESULT 5
D64538
hypothetical protein HP0148 - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C>Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C:Accession: D64538
R:Tombs, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
```

A;Reference number: A64520; MUID:97394467; PMID:9252185  
A;Accession: D64538  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-68 <TOM>  
A;Cross-references: UNIPROT:Q24959; UNIPARC:UPI00000C07EB; GB:AE000536; GB:AE000511; NID

Query Match 7.5%; Score 6; DB 2; Length 68;  
Best Local Similarity 100.0%; Pred. No. 66;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 TLKAIH 35  
|||  
DB 25 TLKAIH 30  
|||

RESULT 6  
S42781  
relaxin - orangutan (fragment)  
C;Species: Pongo pygmaeus (orangutan)  
C;Date: 06-Jan-1995 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: S42781  
R;Evans, B.B.  
submitted to the EMBL Data Library, November 1993  
A;Reference number: S42776  
A;Accession: S42781  
A;Molecule type: DNA  
A;Residues: 1-33 <EVA>  
A;Cross-references: UNIPROT:Q28782; UNIPARC:UPI000008691D; EMBL:Z27230; NID:G415992; PID  
C;Genetics:  
A;Gene: rlx2  
C;Superfamily: insulin  
C;Keywords: disulfide bond; hormone  
P;1-33/Domain: relaxin chain 2B (fragment) #status predicted <RXB2>

Query Match 6.2%; Score 5; DB 2; Length 33;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DEVIK 7  
|||  
DB 5 DEVIK 9  
|||

RESULT 7  
A61232  
pregnancy-associated glycoprotein - bovine (fragment)  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 16-Aug-2004  
C;Accession: A61232  
R;Zoli, A.P.; Beckers, J.F.; Wouters-Ballman, P.; Closset, J.; Falmagne, P.; Ectors, F.  
Biol. Reprod. 45, 1-10, 1991  
A;Title: Purification and characterization of a bovine pregnancy-associated glycoprotein  
A;Reference number: A61232; MUID:91346259; PMID:1908709  
A;Accession: A61232  
A;Molecule type: protein  
A;Residues: 1-39 <ZOL>  
A;Cross-references: UNIPROT:Q7M318; UNIPARC:UPI0000175D6D  
C;Superfamily: Pepsin  
C;Keywords: glycoprotein

Query Match 6.2%; Score 5; DB 2; Length 39;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 KDEPQ 27  
|||  
DB 25 KDEPQ 29  
|||

RESULT 8  
S23804  
homeotic protein lim-2B - African clawed frog (fragment)

C;Species: Xenopus laevis (African clawed frog)  
C;Date: 29-Jan-1998 #sequence\_revision 13-Feb-1998 #text\_change 09-Jul-2004  
C;Accession: S23804  
R;Taira, M.; Jamrich, M.; Good, P.J.; Dawid, I.B.  
Genes Dev. 6, 356-366, 1992  
A;Title: The LIM domain-containing homeo box gene Xlim-1 is expressed specifically in t  
A;Reference number: S23802; MUID:92192449; PMID:1347750  
A;Accession: S23804  
A;Molecule type: mRNA  
A;Residues: 1-39 <TAI>  
A;Cross-references: UNIPROT:P37138; UNIPARC:UPI000012E698; EMBL:Z11588; NID:G64832; PID  
C;Genetics:  
A;Gene: lim-2B  
C;Superfamily: homeotic protein lim-3; homeobox homology; LIM metal-binding repeat homo  
C;Keywords: DNA binding; duplication; embryo; homeobox; nucleus; transcription regulati  
P;1-39/Domain: homeobox homology (fragment) <HOX>

Query Match 6.2%; Score 5; DB 2; Length 39;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 ETLKA 33  
|||  
DB 6 ETLKA 10  
|||

RESULT 9  
S23803  
homeotic protein lim-2A - African clawed frog (fragment)  
C;Species: Xenopus laevis (African clawed frog)  
C;Date: 29-Jan-1998 #sequence\_revision 13-Feb-1998 #text\_change 15-Mar-2004  
C;Accession: S23803  
R;Taira, M.; Jamrich, M.; Good, P.J.; Dawid, I.B.  
Genes Dev. 6, 356-366, 1992  
A;Title: The LIM domain-containing homeo box gene Xlim-1 is expressed specifically in t  
A;Reference number: S23802; MUID:92192449; PMID:1347750  
A;Accession: S23803  
A;Molecule type: mRNA  
A;Residues: 1-39 <TAI>  
A;Cross-references: UNIPARC:UPI000017155C; EMBL:Z11587; NID:G64831; PIDN:CAA7672.1; PI  
A;Note: the authors translated the codon ATT for residue 13 as Ala  
C;Genetics:  
A;Gene: lim-2A  
C;Keywords: DNA binding; duplication; embryo; homeobox; nucleus; transcription regulati  
P;1-39/Domain: homeobox homology (fragment) <HOX>

Query Match 6.2%; Score 5; DB 2; Length 39;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 ETLKA 33  
|||  
DB 6 ETLKA 10  
|||

RESULT 10  
C37264  
E2 Glycoprotein - Barmah Forest virus (fragment)  
C;Species: Barmah Forest virus  
C;Date: 30-Aug-1991 #sequence\_revision 30-Jan-1993 #text\_change 31-Dec-2004  
C;Accession: C37264  
R;Bell, J.R.; Kinney, R.M.; Trent, D.W.; Strauss, E.G.; Strauss, J.H.  
Proc. Natl. Acad. Sci. U.S.A. 81, 4702-4706, 1984  
A;Title: An evolutionary tree relating eight alphaviruses, based on amino-terminal sequ  
A;Reference number: A21774; MUID:84272701; PMID:6087344  
A;Accession: C37264  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-39 <BEL>  
A;Cross-references: UNIPROT:P89946; UNIPARC:UPI000017855E  
C;Keywords: glycoprotein

Query Match 6.2%; Score 5; DB 2; Length 39;

Best Local Similarity 100.0%; Pred. NO. 4.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	41	CGLAG 45
Dd	21	CGLAG 25

RESULT 11

H81591  
hypothetical protein CP0304 [imported] - Chlamydophila pneumoniae (strain AR39)  
C/Species: Chlamydophila pneumoniae, Chlamydia pneumoniae  
C/Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
C/Accession: H81591  
C/Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,  
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,  
Nucleic Acids Res. 28, 1397-1406, 2000  
A/Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.  
A/Reference number: AB1500; MUID:20150255; PMID:10684935  
A/Accession: H81591  
A/Status: preliminary  
A/Molecule type: DNA  
A/Molecule type: DNA  
A/Residues: 1-40 <REA>  
A/Cross-references: UNIPROT:Q9K298; UNIPARC:UPI000000CCCC57; GB:AE002192; GB:AE002161; NITD  
A/Experimental source: strain AR39, HL cells  
C/Genetics:  
A/Gene: CP0304

Query Match	6.2%	Score 5;	DB 2;	Length 40;
Best Local Similarity	100.0%	Pred. No. 4.e+02;		
Matches	5;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;

RESULT 12  
PQ0560 nonstructural protein 3 (clone 8) - hepatitis C virus (fragment)  
C;Species: hepatitis C virus  
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
C;Accession: PQ0560  
R;Kato, N.; Ootsuyama, Y.; Ohkoshi, S.; Nakazawa, T.; Mori, S.; Hijikata, M.; Shimotohno  
Biochem. Biophys. Res. Commun. 181, 279-285, 1991  
A;Title: Distribution of plural HCV types in Japan.  
A;Reference number: PQ0554; MUID:92068204; PMID:1720309  
A;Accession: PQ0560  
A;Molecule type: mRNA  
A;Residues: 1-41 <KAT>  
A;Cross-references: UNIPROT:Q81252; UNIPARC:UP100000F397A; GB:D90519; NID:G222  
C;Superfamily: hepatitis C virus genome polypeptide  
C;Keywords: nonstructural protein

Query Match	6.2%	Score 5;	DB 2;	Length 41;
Best Local Similarity	100.0%;	Pred. No. 4.5e+02;		
Matches 5;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

RESULT 13  
PQ0563 nonstructural protein 3 (clone 11) - hepatitis C virus (fragment)  
C;Species: hepatitis C virus  
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
C;Accession: PQ0563  
R;Kato, N.; Ootsuyama, Y.; Ohkoshi, S.; Nakazawa, T.; Mori, S.; Hijikata, M.; Shimotohno  
Biochem. Biophys. Res. Commun. 181, 279-285, 1991  
A;Title: Distribution of plural HCV types in Japan.  
A;Reference number: PQ0554; MUID:92068204; PMID:1720309

A:Accession: PQ0563  
A:Molecule type: mRNA  
A:Residues: 1-41 <KAT>  
A:Cross-references: UNIPROT:Q81248; UNIPARC:UPI00000EE322; GB:D10566; GB:D90522; NID:922  
C:Superfamily: hepatitis C virus genome polyprotein  
C:Keywords: nonstructural protein

Query Match	6.2%;	Score 5;	DB 2;	Length 41;
Best Local Similarity	100.0%;	Pred. No. 4.5e+02;		
Matches 5;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

RESULT 14  
PQ0564  
nonstructural protein 3 (Clone 4) - hepatitis C virus (fragment)  
C:Species: hepatitis C virus  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
C:Accession: PQ0564  
R:Kato, N.; Ootsuyama, Y.; Ohkoshi, S.; Nakazawa, T.; Mori, S.; Hijikata, M.; Shimotohno  
Biochem. Biophys. Res. Commun. 181, 279-285, 1991  
A:Title: Distribution of plural HCV types in Japan.  
A:Reference number: PQ0554; MUID:92068204; PMID:1720309  
A:Accession: PQ0564  
A:Molecule type: mRNA  
A:Residues: 1-41 <KAT>  
A:Cross-references: UNIPROT:Q81251; UNIPARC:UPI00000P69F4; GB:D10567; GB:D90523; NID:q22  
C:Superfamily: hepatitis C virus genome polyprotein  
C:Keywords: nonstructural protein

Query Match 6.2%; Score 5; DB 2; Length 41;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 15  
PQ0562  
nonstructural protein 3 (Clone 10) - hepatitis C virus (fragment)  
C:Species: hepatitis C virus  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
C:Accession: PQ0562  
R:Kato, N.; Ootsuyama, Y.; Ohkoshi, S.; Nakazawa, T.; Mori, S.; Hijikata, M.; Shimotohno  
Biochem. Biophys. Res. Commun. 181, 279-285, 1991  
A:Title: Distribution of plural HCV types in Japan.  
A:Reference number: PQ0554; MOID:92068204; PMID:1720309  
A:Accession: PQ0562  
A:Molecule type: mRNA  
A:Residues: 1-41 <RAT>  
A:Cross-references: UNIPROT:Q81247; UNIPARC:UPI00000P65F6; GB:D10565; GB:D90521; NID:922  
C:Superfamily: hepatitis C virus genome polyprotein  
C:Keywords: nonstructural protein

Query Match 6.2%; Score 5; DB 2; Length 41;  
Best Local Similarity 100.0%; Pred.No. 4.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: January 20, 2006, 17:50:58  
Job time : 25 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2006, 17:44:52 ; Search time 67 Seconds  
(without alignments)  
842.422 Million cell updates/sec

Title: US-10-619-323-1\_COPY\_113\_192

Perfect score: 80

Sequence: 1 HKDEVIKEVQEFYKDYTNKL.....LETFTVKSCPOAIKEVFDNK 80

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 0

Total number of hits satisfying chosen parameters: 214343

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Listing first 1000 summaries

Database : UniProt\_05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	8.5	29	2	Q4XWD9 PLACH
2	6	7.5	15	1	P10625 microcystis
3	6	7.5	37	2	Q93V77 ATREBE
4	6	7.5	42	2	Q53412_BACSU
5	6	7.5	48	2	Q4RNP3_TETNG
6	6	7.5	51	2	Q4RNP3_TETNG
7	6	7.5	60	1	Y151_UREPA
8	6	7.5	62	2	Q74EK4_GEOSL
9	6	7.5	63	2	Q4FLM6_9RICK
10	6	7.5	66	1	CYT_SOUTU
11	6	7.5	67	2	Q7UUB3_RHOBA
12	6	7.5	68	2	O24959_HELPY
13	6	7.5	71	2	O52950_BACSU
14	6	7.5	71	2	Q728A1_DESVH
15	6	7.5	73	2	Q5BQT7_SCHJA
16	6	7.5	74	2	Q6VXZ4_ECHOL
17	6	7.5	74	2	Q6VXZ4_ECHOL
18	6	7.5	76	2	Q6DL6L_ERWCT
19	6	7.5	79	2	Q7VTU2_BORPE
20	6	7.5	79	2	Q7W4U2_BORBA
21	6	7.5	79	2	Q7WGB9_BORBR
22	5	6.2	15	2	P83071_BACCE
23	5	6.2	18	2	Q9R7B8_BORBU
24	5	6.2	24	2	Q9RQ50_9ENTR
25	5	6.2	25	2	Q4RBM3_TETNG
26	5	6.2	25	2	Q77X16_9HIV1
27	5	6.2	25	2	Q9W8V6_9HIV1
28	5	6.2	26	2	Q4XP56_PLACH
29	5	6.2	29	2	Q4XP92_PLACH
30	5	6.2	30	2	Q4XKQ1_PLACH
31	5	6.2	31	2	Q81G64_BACCR

32	5	6.2	32	2	Q4XWD9 PLACH	Q4xwd9 plasmodium
33	5	6.2	32	2	Q87L58_VIBPA	Q87L58 vibrio para
34	5	6.2	32	2	Q4YI31_PLABE	Q4YI31 plasmodium
35	5	6.2	33	2	Q28782_PONPY	Q28782 pongo pygma
36	5	6.2	35	1	PBP_HYACE	P34175 hyalophora
37	5	6.2	35	2	Q4XJP2_PLACH	Q4xjp2 plasmodium
38	5	6.2	35	2	Q4HDN4_CAMCO	Q4hdn4 campylobact
39	5	6.2	36	2	Q5P857_AZOSE	Q5p857 azoarcus ap
40	5	6.2	38	2	Q7KYM2_HUMAN	Q7kym2 homo sapien
41	5	6.2	38	2	Q4X137_PLACH	Q4x137 plasmodium
42	5	6.2	38	2	Q4Z9S6_9VIRU	Q4z9s6 bacteriopho
43	5	6.2	39	1	LTM2B_XENLA	P37138 xenopus lae
44	5	6.2	39	2	Q7M318_BOVIN	Q7m318 bos taurus
45	5	6.2	39	2	Q5HM83_STABO	Q5hm83 staphylococ
46	5	6.2	39	2	Q8BQGO_MOUSE	Q8bqgo mus musculu
47	5	6.2	40	2	Q7RQC2_PLAYO	Q7rqc2 plasmodium
48	5	6.2	40	2	Q9K298_CHLPN	Q9k298 chlamydia p
49	5	6.2	41	2	Q81Z97_HUMAN	Q81z97 homo sapien
50	5	6.2	41	2	Q9Y3F8_HUMAN	Q9y3f8 homo sapien
51	5	6.2	41	2	Q81247_9HEPC	Q81247 hepatitis c
52	5	6.2	41	2	Q81248_9HEPC	Q81248 hepatitis c
53	5	6.2	41	2	Q81249_9HEPC	Q81249 hepatitis c
54	5	6.2	41	2	Q81252_9HEPC	Q81252 hepatitis c
55	5	6.2	41	2	Q81G73_IRV6	Q81g73 chilo iride
56	5	6.2	41	2	Q8F448_LRPIN	Q8f448 leptospira
57	5	6.2	42	2	Q8FCU6_ECOL6	Q8fcu6 escherichia
58	5	6.2	42	2	Q6URF4_9HIV1	Q6urf4 human immun
59	5	6.2	42	2	Q8ZVGS_SPIKU	Q8zvg5 pyrobaculum
60	5	6.2	43	2	Q8ZVGS_SPIKU	Q8zvg5 pyrobaculum
61	5	6.2	44	2	Q8FYJ6_LRPIN	Q8fyj6 leptospira
62	5	6.2	44	2	Q8ZU36_PYRAE	Q8zu36 pyrobaculum
63	5	6.2	45	2	Q5NDM5_HUMAN	Q5ndms homo sapien
64	5	6.2	45	2	Q5QP28_HUMAN	Q5qp28 homo sapien
65	5	6.2	45	2	Q70E15_HUMAN	Q70e15 homo sapien
66	5	6.2	45	2	Q6UM80_9HEPC	Q6um80 hepatitis c
67	5	6.2	46	2	Q8WML0_HUMAN	Q8wml0 homo sapien
68	5	6.2	46	2	Q96KU2_HUMAN	Q96ku2 homo sapien
69	5	6.2	46	2	Q9UK69_HUMAN	Q9uk69 homo sapien
70	5	6.2	46	2	Q91361_PSEAE	Q91361 pseudomonas
71	5	6.2	46	2	Q36214_9HIV1	Q36214 human immun
72	5	6.2	46	2	Q8NFY0_HUMAN	Q8nfy0 homo sapien
73	5	6.2	47	2	Q9UN35_HUMAN	Q9un35 homo sapien
74	5	6.2	47	2	Q7XJ45_ARATH	Q7xj45 arabidopsis
75	5	6.2	47	2	Q91F15_IRV6	Q91fi5 chilo iride
76	5	6.2	47	2	Q87307_SIVCZ	Q87307 chimpanzee
77	5	6.2	47	2	Q87319_SIVCZ	Q87319 chimpanzee
78	5	6.2	47	2	Q87322_SIVCZ	Q87322 chimpanzee
79	5	6.2	47	2	Q87334_SIVCZ	Q87334 chimpanzee
80	5	6.2	47	2	Q87335_SIVCZ	Q87335 chimpanzee
81	5	6.2	47	2	Q87366_SIVCZ	Q87366 chimpanzee
82	5	6.2	47	2	Q87370_SIVCZ	Q87370 chimpanzee
83	5	6.2	47	2	Q87396_SIVCZ	Q87396 chimpanzee
84	5	6.2	47	2	Q87396_SIVCZ	Q87396 chimpanzee
85	5	6.2	48	2	Q81Z13_BACAN	Q81z13 bacillus an
86	5	6.2	48	2	Q87310_SIVCZ	Q87310 chimpanzee
87	5	6.2	48	2	Q87313_SIVCZ	Q87313 chimpanzee
88	5	6.2	48	2	Q87325_SIVCZ	Q87325 chimpanzee
89	5	6.2	48	2	Q87331_SIVCZ	Q87331 chimpanzee
90	5	6.2	48	2	Q87373_SIVCZ	Q87373 chimpanzee
91	5	6.2	48	2	Q87376_SIVCZ	Q87376 chimpanzee
92	5	6.2	48	2	Q87400_SIVCZ	Q87400 chimpanzee
93	5	6.2	48	2	Q87403_SIVCZ	Q87403 chimpanzee
94	5	6.2	48	2	Q87406_SIVCZ	Q87406 chimpanzee
95	5	6.2	48	2	Q87412_SIVCZ	Q87412 chimpanzee
96	5	6.2	48	2	Q87415_SIVCZ	Q87415 chimpanzee
97	5	6.2	48	2	Q87421_SIVCZ	Q87421 chimpanzee
98	5	6.2	49	2	Q5BXX4_SCHJA	Q5bxx4 schistosoma
99	5	6.2	49	2	O52865_BACTU	O52865 bacillus th
100	5	6.2	49	2	Q9R169_STRCO	Q9r169 streptomyce
101	5	6.2	49	2	Q4RDS5_TETNG	Q4rds5 tetraodon n
102	5	6.2	49	2	Q87388_SIVCZ	Q87388 chimpanzee
103	5	6.2	49	2	Q87390_SIVCZ	Q87390 chimpanzee
104	5	6.2	49	2	Q87390_SIVCZ	Q87390 chimpanzee

105	5	6.2	49	2	Q87418_SIVCZ	Q87418 chimpanzee	178	5	6.2	59	2	Q7UFE3_RHOBA	Q7ufe3 rhodopirell
106	5	6.2	50	1	VUUT_METJA	P81335 methanococc	179	5	6.2	59	2	Q39817_ENCV	Q39817 encephalomy
107	5	6.2	50	2	Q7RGH1_PLAYO	Q7tgh1 plasmodium	180	5	6.2	59	2	Q80Q55_9VIRU	Q80q55 sen virus.
108	5	6.2	50	2	Q4HKY1_CAMLA	Q4hky1 campylobact	181	5	6.2	59	2	Q90WQ4_9PERO	Q90wq4 paralabrax
109	5	6.2	50	2	Q88FV5_PSEPK	Q88fv5 pseudomonas	182	5	6.2	59	2	Q87394_SIVCZ	Q87394 chimpanzee
110	5	6.2	50	2	Q8XH86_CLOPE	Q8xh86 clostridium	183	5	6.2	59	2	Q4GZX9_9HIV1	Q4gzx9 human immun
111	5	6.2	50	2	Q8HJ54_RHILO	Q8hj54 rhizobium 1	184	5	6.2	59	2	Q4GZX8_9HIV1	Q4gzx8 human immun
112	5	6.2	51	2	Q9HBW4_HUMAN	Q9hbw4 homo sapien	185	5	6.2	60	2	Q94U13_OXYTR	Q94u13 oxytricha t
113	5	6.2	51	2	P96297_ALCEU	P96297 alcaligenes	186	5	6.2	60	2	Q8HWV2_DYMA	Q8hwv2 daubentonia
114	5	6.2	51	2	Q7U3X5_SYNXP	Q7u3x5 synechococc	187	5	6.2	60	2	Q5GTCL_WOLTR	Q5gtcl wolbachia s
115	5	6.2	51	2	Q7FP13_COREF	Q7fp13 corynebacte	188	5	6.2	60	2	Q81RQ0_BACAN	Q81rq0 bacillus an
116	5	6.2	51	2	Q8XMC1_CLOPE	Q8xmc1 clostridium	189	5	6.2	60	2	Q9ZC06_STRCO	Q9zc06 streptomyc
117	5	6.2	52	2	Q9S6X0_MYCBO	Q9s6x0 mycobacteri	190	5	6.2	60	2	Q4RDJ3_TETNG	Q4rdj3 tetracodon n
118	5	6.2	52	2	Q6SVF1_MANSM	Q6svf1 manheimia	191	5	6.2	60	2	Q87435_SIVCZ	Q87435 chimpanzee
119	5	6.2	52	2	Q8P062_LEPIN	Q8p062 leptospira	192	5	6.2	61	1	PPD1_BOVIN	P15396 bos taurus
120	5	6.2	52	2	Q31335_ALIMI	Q31335 alligator m	193	5	6.2	61	2	Q4X1X1_ASPFU	Q4x1x1 aspergillus
121	5	6.2	52	2	Q31337_ALIMI	Q31337 alligator m	194	5	6.2	61	2	Q5BZY6_SCHJA	Q5bzy6 schistosoma
122	5	6.2	53	2	Q33SD2_HUMAN	Q33sd2 homo sapien	195	5	6.2	61	2	Q9BPF9_CONTE	Q9bpf9 conus texti
123	5	6.2	53	2	Q54HU1_DICDI	Q54hu1 dictyosteli	196	5	6.2	61	2	Q6JDX0_9DIPT	Q6jdx0 cuterebra g
124	5	6.2	53	2	Q7RJH6_PLAYO	Q7rjh6 plasmodium	197	5	6.2	61	2	Q4KPE5_PSEFS	Q4kfe5 pseudomonas
125	5	6.2	53	2	Q4XSV2_PLACH	Q4xsv2 plasmodium	198	5	6.2	61	2	Q8CZ64_STRR6	Q8cz64 streptococc
126	5	6.2	53	2	Q4Z5L8_PLABE	Q4z5l8 plasmodium	199	5	6.2	61	2	Q8P1S7_STRP8	Q8p1s7 streptococc
127	5	6.2	53	2	Q30452_EQUAS	Q30452 equus asinu	200	5	6.2	61	2	Q75QV1_HRSV	Q75qv1 human respi
128	5	6.2	53	2	Q30469_HORSE	Q30469 equus cabal	201	5	6.2	61	2	Q8JL51_9CAUD	Q8jls1 virus phich
129	5	6.2	53	2	Q30472_HORSE	Q30472 equus cabal	202	5	6.2	61	2	Q4TFM4_TETNG	Q4tfm4 tetracodon n
130	5	6.2	53	2	Q30473_HORSE	Q30473 equus cabal	203	5	6.2	61	2	Q87352_SIVCZ	Q87352 chimpanzee
131	5	6.2	53	2	Q30474_HORSE	Q30474 equus cabal	204	5	6.2	61	2	Q87432_SIVCZ	Q87432 chimpanzee
132	5	6.2	53	2	Q30477_HORSE	Q30477 equus cabal	205	5	6.2	62	1	QX54A_CONMR	Q87432 chimpanzee
133	5	6.2	53	2	Q30478_HORSE	Q30478 equus cabal	206	5	6.2	62	2	Q54V25_DICDI	Q54v25 dictyosteli
134	5	6.2	53	2	Q30480_HORSE	Q30480 equus cabal	207	5	6.2	62	2	Q64995_9ERIC	Q64995 rhododendro
135	5	6.2	53	2	Q9BCX7_HORSE	Q9bcx7 equus cabal	208	5	6.2	62	2	Q64996_9ERIC	Q64996 gaultheria
136	5	6.2	53	2	Q6XQE3_9CAUD	Q6xqe3 enterobacte	209	5	6.2	62	2	Q6ZF43_ORYSA	Q6zfa3 gryza sativ
137	5	6.2	53	2	Q75ZBE_ECOLI	Q75zeb escherichia	210	5	6.2	62	2	Q8EIC2_STRAS	Q8eic2 streptococc
138	5	6.2	53	2	Q4LAI0_STAHH	Q4lai0 staphylococ	211	5	6.2	62	2	Q8R7E0_THETN	Q8r7e0 thermoanaer
139	5	6.2	53	2	Q81EHO_BACCR	Q81eho bacillus ce	212	5	6.2	62	2	Q6APL1_DESPS	Q6apl1 desulfotale
140	5	6.2	53	2	Q5RGF4_BRARE	Q5rgf4 brachydanio	213	5	6.2	63	1	CSRA_HA3IN	P44879 haemophilus
141	5	6.2	53	2	P88733_9HIV1	P88733 human immun	214	5	6.2	63	1	QX51_CONGL	Q9u629 conus glori
142	5	6.2	53	2	P88743_9HIV1	P88743 human immun	215	5	6.2	63	1	PER_MOOTH	P02023 moorella th
143	5	6.2	53	2	P88747_9HIV1	P88747 human immun	216	5	6.2	63	2	Q9BPG7_CONTE	Q9bpg7 conus texti
144	5	6.2	54	1	QX54B_CONMR	Q68ip5 conus marmo	217	5	6.2	63	2	Q9BPH0_CONTE	Q9bph0 conus texti
145	5	6.2	54	1	QX5B_CONVC	P69766 conus victo	218	5	6.2	63	2	Q4Z9J0_9VIRU	Q4z9j0 bacterioph
146	5	6.2	54	2	Q7R1E9_GIALA	Q7r1e9 giardia lam	219	5	6.2	63	2	Q6M799_CORGL	Q6m799 corynebacte
147	5	6.2	54	2	Q7RMS3_PLAYO	Q7rms3 plasmodium	220	5	6.2	63	2	Q938X2_CAMJE	Q938x2 campylobact
148	5	6.2	54	2	Q8LNPE_ORYSA	Q8lnpe oryza sativ	221	5	6.2	63	2	Q9EUM6_LISIV	Q9eum6 listeria in
149	5	6.2	55	2	Q4XUD5_PLACH	Q4xud5 plasmodium	222	5	6.2	63	2	Q9EUM0_LISIV	Q9eum0 listeria iv
150	5	6.2	55	2	Q56Z81_ARATH	Q56z81 arabidopsis	223	5	6.2	63	2	Q4QM87_HAB18	Q4qm87 haemophilus
151	5	6.2	55	2	Q83AY7_COXBU	Q83ay7 coxiella bu	224	5	6.2	64	1	QX51A_CONMR	Q6pn86 conus marmo
152	5	6.2	56	2	Q4YGT7_PLABE	Q4ygt7 plasmodium	225	5	6.2	64	1	QX53_CONMR	Q6pn83 conus marmo
153	5	6.2	56	2	Q69TP0_ORYSA	Q69tp0 oryza sativ	226	5	6.2	64	1	NINH_BP913	P69176 bacterioph
154	5	6.2	56	2	Q6GHE8_STAAR	Q6ghe8 staphylococ	227	5	6.2	64	1	NINH_BPH19	O48428 bacterioph
155	5	6.2	56	2	Q7ASW8_STAAR	Q7asw8 staphylococ	228	5	6.2	64	1	NINH_BPVT2	P69177 bacterioph
156	5	6.2	56	2	Q99U16_STAAM	Q99u16 staphylococ	229	5	6.2	64	2	Q777W6_9VIRU	Q777w6 bacterioph
157	5	6.2	57	2	O17546_CABEL	O17546 caenorhabdi	230	5	6.2	64	2	Q7Y277_9CAUD	Q7y277 phage phi 4
158	5	6.2	57	2	Q5DN40_9CAUD	Q5dn40 bacterioph	231	5	6.2	64	2	Q8X5E8_9VIRU	Q8x5e8 bacterioph
159	5	6.2	57	2	Q65J65_BACLD	Q65j65 bacillus li	232	5	6.2	64	2	Q937S6_YEREN	Q937s6 yersinia en
160	5	6.2	57	2	Q8K6T6_STRP3	Q8k6t6 streptococc	233	5	6.2	64	2	Q93MP6_CAMJE	Q93mp6 campylobact
161	5	6.2	57	2	Q4PR74_CASFI	Q4pr74 castor fibe	234	5	6.2	64	2	Q49384_MYCGE	Q49384 mycoplasma
162	5	6.2	57	2	Q4PR73_CASFI	Q4pr73 castor fibe	235	5	6.2	64	2	Q50FZ8_CAMJE	Q50fz8 campylobact
163	5	6.2	57	2	Q4PR71_CASFI	Q4pr71 castor fibe	236	5	6.2	64	2	Q7AKJ7_ECO57	Q7akj7 escherichia
164	5	6.2	57	2	Q4PR70_CASFI	Q4pr70 castor fibe	237	5	6.2	64	2	O4MJA5_BACCE	O4mja5 bacillus ce
165	5	6.2	57	2	Q4PR69_CASFI	Q4pr69 castor fibe	238	5	6.2	64	2	O4MUV2_BACCE	O4muv2 bacillus ce
166	5	6.2	57	2	Q4PR66_CASFI	Q4pr66 castor fibe	239	5	6.2	64	2	Q9EUV3_LISWE	Q9euv3 listeria we
167	5	6.2	57	2	Q6JKD3_9NUCL	Q6jkd3 neodiprion	240	5	6.2	64	2	Q650L5_BACFR	Q650l5 bacteroides
168	5	6.2	57	2	Q6US16_9CALL	Q6us16 norwalk-lik	241	5	6.2	64	2	Q8FIH8_LEPIN	Q8fih8 leptospira
169	5	6.2	58	1	AXPI_ANTAP	Q8jis1 anthopleura	242	5	6.2	64	2	O6N4V1_RHOPA	O6n4v1 rhodopseu
170	5	6.2	58	2	Q8GIT8_SYN7P	Q8git8 synechococc	243	5	6.2	64	2	O82LX8_STRAW	O82lx8 streptomyc
171	5	6.2	58	2	Q5NY78_AZOSE	Q5ny78 azoarcus sp	244	5	6.2	65	1	AMYL_LACAM	P80696 lactobacill
172	5	6.2	58	2	Q7USR3_RHOBA	Q7use3 rhodopirell	245	5	6.2	65	1	QX51B_CONMR	Q6pn85 conus marmo
173	5	6.2	58	2	Q87382_SIVCZ	Q87382 chimpanzee	246	5	6.2	65	1	SAS3_EACME	Q8pn85 bacillus me
174	5	6.2	59	1	VXIS_EPL54	P20710 bacterioph	247	5	6.2	65	2	Q6TYT5_ORYSA	Q6tyt5 oryza sativ
175	5	6.2	59	2	Q4ZB09_9VIRU	Q4zb09 bacterioph	248	5	6.2	65	2	Q8LLD2_SCUBA	Q8lld2 scutellaria
176	5	6.2	59	2	Q4ZBP0_9VIRU	Q4zbp0 bacterioph	249	5	6.2	65	2	Q7BRU8_BACME	Q7bru8 bacillus me
177	5	6.2	59	2	Q4ZDJ6_9VIRU	Q4zdj6 bacterioph	250	5	6.2	65	2	Q5GRX8_WOLTR	Q5grx8 wolbachia s

251	5	6.2	65	2	Q5XCUS_STRP6	Q5xcu5 streptococc	324	5	6.2	68	2	Q8ATQ9_9HIV1	Q8atq9 human immun
252	5	6.2	65	2	Q9A0F2_STRPY	Q9a0f2 streptococc	325	5	6.2	68	2	Q8ATRO_9HIV1	Q8atro human immun
253	5	6.2	65	2	Q5L2L4_STRT1	Q5l2l4 streptococc	326	5	6.2	68	2	Q8ATRI_9HIV1	Q8atri human immun
254	5	6.2	65	2	Q5M467_STRT2	Q5m467 streptococc	327	5	6.2	68	2	Q8ATR2_9HIV1	Q8atr2 human immun
255	5	6.2	65	2	Q5NGL6_FTRAT	Q5ngl6 francisella	328	5	6.2	68	2	Q8ATR6_9HIV1	Q8atr6 human immun
256	5	6.2	65	2	Q7NUH6_GLOVI	Q7njh6 gloebacter	329	5	6.2	68	2	Q8ATR7_9HIV1	Q8atr7 human immun
257	5	6.2	65	2	Q8NSJ8_CORGL	Q8nsj8 corynebacte	330	5	6.2	68	2	Q8ATR9_9HIV1	Q8atr9 human immun
258	5	6.2	65	2	Q7CFP3_STRP3	Q7cfp3 streptococc	331	5	6.2	68	2	Q8ATS2_9HIV1	Q8ats2 human immun
259	5	6.2	65	2	Q7CNC6_STRP8	Q7cnc6 streptococc	332	5	6.2	68	2	Q8QEH7_9HIV1	Q8qeh7 human immun
260	5	6.2	65	2	Q8DYT6_STRAS	Q8dyt6 streptococc	333	5	6.2	68	2	Q8QEH8_9HIV1	Q8qeh8 human immun
261	5	6.2	65	2	Q8E4E4_STRAS	Q8e4e4 streptococc	334	5	6.2	68	2	Q8QEH9_9HIV1	Q8qeh9 human immun
262	5	6.2	65	2	Q80212_MOUSE	Q80212 mus musculu	335	5	6.2	68	2	Q8QEI0_9HIV1	Q8qei0 human immun
263	5	6.2	65	2	Q6XD88_9REOV	Q6xd88 human rotav	336	5	6.2	68	2	Q8QEI1_9HIV1	Q8qei1 human immun
264	5	6.2	65	2	Q9MMJ1_9EMBB	Q9mmj1 geospiza co	337	5	6.2	68	2	Q8QEI8_9HIV1	Q8qei8 human immun
265	5	6.2	65	2	Q9MMJ7_9EMBB	Q9mmj7 geospiza co	338	5	6.2	68	2	Q8QEI9_9HIV1	Q8qei9 human immun
266	5	6.2	66	1	CX52_CONMR	Q6pu84 conus marmo	339	5	6.2	69	1	SEML_ASHGO	P62499 ashbya goss
267	5	6.2	66	1	RL35_BRAJA	Q89wh9 bradyrhizob	340	5	6.2	69	1	YFXX_AZOCA	P26486 azornisoboli
268	5	6.2	66	1	RL35_CAUCR	Q9a9e2 caulobacter	341	5	6.2	69	2	Q95ZG8_DICDI	Q95z98 dictyostelli
269	5	6.2	66	1	RL35_RHOPA	Q6ndr5 rhodopseudo	342	5	6.2	69	2	Q4YRL2_PLABE	Q4yrl2 plasmodium
270	5	6.2	66	1	Q54B11_DICDI	Q54b11 dictyosteli	343	5	6.2	69	2	Q4Z755_PLABE	Q4z755 plasmodium
271	5	6.2	66	2	Q5F6D5_NEIG1	Q5f6d5 neisseria g	344	5	6.2	69	2	Q93YL6_BRANA	Q93yl6 brassica na
272	5	6.2	66	2	Q5F7Q0_NEIG1	Q5f7q0 neisseria g	345	5	6.2	69	2	Q9LZ32_ARATH	Q9l322 arabidopsis
273	5	6.2	66	2	Q5P8C4_NEIG1	Q5p8c4 neisseria g	346	5	6.2	69	2	Q4TSC3_9SPHN	Q4tsc3 erythrobact
274	5	6.2	66	2	Q5F8H6_EHRHG	Q5fh68 ehrlichia r	347	5	6.2	69	2	Q5P5W6_AZOSE	Q5p5w6 azoarcus sp
275	5	6.2	66	2	Q8PLS3_STRP3	Q8pls3 streptococc	348	5	6.2	69	2	Q72UT4_LEPIC	Q72ut4 leptospira
276	5	6.2	66	2	Q5XB43_SILPO	Q5xb43 silicibacte	349	5	6.2	69	2	Q8OSG0_9PICO	Q8osg0 human rhino
277	5	6.2	66	2	Q99Y22_STRPY	Q99y22 streptococc	350	5	6.2	69	2	Q8OSG2_9PICO	Q8osg2 human rhino
278	5	6.2	66	2	Q7CNE4_STRP8	Q7cnev4 streptococc	351	5	6.2	69	2	Q8OSG4_9PICO	Q8osg4 human rhino
279	5	6.2	66	2	Q5PEV4_ANAMM	Q5pev4 anaplasm m	352	5	6.2	69	2	Q8OSG6_9PICO	Q8osg6 human rhino
280	5	6.2	66	2	Q5HC38_EHRRW	Q5hc38 ehrlichia r	353	5	6.2	69	2	Q8OSH0_9PICO	Q8osh0 human rhino
281	5	6.2	66	2	Q52KL6_MOUSE	Q52kl6 mus musculu	354	5	6.2	69	2	Q8OSH1_9PICO	Q8osh1 human rhino
282	5	6.2	66	2	Q4SBW7_TETNG	Q4sbw7 tetraodon n	355	5	6.2	69	2	Q8OSH4_9PICO	Q8osh4 human rhino
283	5	6.2	66	2	RL35_RICPR	Q9zcv1 rickettsia	356	5	6.2	69	2	Q8OSH7_9PICO	Q8osh7 human rhino
284	5	6.2	67	1	RL35_WOLPM	Q4xm94 plasmodium	357	5	6.2	69	2	Q8OSH8_9PICO	Q8osh8 human rhino
285	5	6.2	67	2	Q4XM94_PLACH	Q8snq8 propithecus	358	5	6.2	69	2	Q8OSI2_9PICO	Q8osi2 human rhino
286	5	6.2	67	2	Q8SNQ8_PROVE	Q5cbp4 thermotoga	359	5	6.2	69	2	Q8OSI3_9PICO	Q8osi3 human rhino
287	5	6.2	67	2	Q5CBP4_9THEM	Q4vip8 bacillus ce	360	5	6.2	69	2	Q8OSI4_9PICO	Q8osi4 human rhino
288	5	6.2	67	2	Q4V1P8_BACCZ	Q4r2t6 hydrogenoba	361	5	6.2	69	2	Q8OSI5_9PICO	Q8osi5 human rhino
289	5	6.2	67	2	Q4R2T6_HYDTH	Q4nxb4 anaeronyxob	362	5	6.2	69	2	Q8OSI6_9PICO	Q8osi6 human rhino
290	5	6.2	67	2	Q4NKB4_9DELT	Q8lxb1 bacillus ce	363	5	6.2	69	2	Q8OSJ2_9PICO	Q8osj2 human rhino
291	5	6.2	67	2	Q8LXB1_BACCR	Q5nmc0 zymomonas m	364	5	6.2	69	2	Q8OSJ5_9PICO	Q8osj5 human rhino
292	5	6.2	67	2	Q5NNC0_ZYMMO	Q9qej0 human immun	365	5	6.2	69	2	Q8OSJ6_9PICO	Q8osj6 human rhino
293	5	6.2	67	2	Q9QEI0_9HIV1	P01094 saccharomyc	366	5	6.2	69	2	Q8OSJ7_9PICO	Q8osj7 human rhino
294	5	6.2	68	1	IPA3_YEAST	Q92h38 rickettsia	367	5	6.2	69	2	Q8OSJ8_9PICO	Q8osj8 human rhino
295	5	6.2	68	1	RL35_RICCN	Q73gr8 wolbachia p	368	5	6.2	69	2	Q8OSJ9_9PICO	Q8osj9 human rhino
296	5	6.2	68	1	RL35_WOLPM	P17l04 haubacteri	369	5	6.2	69	2	Q8OSK0_9PICO	Q8osk0 human rhino
297	5	6.2	68	1	Y1110_HALSA	Q973k1 sulfolobus	370	5	6.2	69	2	Q8OSK1_9PICO	Q8osk1 human rhino
298	5	6.2	68	2	Q973K1_SULTO	Q95304 homo sapien	371	5	6.2	69	2	Q8OSK2_9PICO	Q8osk2 human rhino
299	5	6.2	68	2	Q95304_HUMAN	Q5xyv4 borrelia ga	372	5	6.2	69	2	Q8OSK3_9PICO	Q8osk3 human rhino
300	5	6.2	68	2	Q5XYZ4_BORGA	Q6shm8 uncultured	373	5	6.2	69	2	Q8OSK4_9PICO	Q8osk4 human rhino
301	5	6.2	68	2	Q6SHM8_9BACT	Q7p970 rickettsia	374	5	6.2	69	2	Q8OSK5_9PICO	Q8osk5 human rhino
302	5	6.2	68	2	Q7P970_RICSI	Q4umk7 rickettsia	375	5	6.2	69	2	Q8OSK9_9PICO	Q8osk9 human rhino
303	5	6.2	68	2	Q4UMK7_RICFE	Q4fnh7 candidatus	376	5	6.2	69	2	Q8OSL0_9PICO	Q8osl0 human rhino
304	5	6.2	68	2	Q4FNH7_RICCK	Q73f41 bacillus ce	377	5	6.2	69	2	Q8OSL2_9PICO	Q8osl2 human rhino
305	5	6.2	68	2	Q73F41_BACC1	Q73f42 bacillus ce	378	5	6.2	69	2	Q8OSL5_9PICO	Q8osl5 human rhino
306	5	6.2	68	2	Q73F42_BACC1	Q9zmt2 helicobacte	379	5	6.2	69	2	Q8OSL6_9PICO	Q8osl6 human rhino
307	5	6.2	68	2	Q9ZMT2_HELPJ	Q8lqal bacillus an	380	5	6.2	69	2	Q8OSL8_9PICO	Q8osl8 human rhino
308	5	6.2	68	2	Q8LQAL_BACAN	Q6no26 rhodopseudo	381	5	6.2	69	2	Q8OSL9_9PICO	Q8osl9 human rhino
309	5	6.2	68	2	Q6NO26_RHOPA	Q68wd1 rickettsia	382	5	6.2	69	2	Q8OSM0_9PICO	Q8osm0 human rhino
310	5	6.2	68	2	Q68WD1_RICTY	Q8v0q2 papaya mosa	383	5	6.2	69	2	Q8OSM1_9PICO	Q8osm1 human rhino
311	5	6.2	68	2	Q8V0Q2_PMV	Q8v0q5 papaya mosa	384	5	6.2	69	2	Q8OSM3_9PICO	Q8osm3 human rhino
312	5	6.2	68	2	Q8V0Q5_PMV	Q8atp5 human immun	385	5	6.2	69	2	Q8OSM5_9PICO	Q8osm5 human rhino
313	5	6.2	68	2	Q8ATP5_9HIV1	Q8atp6 human immun	386	5	6.2	69	2	Q8OSM7_9PICO	Q8osm7 human rhino
314	5	6.2	68	2	Q8ATP6_9HIV1	Q8atp7 human immun	387	5	6.2	69	2	Q8OSM9_9PICO	Q8osm9 human rhino
315	5	6.2	68	2	Q8ATP7_9HIV1	Q8atq1 human immun	388	5	6.2	69	2	Q8OSN0_9PICO	Q8osn0 human rhino
316	5	6.2	68	2	Q8ATP9_9HIV1	Q8atq2 human immun	389	5	6.2	69	2	Q8OSN4_9PICO	Q8osn4 human rhino
317	5	6.2	68	2	Q8ATQ0_9HIV1	Q8atq3 human immun	390	5	6.2	69	2	Q8OSN5_9PICO	Q8osn5 human rhino
318	5	6.2	68	2	Q8ATQ1_9HIV1	Q8atq5 human immun	391	5	6.2	69	2	Q8OSN7_9PICO	Q8osn7 human rhino
319	5	6.2	68	2	Q8ATQ2_9HIV1	Q8atq7 human immun	392	5	6.2	69	2	Q8OSPO_9PICO	Q8osp0 human rhino
320	5	6.2	68	2	Q8ATQ3_9HIV1		393	5	6.2	69	2		
321	5	6.2	68	2	Q8ATQ4_9HIV1		394	5	6.2	69	2		
322	5	6.2	68	2	Q8ATQ5_9HIV1		395	5	6.2	69	2		
323	5	6.2	68	2	Q8ATQ7_9HIV1		396	5	6.2	69	2		



397	5	6.2	69	2	Q80SP1_9PICO	Q80sp1 human rhino
398	5	6.2	69	2	Q80SP3_HRV16	Q80sp3 human rhino
399	5	6.2	69	2	Q80SPA_9PICO	Q80sp4 human rhino
400	5	6.2	69	2	Q80SP5_9PICO	Q80sp5 human rhino
401	5	6.2	69	2	Q80SP7_9PICO	Q80sp7 human rhino
402	5	6.2	69	2	Q80SP8_9PICO	Q80sp8 human rhino
403	5	6.2	69	2	Q80SP9_9PICO	Q80sp9 human rhino
404	5	6.2	69	2	Q80SQ1_9PICO	Q80sq1 human rhino
405	5	6.2	69	2	Q80SQ6_HRV2	Q80sq6 human rhino
406	5	6.2	69	2	Q80SQ7_HRV1A	Q80sq7 human rhino
407	5	6.2	69	2	Q80JYL7_9REOV	Q80jyl7 bovine rota
408	5	6.2	69	2	Q8QMH4_9ENTO	Q8qmh4 human coxsa
409	5	6.2	70	2	Q8NKU7_ACIAM	Q8nku7 acidianus a
410	5	6.2	70	2	Q8UWV4_HALMA	Q8uwv4 haloarcula
411	5	6.2	70	2	Q8S8N7_9CAUD	Q8s8n7 lactococcus
412	5	6.2	70	2	Q80165_9SCCE	Q80165 secale cere
413	5	6.2	70	2	Q94KK3_LOLPR	Q94kk3 lolium pere
414	5	6.2	70	2	Q9F654_ECOLI	Q9f654 escherichia
415	5	6.2	70	2	Q4HB47_9DEIO	Q4hb47 deinococcus
416	5	6.2	70	2	Q8A758_BACTN	Q8a758 bacteroides
417	5	6.2	70	2	Q8RE06_FUSNN	Q8re06 fusobacteri
418	5	6.2	70	2	Q80XV5_9MURI	Q80xv5 rattus sp.
419	5	6.2	71	2	Q8TZV7_PYRFU	Q8tzv7 pyrococcus
420	5	6.2	71	2	Q68YW3_LEPMC	Q68yw3 leptospaer
421	5	6.2	71	2	Q80146_9CAUD	Q80146 bacterioph
422	5	6.2	71	2	Q9PDH9_XYLFA	Q9pdh9 xylella fas
423	5	6.2	71	2	Q6G9S6_STAAS	Q6g9s6 staphylococ
424	5	6.2	71	2	Q7P197_CHRVO	Q7p197 chromobacte
425	5	6.2	71	2	Q8HGE4_STAAC	Q8hge4 staphylococ
426	5	6.2	71	2	Q8NMY2_STAAN	Q8nmy2 staphylococ
427	5	6.2	71	2	Q9WK37_EMCV	Q9wk37 encephalomy
428	5	6.2	71	2	Q9VPL9_EMCV	Q9vpl9 encephalomy
429	5	6.2	71	2	Q9YPS3_9HIV1	Q9yps3 human immun
430	5	6.2	71	2	Q1P554_9HIV1	Q9yp54 human immun
431	5	6.2	72	1	X358_MANSN	Q65vp5 mantheimia
432	5	6.2	72	2	Q4YFM4_PLABE	Q4yfm4 plasmodium
433	5	6.2	72	2	Q6A211_GORBE	Q6a211 gorilla gor
434	5	6.2	72	2	Q6A215_GORBE	Q6a215 gorilla gor
435	5	6.2	72	2	Q6A216_GORBE	Q6a216 gorilla gor
436	5	6.2	72	2	Q6A218_GORGO	Q6a218 gorilla gor
437	5	6.2	72	2	Q6A219_GORGO	Q6a219 gorilla gor
438	5	6.2	72	2	Q76FP0_CANFA	Q76fp0 canis famli
439	5	6.2	72	2	Q6X3F8_PSEAE	Q6x3f8 pseudomonas
440	5	6.2	72	2	Q4L5A4_STAHTJ	Q4l5a4 staphylococ
441	5	6.2	72	2	Q88VB0_LACPL	Q88vb0 lactobacill
442	5	6.2	72	2	Q74L22_LACJO	Q74l22 lactobacill
443	5	6.2	72	2	Q5HQ79_STAEO	Q5hq79 staphylococ
444	5	6.2	72	2	Q8CT15_STAEP	Q8ct15 staphylococ
445	5	6.2	73	2	Q56H83_9EUC	Q56h83 farfantepen
446	5	6.2	73	2	Q56H84_9EUC	Q56h84 farfantepen
447	5	6.2	73	2	Q58LL3_9CAUD	Q58ll3 cyanophage
448	5	6.2	73	2	Q6K3N0_ORYSA	Q6k3n0 oryza sativ
449	5	6.2	73	2	Q72CU5_DESVH	Q72cu5 desulfovibr
450	5	6.2	73	2	Q9YPL4_EMCV	Q9ypl4 encephalomy
451	5	6.2	73	2	Q9YPL6_EMCV	Q9ypl6 encephalomy
452	5	6.2	73	2	Q4S123_TETNG	Q4s123 tetraodon n
453	5	6.2	73	2	Q85464_9RETR	Q85464 avian sarco
454	5	6.2	74	2	Q8ZMG6_PYRAE	Q8zwg6 pyrobaculum
455	5	6.2	74	2	Q8ZZW1_PYRAE	Q8zzw1 pyrobaculum
456	5	6.2	74	2	Q6TLS0_DROME	Q6tls0 drosophila
457	5	6.2	74	2	Q4X551_PLACH	Q4x551 plasmodium
458	5	6.2	74	2	Q6LE72_SALTY	Q6le72 salmonella
459	5	6.2	74	2	Q4UZ19_XANCP	Q4uz19 xanthomonas
460	5	6.2	74	2	Q831J4_ENTFA	Q831j4 enterococcu
461	5	6.2	74	2	Q8P512_XANCP	Q8p512 xanthomonas
462	5	6.2	74	2	Q77AU0_EMCV	Q77au0 encephalomy
463	5	6.2	74	2	Q9W8B2_EMCV	Q9w8b2 encephalomy
464	5	6.2	75	1	TRAY3_ECOLI	P05835 escherichia
465	5	6.2	75	2	Q552L0_DICDI	Q552l0 dictyosteli
466	5	6.2	75	2	Q5ZCF4_ORYSA	Q5zcf4 oryza sativ
467	5	6.2	75	2	O05554_LEGPN	O05554 legionella
468	5	6.2	75	2	Q74WA0_YERPE	Q74wa0 yersinia pe
469	5	6.2	75	2	Q6SJ27_ECOLI	Q6sj27 escherichia

470	5	6.2	75	2	Q57BT4_BRUAB	Q57bt4 brucella ab
471	5	6.2	75	2	Q72P13_LEPIC	Q72p13 leptospira
472	5	6.2	75	2	Q8FZA3_BRUSU	Q8fza3 brucella su
473	5	6.2	75	2	Q8YIL3_BRUME	Q8yil3 brucella me
474	5	6.2	75	2	Q7AK74_922Z2	Q7ak74 plasmid r10
475	5	6.2	75	2	Q5Y1H1_9HEPC	Q5y1h1 hepatitis c
476	5	6.2	75	2	Q8JM20_9NUCL	Q8jm20 mamestra co
477	5	6.2	75	2	Q9WK35_EMCV	Q9wk35 encephalomy
478	5	6.2	75	2	Q9YFX2_EMCV	Q9ypx2 porcine enc
479	5	6.2	76	1	PIA1_PLEOS	Q7m4t6 pleurotus o
480	5	6.2	76	1	PIA2_PLEOS	Q7m4t5 pleurotus o
481	5	6.2	76	2	Q28492_ARCFU	O28492 archaeoglob
482	5	6.2	76	2	Q46813_EQUAS	O46813 equus asinu
483	5	6.2	76	2	Q46815_EQUAS	O46815 equus asinu
484	5	6.2	76	2	Q7Y3W1_9CAUD	Q7y3w1 bacterioph
485	5	6.2	76	2	Q8HAA4_9CAUD	Q8haa4 salmonella
486	5	6.2	76	2	Q69SR5_ORYSA	Q69sr5 oryza sativ
487	5	6.2	76	2	Q6Z4F9_ORYSA	Q6z4f9 oryza sativ
488	5	6.2	76	2	Q761Z1_ORYSA	Q761z1 oryza sativ
489	5	6.2	76	2	Q9S953_MESCR	O9s953 mesembryant
490	5	6.2	76	2	Q87892_NEIME	O87892 neisseria m
491	5	6.2	76	2	Q7P3X3_FUSNV	Q7p3x3 fusobacteri
492	5	6.2	76	2	Q9CKJ0_PASMU	Q9ckj0 pasteurella
493	5	6.2	76	2	Q8AKB9_DESPS	Q8akb9 desulfotale
494	5	6.2	76	2	Q8JX76_9VIRU	Q8jx76 sen virus.
495	5	6.2	76	2	Q4T4C9_TETNG	Q4t4c9 tetraodon n
496	5	6.2	77	2	Q8W1M3_SOLCH	Q8w1m3 solanum cha
497	5	6.2	77	2	Q6ZUM1_BACLD	Q6zum1 bacillus li
498	5	6.2	77	2	Q97LU9_CIOAB	Q97lu9 clostridium
499	5	6.2	77	2	Q8G2J6_BRUSU	Q8g2j6 brucella su
500	5	6.2	77	2	Q8QTI3_9INFA	Q8qti3 influenza a
501	5	6.2	77	2	Q8QTI4_9INFA	Q8qti4 influenza a
502	5	6.2	77	2	Q4T544_TETNG	Q4t544 tetraodon n
503	5	6.2	78	1	RR16_ADICA	Q85fn9 adiantum ca
504	5	6.2	78	1	Y022_CHICV	Q824w6 chlamydophi
505	5	6.2	78	1	Y720_CHLPN	Q927i5 chlamydia p
506	5	6.2	78	2	Q9V2K5_PVRAB	Q9v2k5 pyrococcus
507	5	6.2	78	2	Q8ND26_HUMAN	Q8nd26 homo sapien
508	5	6.2	78	2	Q7RAS0_PLAYO	Q7ras0 plasmodium
509	5	6.2	78	2	Q5NVK9_PONFY	Q5nvk9 pongo pygma
510	5	6.2	78	2	Q6W3R0_ACIJB	Q6w3r0 acinonyx ju
511	5	6.2	78	2	Q66T53_GOSHI	Q66t53 gossypium h
512	5	6.2	78	2	Q7P9U1_RICSI	Q7p9u1 rickettsia
513	5	6.2	78	2	Q5L788_CHLAB	Q5l788 chlamydophi
514	5	6.2	78	2	Q88VY2_RICTY	Q88vy2 rickettsia
515	5	6.2	79	1	Y1306_LISMO	P67288 listeria mo
516	5	6.2	79	1	Y1324_LISMF	Q720b5 listeria mo
517	5	6.2	79	1	Y1344_LISIN	P67289 listeria in
518	5	6.2	79	2	Q7S8A7_NEUCR	Q7s8a7 neurospora
519	5	6.2	79	2	Q81F84_PLAFA	Q81fr4 plasmodium
520	5	6.2	79	2	Q8BP73_9CAEN	Q8bp73 conus tessu
521	5	6.2	79	2	Q4XHV5_PLACH	Q4xhv5 plasmodium
522	5	6.2	79	2	Q30465_HORSE	Q30465 equus cabal
523	5	6.2	79	2	Q80833_ARATH	O80833 arabidopsis
524	5	6.2	79	2	Q8H365_ORYSA	O8h365 oryza sativ
525	5	6.2	79	2	Q81883_ARATH	O81883 arabidopsis
526	5	6.2	79	2	P77080_ECOLI	P77060 escherichia
527	5	6.2	79	2	Q9AIU5_ZOORA	Q9aius zoogloeas ra
528	5	6.2	79	2	Q34958_BACSU	O34958 bacillus su
529	5	6.2	79	2	Q9WZ91_THEME	Q9wz91 thermotoga
530	5	6.2	79	2	Q7NZN4_CHRVO	Q7nzn4 chromobacte
531	5	6.2	79	2	Q65K03_BACLD	Q65k03 bacillus li
532	5	6.2	79	2	Q8CER2_MOUSE	Q8cer2 mus musculu
533	5	6.2	79	2	Q8V3G9_SWPV	Q8v3g9 swinepox vi
534	5	6.2	80	2	Q95575_HUMAN	Q95575 homo sapien
535	5	6.2	80	2	Q54SB2_DICDI	Q54sb2 dictyosteli
536	5	6.2	80	2	Q85J60_ANTGR	O85j60 antonomus
537	5	6.2	80	2	Q76FN9_CANFA	Q76fn9 canis famli
538	5	6.2	80	2	Q4FLJ6_RICK	Q4flj6 candidatus
539	5	6.2	80	2	Q9RZA2_DEIRA	Q9rza2 deinococcus
540	5	6.2	80	2	Q5LYA7_STRT1	Q5lya7 streptococc
541	5	6.2	80	2	Q9YPL2_EMCV	Q9ypl2 encephalomy
542	5	6.2	80	2	Q801C6_LATME	Q801c6 latimeria m



543	4	5.0	9	1	CB22_SPIOL	Q9t2k9 spinacia ol	616	4	5.0	19	2	Q01057_KLULA	Q01057 kluyveromy
544	4	5.0	2	Q7M2N7_BOSIN	Q7m2n7 bos indicus	617	4	5.0	19	2	Q81VK8_HUMAN	Q81vk8 homo sapien	
545	4	5.0	9	P82568_STRPY	P82568 streptococc	618	4	5.0	19	2	Q9UC73_HUMAN	Q9uc73 homo sapien	
546	4	5.0	11	QDA1P_SARBU	P83518 sarcophaga	619	4	5.0	19	2	Q9UKU5_HUMAN	Q9ukus homo sapien	
547	4	5.0	11	Q6LC30_FASHE	Q61c30 fasciola he	620	4	5.0	19	2	Q8TAJ9_HUMAN	Q8taj9 homo sapien	
548	4	5.0	11	Q91UY9_9ZZZZ	Q91uy9 transposon	621	4	5.0	19	2	Q26321_LYNST	Q26321 lynnaea sta	
549	4	5.0	12	Q015_BACSU	P80863 bacillus su	622	4	5.0	19	2	Q5SBS5_SCHJA	Q5sbes schistosoma	
550	4	5.0	12	Q5KSP0_SYMFO	Q5ksp0 symlocarpu	623	4	5.0	19	2	Q9QV38_9MURI	Q9qv38 mus sp. erp	
551	4	5.0	13	Q6WPN0_ARATH	Q6wpn0 arabidopsis	624	4	5.0	19	2	Q9PRG2_SALSA	Q9prg2 salmo majo	
552	4	5.0	13	RS19_ASHYP	Q44592 ash yellowa	625	4	5.0	20	1	CHY3_PAGMA	P83547 pagrus majo	
553	4	5.0	13	Q50038_MYCLE	Q50038 mycobacteri	626	4	5.0	20	1	CRP_MUSCA	P19094 mustelus ca	
554	4	5.0	13	Q6RSM3_COXBU	Q6rsm3 coxiella bu	627	4	5.0	20	1	DAH51_LITDA	P84267 litoria dah	
555	4	5.0	13	Q6LCB1_RAT	Q6lcb1 rattus norv	628	4	5.0	20	1	NF03_NAEFO	P83998 naegleria f	
556	4	5.0	14	HLPI_HYLFU	P84292 hyla puncta	629	4	5.0	20	2	Q7SAL6_NEUCR	Q7sali6 neurospora	
557	4	5.0	14	MAST_VESMA	P04205 vespa manda	630	4	5.0	20	2	Q7M4Q0_HUMAN	Q7m4q0 homo sapien	
558	4	5.0	14	MAST_VESOR	P17238 vespa orien	631	4	5.0	20	2	Q9UCA0_HUMAN	Q9uca0 homo sapien	
559	4	5.0	14	Q5BR70_SCHJA	Q5br70 schistosoma	632	4	5.0	20	2	Q96B47_HUMAN	Q96b47 homo sapien	
560	4	5.0	14	Q8HYM2_FELCA	Q8hym2 felis silve	633	4	5.0	20	2	Q96B47_HUMAN	Q96b47 homo sapien	
561	4	5.0	14	Q56ZE8_ARATH	Q56ze8 arabidopsis	634	4	5.0	20	2	Q4XKU0_PLACH	Q4xku0 plasmodium	
562	4	5.0	14	Q52638_ECOLI	Q52638 escherichia	635	4	5.0	20	2	Q4YCL5_PLABE	Q4ycl5 plasmodium	
563	4	5.0	14	Q52636_9ZZZZ	Q52636 plasmid r12	636	4	5.0	20	2	Q4Z2C1_PLABE	Q4z2c1 plasmodium	
564	4	5.0	14	Q661E1_BORGA	Q661e1 borrelia ga	637	4	5.0	20	2	Q95MJ7_TARSY	Q95mj7 tarsius syr	
565	4	5.0	14	Q6LDY1_9ZZZZ	Q6ldy1 plasmid r38	638	4	5.0	20	2	Q95MJ8_GALMO	Q95mj8 galago moho	
566	4	5.0	14	Q6LEH6_9ZZZZ	Q6leh6 plasmid r53	639	4	5.0	20	2	Q95MK3_ATEBE	Q95mk3 ateles belz	
567	4	5.0	14	Q6LEH7_9ZZZZ	Q6leh7 plasmid r10	640	4	5.0	20	2	Q95MK4_CHEMA	Q95mk4 cheirogaleu	
568	4	5.0	14	Q6LEH8_9ZZZZ	Q6leh8 plasmid col	641	4	5.0	20	2	Q95MK5_VARVR	Q95mk5 varecia var	
569	4	5.0	14	Q6LEH9_9ZZZZ	Q6leh9 plasmid col	642	4	5.0	20	2	Q95MK6_EULCO	Q95mk6 eulemur cor	
570	4	5.0	14	Q6LEI0_9ZZZZ	Q6lei0 plasmid col	643	4	5.0	20	2	Q5IGY2_9CAUD	Q5igy2 bacterioph	
571	4	5.0	14	Q56127_9CIRC	Q56127 porcine cir	644	4	5.0	20	2	Q9R4Y5_HELPY	Q9r4y5 helicobacte	
572	4	5.0	14	Q93202_9CIRC	Q93202 porcine cir	645	4	5.0	20	2	Q9PSI4_ORCKI	Q9psi4 oncorhynch	
573	4	5.0	14	Q77NR3_9CIRC	Q77nr3 porcine cir	646	4	5.0	21	1	DAH52_LITDA	P84268 litoria dah	
574	4	5.0	14	Q77RC0_9CIRC	Q77rc0 porcine cir	647	4	5.0	21	1	MCPT3_MOUSE	P21843 mus musculu	
575	4	5.0	14	Q77RM6_9CIRC	Q77rm6 porcine cir	648	4	5.0	21	2	Q9UWH7_9CREN	Q9uwh7 sulfolobus.	
576	4	5.0	14	Q77S02_9CIRC	Q77s02 porcine cir	649	4	5.0	21	2	Q7JPS8_LYNST	Q7jps8 lymanaea sta	
577	4	5.0	14	Q77S09_9CIRC	Q77s09 porcine cir	650	4	5.0	21	2	Q7R9Y0_PLAYO	Q7r9y0 plasmodium	
578	4	5.0	14	Q77S13_9CIRC	Q77s13 porcine cir	651	4	5.0	21	2	Q4XLR2_PLACH	Q4xlr2 plasmodium	
579	4	5.0	15	Q7SBM4_NEUCR	Q7sbm4 neurospora	652	4	5.0	21	2	Q4YCP3_PLABE	Q4ycp3 plasmodium	
580	4	5.0	15	Q9UR90_YEAST	Q9ur90 saccharomyc	653	4	5.0	21	2	Q8HYM1_FELCA	Q8hym1 felis silve	
581	4	5.0	15	Q5K6Q7_CRAGI	Q5k6q7 crassostrea	654	4	5.0	21	2	Q8N4X2_HUMAN	Q8n4x2 homo sapien	
582	4	5.0	15	Q6LDF5_TRICO	Q6ldf5 trichosteon	655	4	5.0	22	2	Q9BZM9_HUMAN	Q9bzm9 homo sapien	
583	4	5.0	15	Q7M319_META	Q7m319 macropus sp	656	4	5.0	22	2	Q5BY01_SCHJA	Q5by01 schistosoma	
584	4	5.0	15	Q52304_9ZZZZ	Q52304 plasmid r1-	657	4	5.0	22	2	Q9NFG2_PLAFA	Q9nfg2 plasmodium	
585	4	5.0	15	Q80X05_MESAU	Q80x05 mesocricetu	658	4	5.0	22	2	Q7RLB6_PLAYO	Q7rlb6 plasmodium	
586	4	5.0	15	Q79ED5_9ZZZZ	Q79ed5 plasmid r12	659	4	5.0	22	2	Q7RMV4_PLAYO	Q7rmv4 plasmodium	
587	4	5.0	15	Q9PTM6_POEGU	Q9ptm6 poephilla gu	660	4	5.0	22	2	Q4XI70_PLACH	Q4xi70 plasmodium	
588	4	5.0	16	Q5B8M1_EMENI	Q5b8m1 aspergillus	661	4	5.0	22	2	Q4XS26_PLACH	Q4xs26 plasmodium	
589	4	5.0	16	Q9URB8_YEAST	Q9urb8 saccharomyc	662	4	5.0	22	2	Q4YG66_PLABE	Q4yg66 plasmodium	
590	4	5.0	16	Q9TRA2_PIG	Q9tra2 sus scrofa	663	4	5.0	22	2	P82162_SPIOL	P82162 spinacia ol	
591	4	5.0	16	P82161_SPIOL	P82161 spinacia ol	664	4	5.0	22	2	Q34195_EHRII	Q34195 ehrlichia r	
592	4	5.0	16	Q6RSJ3_COXBU	Q6rsj3 coxiella bu	665	4	5.0	22	2	Q9ZG44_CHLTR	Q9zga4 chlamydia t	
593	4	5.0	16	Q9RSK1_PSEPU	Q9rsk1 pseudomonas	666	4	5.0	22	2	Q9QV15_9MURI	Q9qv15 mus sp. . syn	
594	4	5.0	16	Q6LXB8_PSEAE	Q6lxb8 pseudomonas	667	4	5.0	22	2	Q9QW14_9MURI	Q9qw14 mus sp. . p	
595	4	5.0	16	Q9PRY2_PETMA	Q9pry2 petromyzon	668	4	5.0	23	1	ACHG_ELEEL	P09692 electrophor	
596	4	5.0	17	UN15_CLOPA	P81354 clostridium	669	4	5.0	23	1	AUR41_LITAU	P82397 litoria aur	
597	4	5.0	17	Q9GZT7_HUMAN	Q9gz77 homo sapien	670	4	5.0	23	1	AUR42_LITAU	P69025 litoria aur	
598	4	5.0	17	Q9UD18_HUMAN	Q9ud18 homo sapien	671	4	5.0	23	1	PS3_PSEPD	P69024 litoria ran	
599	4	5.0	17	Q6LER4_HUMAN	Q6ler4 homo sapien	672	4	5.0	23	1	PS4_PSEPD	P8190 pseudis par	
600	4	5.0	17	P90402_9HIV1	P90402 human immun	673	4	5.0	23	1	PS4_PSEPD	P83191 pseudis par	
601	4	5.0	17	Q8UT86_9HIV1	Q8ut86 human immun	674	4	5.0	23	2	Q5DVF3_9CREN	Q5dvf3 sulfolobus	
602	4	5.0	17	Q9Q709_9HIV1	Q9q709 human immun	675	4	5.0	23	2	Q8N5P5_HUMAN	Q8n5p5 homo sapien	
603	4	5.0	18	Q69Y10_HUMAN	Q69y10 homo sapien	676	4	5.0	23	2	Q7RJKO_PLAYO	Q7rjko plasmodium	
604	4	5.0	18	Q9UET8_HUMAN	Q9uet8 homo sapien	677	4	5.0	23	2	Q7RLB8_PLAYO	Q7rlb8 plasmodium	
605	4	5.0	18	Q6RSD8_9DIPT	Q6rsd8 chironomus	678	4	5.0	23	2	Q4XNB0_PLACH	Q4xnb0 plasmodium	
606	4	5.0	18	Q4TZV7_PAPHA	Q4tzv7 papio hamad	679	4	5.0	23	2	Q4XY15_PLACH	Q4xy15 plasmodium	
607	4	5.0	18	Q9X3N3_NEIME	Q9x3n3 neisseria m	680	4	5.0	23	2	Q4Y655_PLACH	Q4y655 plasmodium	
608	4	5.0	18	P95811_STRPY	P95811 streptococc	681	4	5.0	23	2	Q4Y686_PLACH	Q4y686 plasmodium	
609	4	5.0	18	P97166_STRPY	P97166 streptococc	682	4	5.0	23	2	Q4YGG2_PLABE	Q4ygg2 plasmodium	
610	4	5.0	18	Q81CS8_BACCR	Q81cs8 bacillus ce	683	4	5.0	23	2	Q4YIN7_PLABE	Q4yin7 plasmodium	
611	4	5.0	18	Q9DSS9_ADE04	Q9das9 human adeno	684	4	5.0	23	2	Q9S8D9_MAIZE	Q9s8d9 zea mays (m	
612	4	5.0	19	H170_RAT	P21794 rattus norv	685	4	5.0	23	2	Q9R410_BORPE	Q9r410 bordetella	
613	4	5.0	19	NF37_NAEFO	P83727 naegleria f	686	4	5.0	23	2	Q9R5T0_TREDE	Q9r5t0 treponema d	
614	4	5.0	19	UKA1_HUMAN	P31940 homo sapien	687	4	5.0	23	2	Q43887_ANAAZ	Q43887 anabaena az	
615	4	5.0	19	Q9UWJ8_ARCFU	Q9uwj8 archaeoglob	688	4	5.0	23	2	Q61DX6_9PTCO	Q61dx6 human rhino	

689	4	5.0	24	1	CT31_LITCI	P81851	litoria cit	762	4	5.0	27	2	Q9Q193_9HEPC	Q9q193	hepatitis c
690	4	5.0	24	1	IR31_HAEIN	P35756	haemophilus	763	4	5.0	27	2	Q9Q194_9HEPC	Q9q194	hepatitis c
691	4	5.0	24	2	Q6QN8_9CNID	Q6qn8	anthopleura	764	4	5.0	27	2	Q9Q195_9HEPC	Q9q195	hepatitis c
692	4	5.0	24	2	Q4X15_PLACH	Q4x15	plasmodium	765	4	5.0	27	2	Q9Q196_9HEPC	Q9q196	hepatitis c
693	4	5.0	24	2	Q4XC56_PLACH	Q4xc56	plasmodium	766	4	5.0	27	2	Q9Q197_9HEPC	Q9q197	hepatitis c
694	4	5.0	24	2	Q4YMI4_PLACH	Q4ym14	plasmodium	767	4	5.0	27	2	Q9Q198_9HEPC	Q9q198	hepatitis c
695	4	5.0	24	2	Q4THA3_TETNG	Q4tha3	tetraodon n	768	4	5.0	27	2	Q9Q199_9HEPC	Q9q199	hepatitis c
696	4	5.0	24	1	CHY1_PAGNA	P83545	pagrus majo	769	4	5.0	27	2	Q9Q1A0_9HEPC	Q9q1A0	hepatitis c
697	4	5.0	25	1	CH12_PAGNA	P83546	pagrus majo	770	4	5.0	27	2	Q9Q1A1_9HEPC	Q9q1A1	hepatitis c
698	4	5.0	25	2	Q9UWQ3_SULSO	Q9uwq3	sulfolobus	771	4	5.0	27	2	Q9Q1A2_9HEPC	Q9q1A2	hepatitis c
699	4	5.0	25	2	Q9BQJ6_HUMAN	Q9bqj6	homo sapien	772	4	5.0	27	2	Q9Q1A3_9HEPC	Q9q1A3	hepatitis c
700	4	5.0	25	2	Q5C4Z9_SCHJA	Q5c4z9	schistosoma	773	4	5.0	27	2	Q9Q1A4_9HEPC	Q9q1A4	hepatitis c
701	4	5.0	25	2	Q9BM60_9BILA	Q9bm60	sagitta sp.	774	4	5.0	27	2	Q9Q1A5_9HEPC	Q9q1A5	hepatitis c
702	4	5.0	25	2	Q4XK95_PLACH	Q4xk95	plasmodium	775	4	5.0	27	2	Q9Q1A6_9HEPC	Q9q1A6	hepatitis c
703	4	5.0	25	2	Q7M3G0_BOVIN	Q7m3g0	bos taurus	776	4	5.0	27	2	Q9Q1A7_9HEPC	Q9q1A7	hepatitis c
704	4	5.0	25	2	Q9LSWT_ARATH	Q9lsw1	arabidopsis	777	4	5.0	27	2	Q9Q1A8_9HEPC	Q9q1A8	hepatitis c
705	4	5.0	25	2	Q9K2K4_STAAR	Q9k2k4	staphylococ	778	4	5.0	27	2	Q9Q1A9_9HEPC	Q9q1A9	hepatitis c
706	4	5.0	25	2	Q9X9U4_STRCO	Q9x9u4	streptomyce	779	4	5.0	27	2	Q91KU2_9HEPC	Q91ku2	hepatitis c
707	4	5.0	25	2	Q4LA85_STAAR	Q4la85	staphylococ	780	4	5.0	27	2	Q91L83_9HEPC	Q91l83	hepatitis c
708	4	5.0	25	2	Q6RVE7_MESAU	Q6rve7	mesocricetu	781	4	5.0	27	2	Q91L84_9HEPC	Q91l84	hepatitis c
709	4	5.0	25	2	Q9QUZ2_9MURI	Q9quz2	mus sp. . 5	782	4	5.0	27	2	Q91L85_9HEPC	Q91l85	hepatitis c
710	4	5.0	25	2	Q69474_HHV1	Q69474	human herpe	783	4	5.0	27	2	Q91L86_9HEPC	Q91l86	hepatitis c
711	4	5.0	25	2	Q9PSB0_XENBO	Q9psb0	xenopus bor	784	4	5.0	27	2	Q91L87_9HEPC	Q91l87	hepatitis c
712	4	5.0	25	2	Q58Q30_9HIV1	Q58q30	human immun	785	4	5.0	27	2	Q91L88_9HEPC	Q91l88	hepatitis c
713	4	5.0	25	2	Q58Q37_9HIV1	Q58q37	human immun	786	4	5.0	27	2	Q91L89_9HEPC	Q91l89	hepatitis c
714	4	5.0	25	2	Q58Q68_9HIV1	Q58q68	human immun	787	4	5.0	27	2	Q91L90_9HEPC	Q91l90	hepatitis c
715	4	5.0	25	2	Q58Q98_9HIV1	Q58q98	human immun	788	4	5.0	27	2	Q91L91_9HEPC	Q91l91	hepatitis c
716	4	5.0	25	2	Q58QA5_9HIV1	Q58qa5	human immun	789	4	5.0	27	2	Q91L92_9HEPC	Q91l92	hepatitis c
717	4	5.0	25	2	Q9WRF2_9HIV1	Q9wrf2	human immun	790	4	5.0	27	2	Q91L93_9HEPC	Q91l93	hepatitis c
718	4	5.0	26	1	ARALB_ARABL	P83573	aralia elat	791	4	5.0	27	2	Q91L94_9HEPC	Q91l94	hepatitis c
719	4	5.0	26	1	STP_BFLZ3	P62766	bacterioph	792	4	5.0	27	2	Q91L95_9HEPC	Q91l95	hepatitis c
720	4	5.0	26	1	STP_BFLZ5	P62767	bacterioph	793	4	5.0	27	2	Q91L96_9HEPC	Q91l96	hepatitis c
721	4	5.0	26	1	STP_BPT4	P62765	bacterioph	794	4	5.0	27	2	Q91L97_9HEPC	Q91l97	hepatitis c
722	4	5.0	26	1	X507_HELPY	P64662	helicobacte	795	4	5.0	27	2	Q91L98_9HEPC	Q91l98	hepatitis c
723	4	5.0	26	1	Y560_HELPY	P64661	helicobacte	796	4	5.0	27	2	Q91L99_9HEPC	Q91l99	hepatitis c
724	4	5.0	26	1	YFHA_KLEOX	P21710	klebsiella	797	4	5.0	27	2	Q91LA0_9HEPC	Q91la0	hepatitis c
725	4	5.0	26	2	Q9UW7_SULSO	Q9uw7	sulfolobus	798	4	5.0	27	2	Q91LA1_9HEPC	Q91la1	hepatitis c
726	4	5.0	26	2	Q50833_METVA	Q50835	methanococc	799	4	5.0	27	2	Q91LA2_9HEPC	Q91la2	hepatitis c
727	4	5.0	26	2	Q68K4_DROMR	Q68k4	drosophila	800	4	5.0	27	2	Q91LA3_9HEPC	Q91la3	hepatitis c
728	4	5.0	26	2	Q4XE15_PLACH	Q4xe15	plasmodium	801	4	5.0	27	2	Q91LC3_9HEPC	Q91lc3	hepatitis c
729	4	5.0	26	2	Q4XQ31_PLACH	Q4xq31	plasmodium	802	4	5.0	27	2	Q91LD2_9HEPC	Q91ld2	hepatitis c
730	4	5.0	26	2	Q4YE51_PLACH	Q4ye51	plasmodium	803	4	5.0	27	2	Q91LE2_9HEPC	Q91le2	hepatitis c
731	4	5.0	26	2	Q8HYW8_BOVIN	Q8hyw8	bos taurus	804	4	5.0	27	2	Q9J5U8_9HEPC	Q9j5u8	hepatitis c
732	4	5.0	26	2	Q38084_9CAUD	Q38084	bacterioph	805	4	5.0	27	2	Q9J5U9_9HEPC	Q9j5u9	hepatitis c
733	4	5.0	26	2	Q56289_THIFE	Q56289	thiobacillu	806	4	5.0	27	2	Q9J5V0_9HEPC	Q9j5v0	hepatitis c
734	4	5.0	26	2	Q6V7G4_VIBCH	Q6v7g4	vibrio chol	807	4	5.0	27	2	Q9J5V1_9HEPC	Q9j5v1	hepatitis c
735	4	5.0	26	2	Q8VVF8_STRSU	Q8vvf8	streptococc	808	4	5.0	27	2	Q9J5V2_9HEPC	Q9j5v2	hepatitis c
736	4	5.0	26	2	Q64FW9_9VIRU	Q64fw9	cauliflower	809	4	5.0	27	2	Q9QHK3_9HEPC	Q9qhk3	hepatitis c
737	4	5.0	26	2	Q13159_CHICK	Q13159	gallus gall	810	4	5.0	27	2	Q9QHK4_9HEPC	Q9qhk4	hepatitis c
738	4	5.0	26	2	Q8UVE1_CHICK	Q8uve1	gallus gall	811	4	5.0	27	2	Q9QHK5_9HEPC	Q9qhk5	hepatitis c
739	4	5.0	26	2	Q9PSB3_XENLA	Q9psb3	xenopus lae	812	4	5.0	27	2	Q9QHK7_9HEPC	Q9qhk7	hepatitis c
740	4	5.0	26	2	Q4PU49_9HIV1	Q4pu49	human immun	813	4	5.0	27	2	Q9QHK8_9HEPC	Q9qhk8	hepatitis c
741	4	5.0	26	2	Q4PU54_9HIV1	Q4pu54	human immun	814	4	5.0	27	2	Q9QHK9_9HEPC	Q9qhk9	hepatitis c
742	4	5.0	26	2	Q4PU59_9HIV1	Q4pu59	human immun	815	4	5.0	27	2	Q9QHL0_9HEPC	Q9qhl0	hepatitis c
743	4	5.0	27	1	R82CB_FANCL	P82879	rana clamit	816	4	5.0	27	2	Q9QHL1_9HEPC	Q9qhl1	hepatitis c
744	4	5.0	27	2	Q8YTK0_CHRQI	Q8ytk4	chrysosora q	817	4	5.0	27	2	Q9QHL2_9HEPC	Q9qhl2	hepatitis c
745	4	5.0	27	2	Q4Y2T0_PLACH	Q4y2t0	plasmodium	818	4	5.0	27	2	Q9QHL5_9HEPC	Q9qhl5	hepatitis c
746	4	5.0	27	2	Q4YE00_PLACH	Q4ye00	plasmodium	819	4	5.0	27	2	Q9QHL7_9HEPC	Q9qhl7	hepatitis c
747	4	5.0	27	2	Q4YVK2_PLACH	Q4yvk2	plasmodium	820	4	5.0	27	2	Q9QHL8_9HEPC	Q9qhl8	hepatitis c
748	4	5.0	27	2	Q46119_CAMJE	Q46119	campylobact	821	4	5.0	27	2	Q9QHL9_9HEPC	Q9qhl9	hepatitis c
749	4	5.0	27	2	Q4NGE1_BACCE	Q4nge1	bacillus ce	822	4	5.0	27	2	Q9QHM0_9HEPC	Q9qhm0	hepatitis c
750	4	5.0	27	2	Q9QVS1_9MURI	Q9qvs1	mus sp. . 1	823	4	5.0	27	2	Q9QHM1_9HEPC	Q9qhm1	hepatitis c
751	4	5.0	27	2	O57153_9BETA	O57153	human herpe	824	4	5.0	27	2	Q9QHM2_9HEPC	Q9qhm2	hepatitis c
752	4	5.0	27	2	O57154_9BETA	O57154	human herpe	825	4	5.0	27	2	Q9QI33_9HEPC	Q9qi33	hepatitis c
753	4	5.0	27	2	Q6SXX2_9HEPC	Q6sxx2	hepatitis c	826	4	5.0	27	2	Q9QI37_9HEPC	Q9qi37	hepatitis c
754	4	5.0	27	2	Q9QHC2_9HEPC	Q9qhc2	hepatitis c	827	4	5.0	27	2	Q9QI38_9HEPC	Q9qi38	hepatitis c
755	4	5.0	27	2	Q9QHC5_9HEPC	Q9qhc5	hepatitis c	828	4	5.0	27	2	Q9QI39_9HEPC	Q9qi39	hepatitis c
756	4	5.0	27	2	Q9QHC9_9HEPC	Q9qhc9	hepatitis c	829	4	5.0	27	2	Q9QI40_9HEPC	Q9qi40	hepatitis c
757	4	5.0	27	2	Q9QHC9_9HEPC	Q9qhc9	hepatitis c	830	4	5.0	27	2	Q9QI42_9HEPC	Q9qi42	hepatitis c
758	4	5.0	27	2	Q9QHD4_9HEPC	Q9qhd4	hepatitis c	831	4	5.0	27	2	Q9QI43_9HEPC	Q9qi43	hepatitis c
759	4	5.0	27	2	Q9QI46_9HEPC	Q9qi46	hepatitis c	832	4	5.0	27	2	Q9QI45_9HEPC	Q9qi45	hepatitis c
760	4	5.0	27	2	Q9Q191_9HEPC	Q9q191	hepatitis c	833	4	5.0	27	2	Q9Q149_9HEPC	Q9qi49	hepatitis c
761	4	5.0	27	2	Q9Q192_9HEPC	Q9q192	hepatitis c	834	4	5.0	27	2	Q9Q150_9HEPC	Q9qi50	hepatitis c

835	4	5.0	27	2	Q4TX84_9HEPC	Q4tx84 hepatitis c	908	4	5.0	30	2	Q7M241_ORYSA	Q7m241 oryza sativ
836	4	5.0	27	2	Q4TX85_9HEPC	Q4tx85 hepatitis c	909	4	5.0	30	2	Q8QP81_STRTK	Q8qp81 streptococc
837	4	5.0	27	2	Q4TX86_9HEPC	Q4tx86 hepatitis c	910	4	5.0	30	2	Q4LB43_ECOLI	Q4lb43 escherichia
838	4	5.0	27	2	Q4TX88_9HEPC	Q4tx88 hepatitis c	911	4	5.0	30	2	Q4MUK5_BACCE	Q4muk5 bacillus ce
839	4	5.0	27	2	Q4TX90_9HEPC	Q4tx90 hepatitis c	912	4	5.0	30	2	Q4HI47_CAMCO	Q4hi47 campylobact
840	4	5.0	27	2	Q4TX93_9HEPC	Q4tx93 hepatitis c	913	4	5.0	30	2	Q4JVV9_CORJK	Q4jvv9 corynebacte
841	4	5.0	27	2	Q4TX95_9HEPC	Q4tx95 hepatitis c	914	4	5.0	30	2	Q7MVC5_PORGI	Q7mvc5 porphyromon
842	4	5.0	27	2	Q4TX98_9HEPC	Q4tx98 hepatitis c	915	4	5.0	30	2	Q8EJP3_SHEON	Q8ejp3 shewanella
843	4	5.0	27	2	Q4TX99_9HEPC	Q4tx99 hepatitis c	916	4	5.0	30	2	Q9PPG5_CAMJE	Q9ppg5 campylobact
844	4	5.0	27	2	Q4TXA1_9HEPC	Q4txa1 hepatitis c	917	4	5.0	30	2	Q83B13_COXBU	Q83b13 coxiella bu
845	4	5.0	27	2	Q4TXA2_9HEPC	Q4txa2 hepatitis c	918	4	5.0	30	2	Q8HIF8_STAAC	Q8hif8 staphylococ
846	4	5.0	27	2	Q71608_CHICK	Q73608 gallus gall	919	4	5.0	30	2	Q9JL14_RHILO	Q9jl14 rhizobium l
847	4	5.0	27	2	Q4SQF1_TETNG	Q4sqf1 tetraodon n	920	4	5.0	30	2	Q9JXT7_NEIMB	Q9jxt7 neisseria m
848	4	5.0	28	1	LECA_IRIHO	P25513 iris hollan	921	4	5.0	30	2	Q7M031_RAT	Q7m031 rattus norv
849	4	5.0	28	1	ORDN_PLAOR	P25513 placobdella	922	4	5.0	30	2	Q88549_MSAU	Q88549 mesocricetu
850	4	5.0	28	2	Q26318_LYMST	Q26318 lymnaea sta	923	4	5.0	30	2	Q96630_ADEB2	Q96630 bovine aden
851	4	5.0	28	2	Q26319_LYMST	Q26319 lymnaea sta	924	4	5.0	30	2	Q8QFV5_LAMFL	Q8qfv5 lampetra fl
852	4	5.0	28	2	Q27356_LYMST	Q27356 lymnaea sta	925	4	5.0	31	1	CTRP_PENMO	Q35002 penaeus mon
853	4	5.0	28	2	Q5C2P0_SCHJA	Q4xv8 schistosoma	926	4	5.0	31	1	PETL_PORPU	P51221 porphyra pu
854	4	5.0	28	2	Q4XV8_PLACH	Q4xv8 schistosoma	927	4	5.0	31	2	Q9USG3_SCHPO	Q9usg3 schizosacch
855	4	5.0	28	2	Q4YXV8_PLACH	Q4yc14 plasmodium	928	4	5.0	31	2	Q9BZZ6_HUMAN	Q9bzz6 homo sapien
856	4	5.0	28	2	Q4YXV8_PLACH	Q4yc14 plasmodium	929	4	5.0	31	2	Q5BZR3_SCHJA	Q5bzz3 schistosoma
857	4	5.0	28	2	Q4YXA7_PLABE	Q4yya7 plasmodium	930	4	5.0	31	2	Q7RPU7_PLAYO	Q7rpu7 plasmodium
858	4	5.0	28	2	Q7RFX0_IPONI	Q75rx0 ipomoea nil	931	4	5.0	31	2	Q4XGX2_PLACH	Q4xgx2 plasmodium
859	4	5.0	28	2	Q7RFX0_IPONI	Q75rx0 ipomoea nil	932	4	5.0	31	2	Q53411_BACSU	Q53411 bacillus su
860	4	5.0	28	2	Q9XK42_9STRA	Q9xk42 aureococcus	933	4	5.0	31	2	Q57CN6_BRUAB	Q57cn6 bruceella ab
861	4	5.0	28	2	Q47565_ECOLI	Q47565 escherichia	934	4	5.0	31	2	Q4L3L7_STAHL	Q4l3l7 staphylococ
862	4	5.0	28	2	Q9R5E6_THEAQ	Q9r5e6 thermus aqu	935	4	5.0	31	2	Q8DTU2_STRMU	Q8dtu2 streptococc
863	4	5.0	28	2	Q9R5E6_THEAQ	Q9r5e6 thermus aqu	936	4	5.0	31	2	Q9KST7_VIBCH	Q9kzt7 vibrio chol
864	4	5.0	28	2	Q8OKG6_9RHAB	Q8okg6 rabies viru	937	4	5.0	31	2	Q6MK47_BDEBA	Q6mk47 bdellovibri
865	4	5.0	28	2	Q8OKK0_9RHAB	Q8okk0 rabies viru	938	4	5.0	31	2	Q87IO9_VIBPA	Q87io9 vibrio para
866	4	5.0	28	2	Q9QCD4_ADE02	Q9qcd4 human adeno	939	4	5.0	31	2	Q8G058_BRUSU	Q8g058 bruceella su
867	4	5.0	28	2	Q9QCD5_9ADEN	Q9qcd5 human adeno	940	4	5.0	31	2	Q9CMC7_9MURI	Q9cmc7 rattus sp.
868	4	5.0	28	2	Q9QCD6_9ADEN	Q9qcd6 human adeno	941	4	5.0	31	2	Q9CKD9_MOUSE	Q9ckd9 mus musculu
869	4	5.0	28	2	Q9QCD7_9ADEN	Q9qcd7 human adeno	942	4	5.0	31	2	Q84108_IANT6	Q84108 influenza a
870	4	5.0	28	2	Q9QCD8_ADE08	Q9qcd8 human adeno	943	4	5.0	31	2	Q91AA4_CHICK	Q91aa4 gallus gall
871	4	5.0	28	2	Q9QD08_9RHAB	Q9qcd8 rabies viru	944	4	5.0	31	2	Q85512_9RETR	Q85512 avian eryth
872	4	5.0	28	2	Q9QC15_9HEPC	Q9qc15 hepatitis c	945	4	5.0	32	2	Q7M553_HALMA	Q7m553 haloacteri
873	4	5.0	28	2	Q9YXK8_9VIRU	Q9yxk8 acute bee p	946	4	5.0	32	2	Q5UMX3_HALMA	Q5umx3 haloarcula
874	4	5.0	29	1	NUO1_SOLTU	P80267 solanum tub	947	4	5.0	32	2	Q8TGT3_YEAST	Q8tgt3 saccharomyc
875	4	5.0	29	1	PSB1_SYNVU	P12240 synechococc	948	4	5.0	32	2	Q96S24_HUMAN	Q96s24 homo sapien
876	4	5.0	29	1	PSHDQ3_CANRU	Q9hdq3 candida rug	949	4	5.0	32	2	Q5BRP2_SCHJA	Q5brp2 schistosoma
877	4	5.0	29	2	Q69YR8_HUMAN	Q69yr8 homo sapien	950	4	5.0	32	2	Q4X4Q6_PLACH	Q4x4q6 plasmodium
878	4	5.0	29	2	Q53SD1_HUMAN	Q53sd1 homo sapien	951	4	5.0	32	2	Q4XF05_PLACH	Q4xf05 plasmodium
879	4	5.0	29	2	Q4X6D1_PLACH	Q4x6d1 plasmodium	952	4	5.0	32	2	Q4XHI2_PLACH	Q4xhi2 plasmodium
880	4	5.0	29	2	Q4YFJ4_PLABE	Q4yfj4 plasmodium	953	4	5.0	32	2	Q4Y2Q0_PLACH	Q4y2q0 plasmodium
881	4	5.0	29	2	Q4YJ20_PLABE	Q4yj20 plasmodium	954	4	5.0	32	2	Q4YGI2_PLABE	Q4ygi2 plasmodium
882	4	5.0	29	2	Q4YU46_PLABE	Q4yu46 plasmodium	955	4	5.0	32	2	Q4YUS2_PLABE	Q4yus2 plasmodium
883	4	5.0	29	2	Q7OPH1_PIG	Q7oph1 sus scrofa	956	4	5.0	32	2	Q6J9M8_XENNE	Q6j9m8 xenorhabdus
884	4	5.0	29	2	Q9R658_RHOCA	Q9r658 rhodobacter	957	4	5.0	32	2	Q7M016_CIOSY	Q7m016 clostridium
885	4	5.0	29	2	Q9IQJ6_9HIV1	Q9iqj6 human immun	958	4	5.0	32	2	Q7M018_FIRM	Q7m018 veillonella
886	4	5.0	30	1	2ENR_CLOTY	P11887 clostridium	959	4	5.0	32	2	Q9K261_CHLNP	Q9k261 chlamydia p
887	4	5.0	30	1	CXZA_CONBE	P58625 conus betul	960	4	5.0	32	2	Q9R5J6_MYCTU	Q9r5j6 mycobacteri
888	4	5.0	30	1	PSAM_MESVI	Q9mus2 mesostigma	961	4	5.0	32	2	Q57MB8_SALCH	Q57mb8 salmonella
889	4	5.0	30	1	UPB61_UPEIN	P82037 uperoleia i	962	4	5.0	32	2	Q4MFR9_BACCE	Q4mfr9 bacillus ce
890	4	5.0	30	1	UPB62_UPEIN	P82037 uperoleia i	963	4	5.0	32	2	Q4MFR1_BACCE	Q4mfr1 bacillus ce
891	4	5.0	30	2	P78460_HUMAN	P78460 homo sapien	964	4	5.0	32	2	Q4HMX1_CAMLA	Q4hmx1 campylobact
892	4	5.0	30	2	Q26320_LYMST	Q26320 lymnaea sta	965	4	5.0	32	2	Q4MPO8_BACCE	Q4mpo8 bacillus ce
893	4	5.0	30	2	Q5BR16_SCHJA	Q5br16 schistosoma	966	4	5.0	32	2	Q5PE29_SALPA	Q5pe29 salmonella
894	4	5.0	30	2	Q5C004_SCHJA	Q5c004 schistosoma	967	4	5.0	32	2	Q65WI3_MANSM	Q65wi3 manheimia
895	4	5.0	30	2	Q5CAU1_SCHJA	Q5cau1 schistosoma	968	4	5.0	32	2	Q73EA3_BACCI	Q73ea3 bacillus ce
896	4	5.0	30	2	Q7R4B5_GIALA	Q7r4b5 giardia lam	969	4	5.0	32	2	Q73FJ9_BACCI	Q73fj9 bacillus ce
897	4	5.0	30	2	Q8IHP0_PLAF7	Q8ihp0 plasmodium	970	4	5.0	32	2	Q8Z582_SALTI	Q8z582 salmonella
898	4	5.0	30	2	Q7RF34_PLAYO	Q7rf34 plasmodium	971	4	5.0	32	2	Q7NT4_STRPN	Q7nt4 streptococc
899	4	5.0	30	2	Q7RIM6_PLAYO	Q7rim6 plasmodium	972	4	5.0	32	2	Q8IR94_BACAN	Q8ir94 bacillus an
900	4	5.0	30	2	Q4XE18_PLACH	Q4xe18 plasmodium	973	4	5.0	32	2	Q83CC7_COXBU	Q83cc7 coxiella bu
901	4	5.0	30	2	Q4XJP6_PLACH	Q4xjp6 plasmodium	974	4	5.0	32	2	Q7VIX4_HELHP	Q7vix4 helicobacte
902	4	5.0	30	2	Q4XVC7_PLACH	Q4xvc7 plasmodium	975	4	5.0	32	2	Q5HQO6_STAQO	Q5hqo6 staphylococ
903	4	5.0	30	2	Q4XXW6_PLACH	Q4xxw6 plasmodium	976	4	5.0	32	2	Q81JD8_BACAN	Q81jd8 bacillus an
904	4	5.0	30	2	Q4Y299_PLACH	Q4y299 plasmodium	977	4	5.0	32	2	Q73F54_BACCI	Q73f54 bacillus ce
905	4	5.0	30	2	Q4Y489_PLACH	Q4y489 plasmodium	978	4	5.0	32	2	Q80WZ8_9MURI	Q80wz8 met sp. met
906	4	5.0	30	2	Q4YJY1_PLABE	Q4yjy1 plasmodium	979	4	5.0	32	2	Q9QWB2_9MURI	Q9qwb2 rattus sp.
907	4	5.0	30	2	Q5ULW3_9CAUD	Q5ulw3 lactobacill	980	4	5.0	32	2	Q9IWC2_9PAPI	Q9iwc2 phocoena sp

981 4 5.0 32 2 Q502D3 BRARE  
 982 4 5.0 32 2 Q4REX4 TEING  
 983 4 5.0 32 2 Q4SUK1 TETNG  
 984 4 5.0 33 2 Q13375 HUMAN  
 985 4 5.0 33 2 Q9UDT0 HUMAN  
 986 4 5.0 33 2 Q4G105 HUMAN  
 987 4 5.0 33 2 Q9NGN0 STRPU  
 988 4 5.0 33 2 Q4XEP6 PLACH  
 989 4 5.0 33 2 Q4XTB8 PLACH  
 990 4 5.0 33 2 Q9TSW9 CANFA  
 991 4 5.0 33 2 Q29066 PIG  
 992 4 5.0 33 2 Q8H9P9 9CAUD  
 993 4 5.0 33 2 Q5XZ94 BORGA  
 994 4 5.0 33 2 Q711Z4 LACDL  
 995 4 5.0 33 2 Q65SM8 MANSM  
 996 4 5.0 33 2 Q6MNH5 BDEBA  
 997 4 5.0 33 2 Q88AE8 PSESM  
 998 4 5.0 33 2 Q9Z298 RAT  
 999 4 5.0 33 2 Q7M0E6 RAT  
 1000 4 5.0 33 2 Q6EAW6 9CALI

## ALIGNMENTS

RESULT 1  
 Q4XUQ5 PLACH PRELIMINARY; PRT; 29 AA.

AC Q4XUQ5;  
 DT 13-SEP-2005 (TRENBLrel. 31, Created)  
 DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 GN ORFNames=PC105993.00.0;  
 OS Plasmodium chabaudi.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=5825;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,  
 RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,  
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,  
 RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,  
 RA Bidwell S.I., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,  
 RA Janse C.J., Barrall B., Turner C.M.R., Waters A.P., Sinden R.S.;  
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,  
 RT transcriptomic, and proteomic analyses.";  
 RL Science 307:82-86(2005).  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; CAJ01003007; CAH79356.1; -; Genomic\_DNA.  
 KW Hypothetical protein.  
 FT NON TER 1  
 SQ SEQUENCE 29 AA; 3541 MW; A386F2C2D29442CC CRC64;

Query Match 8.8%; Score 7; DB 2; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 18;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 YNKLTK 23  
 |||||  
 Db 2 YNKLTK 8

RESULT 2  
 PLAS MICAE STANDARD; PRT; 15 AA.  
 AC P10625;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-JUL-1989 (Rel. 11, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Plastocyanin (Fragment).

GN Name=pEtE;  
 OS Microcystis aeruginosa.  
 OC Bacteria; Cyanobacteria; Chroococcales; Microcystis.  
 OX NCBI\_TaxID=1126;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=89134784; PubMed=2537099;  
 RA Tan S., Ho K.-K.;  
 RT "Purification of an acidic plastocyanin from Microcystis aeruginosa.";  
 RL Biochim. Biophys. Acta 973:111-117(1989).  
 CC -!- FUNCTION: Participates in electron transfer between P700 and the  
 CC cytochrome b6-f complex in photosystem I.  
 CC -!- SIMILARITY: Contains 1 plastocyanin-like domain.  
 CC -----  
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 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC PIR; S03353; S03353.  
 DR HAMAP; MF 00566; -; 1.  
 DR InterPro; IPR000923; BlueCu 1.  
 DR PROSITE; PS00196; COPPER\_BLUE; PARTIAL.  
 KW Copper; Direct protein sequencing; Electron transport; Metal-binding;  
 KW Transport.  
 FT NON TER 15  
 SQ SEQUENCE 15 AA; 1555 MW; 32B6D4662F44F969 CRC64;

Query Match 7.5%; Score 6; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 EFTTVK 67  
 |||||  
 Db 1 EFTTVK 6

## RESULT 3

Q93Y77 ATREBE PRELIMINARY; PRT; 37 AA.  
 AC Q93Y77;  
 DT 01-DEC-2001 (TRENBLrel. 19, Created)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
 DE Putative multicystatin (Fragment).  
 OS Atropa belladonna (Belladonna) (Deadly nightshade).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 OC asterids; lamiales; Solanales; Solanaceae; Atropa.  
 OX NCBI\_TaxID=33113;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Nouar B.;  
 RL Thesis (2001), Department of Plant Biotechnology, Universite Libre de  
 RL Bruxelles, Brussels, Belgium.  
 RL [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Nouar B., Baucher M., Jaziri M.;  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ309374; CAC40744.1; -; mRNA.  
 DR HSRF; P09229; IBOK.  
 DR GO; GO:0004869; F:cysteine protease inhibitor activity; IEA.  
 DR InterPro; IPR003243; Prot\_inh\_I25A\_B.  
 DR ProDom; PD001231; Prot\_inh\_I25A\_B; 1.  
 FT NON TER 1  
 SQ SEQUENCE 37 AA; 4403 MW; 37285565D81A4284 CRC64;

Query Match 7.5%; Score 6; DB 2; Length 37;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KEVQEF 12

```
Db      23 KEVQEF 28
|||||
RESULT 4
O53412 BACSU
ID Q53412_BACSU PRELIMINARY; PRT; 42 AA.
AC Q53412;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Clone pS77 product protein (Fragment).
GN Name-clone pS77 product;
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94271615; PubMed=7545933;
RA Luo J., Li W., Zhang T., Chai S., Wang H.;
RT "Cloning and sequencing of promoter and signal sequence coding regions
from Bacillus subtilis.";
RL I Chuan Hsueh Pao 21:74-80(1994).
DR EMBL; S70232; AAB31052.1; -; Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 42 AA; 4834 MW; B868407FA47BE164 CRC64;

Query Match 7.5%; Score 6; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EVIKEV 9
Db 16 EVIKEV 21
|||||

RESULT 5
Q4RNV7 TETNG
ID Q4RNV7 TETNG PRELIMINARY; PRT; 48 AA.
AC Q4RNV7;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 10 SCAP15009, whole genome shotgun sequence.
GN ORFNames=GSTENG00031353001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salancoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Kellis M., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DDAJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC Q53412;
DR EMBL; CAAE01015009; CAG09859.1; -; Genomic DNA.
SQ SEQUENCE 51 AA; 5947 MW; 30A95DD8BEA7CA83 CRC64;

Query Match 7.5%; Score 6; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 PKKQVL 61
Db 20 PKKQVL 25
|||||

RESULT 7
Y151_UREPA
ID Y151_UREPA STANDARD; PRT; 60 AA.
AC Q9PQZ3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Hypothetical protein UUI151.
```

```
GN OrderedLocusNames=U1151;
OS Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.
OX NCBI_TaxID=134821;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 700970 / Serovar 3;
RX MEDLINE=20500219; PubMed=11048724; DOI=10.1038/35037619;
RA Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,
  Caswell G.H.;
RT "The complete sequence of the mucosal pathogen Ureaplasma
  urealyticum.";
RL Nature 407:757-762(2000).
CC -----
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CC removed.
CC -----
DR EMBL; AE002115; AAF30557.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 60 AA; 7313 MW; 49AB0B55342E43F3 CRC64;

Query Match 7.5%; Score 6; DB 1; Length 60;
Best Local Similarity 100.0%; Pred. No. 3.7e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0;

Qy 3 DEVIKE 8
Db 50 DEVIKE 55

RESULT 8
Q74EK4 GEOSL
ID Q74EK4 GEOSL PRELIMINARY; PRT; 62 AA.
AC Q74EK4
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DE Lipoprotein, putative.
GN OrderedLocusNames=GSU0958;
OS Geobacter sulfurreducens;
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
OC Geobacteraceae; Geobacter.
OX NCBI_TaxID=35554;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PCA / ATCC 51573;
RX PubMed=14671304; DOI=10.1126/science.1088727;
RA Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
  Heidelberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J.,
  Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
  Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
  Daviden T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
  Weidman J.F., Khouri H.M., Feldblyum T.V., Utterback T.R.,
  Van Aken S.E., Lovley D.R., Fraser C.M.;
RT "Genome of Geobacter sulfurreducens: metal reduction in subsurface
  environments.";
RL Science 302:1967-1969(2003).
DR EMBL; AE017180; AAR34285.1; -; Genomic_DNA.
DR TIGR; GSU0958; -.
KW Complete proteome; Lipoprotein.
SQ SEQUENCE 62 AA; 6629 MW; 189C7B0BE509B16E CRC64;

Query Match 7.5%; Score 6; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 3.8e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0;

Qy 42 GLAGGV 47
Db 16 GLAGGV 21
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```
RESULT 9
Q4FLM6 GRICK
ID Q4FLM6 GRICK PRELIMINARY; PRT; 63 AA.
AC Q4FLM6
DT 13-SEP-2005 (TRENBLrel. 31, Created)
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE Ribosomal L29 protein.
GN Name=rpMc; ORFNames=SR11_1109;
OS Candidatus Pelagibacter ubique HTCC1062.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC SAR11 cluster; Candidatus Pelagibacter.
OX NCBI_TaxID=335992;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HTCC1062;
RA Giovannoni S.J., Tripp H.J., Givan S.A., Podar M., Vergin K.L.,
  Baptista D., Bibbs L., Eads J., Richardson T.H., Noordwehr M.,
  Rappe M.S., Short J., Carrington J.C., Mathur E.J.;
RT "Genome Streamlining in a Cosmopolitan Oceanic Bacterium.";
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000084; AAZ21912.1; -; Genomic DNA.
SQ SEQUENCE 63 AA; 7318 MW; A52A50C9AED6670F CRC64;

Query Match 7.5%; Score 6; DB 2; Length 63;
Best Local Similarity 100.0%; Pred. No. 3.8e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0;

Qy 2 KDEVIK 7
Db 11 KDEVIK 16

RESULT 10
CVT_SOLTU
ID CVT_SOLTU STANDARD; PRT; 66 AA.
AC Q03I96;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Cysteine proteinase inhibitor (Fragment).
GN Name=CYS-PIN;
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=cv. Desiree; TISSUE=Leaf;
RX MEDLINE=93005746; PubMed=1392612; DOI=10.1105/tpc.4.9.1157;
RA Hildmann T., Ebneth M., Pena-Cortes H., Sanchez-Serrano J.J.,
  Willmitzer L., Prath S.;
RT "General roles of abscisic and jasmonic acids in gene activation as a
  result of mechanical wounding.";
RL Plant Cell 4:1157-1170(1992).
CC -!- TISSUE SPECIFICITY: In tubers of untreated plants. After ABA
  treatment or mechanical wounding is mostly accumulated in leaves,
  to a lesser extent in stems, but not in roots.
CC -!- INDUCTION: By abscisic acid (ABA), jasmonic acid (JA) and
  wounding.
CC -!- SIMILARITY: Belongs to the cystatin family. Phytocystatin
  subfamily.
CC -----
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CC removed.
CC -----
DR EMBL; X67844; CAA48037.1; -; mRNA.
DR PIR; PQ0469; PQ0469.
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DR InterPro; IPR000010; Prot_inh_cystat.
DR InterPro; IPR003243; Prot_inh_I25A_B.
DR Pfam; PF00031; Cystatin; 1.
DR ProDom; PD001231; Prot_inh_I25A_B; 1.
DR SMART; SM00043; CV; 1.
DR PROSITE; PS00287; CYSTATIN; 1.
KW Protease inhibitor; Thiol protease inhibitor.
FT MOTIF 18 22 Secondary area of contact.
FT NON_TER 1 1
SQ SEQUENCE 66 AA; 7906 MW; 70C2832D0E777631 CRC64;

Query Match 7.5%; Score 6; DB 1; Length 66;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KEVQEF 12
DB 53 KEVQEF 58

RESULT 11
Q7UB3_RHOBA PRELIMINARY; PRT; 67 AA.
AC Q7UB3;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
DE OrderedLocNames=RB3398;
OS Rhodopirellula baltica.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=117;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
RA Schlesner H., Amann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
RT strain 1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
DR EMBL; BX294138; CAD73168.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 67 AA; 7569 MW; 217C390C6105CABE CRC64;

Query Match 7.5%; Score 6; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 ALNCCG 42
DB 46 ALNCCG 51

RESULT 12
O24959_HELPY PRELIMINARY; PRT; 68 AA.
AC O24959;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein HP0148.
GN OrderedLocNames=HP0148;
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=26695 / ATCC 700392;
RX MEDLINE=97394467; PubMed=9252185; DOI=10.1038/41483;

RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R.,
RA Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness E.F.,
RA Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khalak H.G.,
RA Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D.,
RA Hickey E.K., Berg D.E., Gocayne J.D., Uterback T.R., Peterson J.D.,
RA Kelley J.M., Cotton M.D., Weidman J.F., Fujii C., Bowman C.,
RA Watthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D.,
RA Smith H.O., Fraser C.M., Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori.";
RL Nature 388:539-547(1997).
DR EMBL; AE000536; AAD07229.1; -; Genomic_DNA.
DR PIR; D64538; D64538.
DR TIGR; HP0148; -.
KW Complete proteome.
SQ SEQUENCE 68 AA; 7790 MW; 6329CF386CC93B5D CRC64;

Query Match 7.5%; Score 6; DB 2; Length 68;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 TLKAIH 35
DB 25 TLKAIH 30

RESULT 13
OS2950_BACSU PRELIMINARY; PRT; 71 AA.
ID OS2950;
AC OS2950;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Plasmid pLS32 DNA for thymidine kinase, replication protein, complete
DE cds.
OS Bacillus subtilis.
OG Plasmid pLS32.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=IAM1163;
RX MEDLINE=98149660; PubMed=9490016; DOI=10.1016/S0014-5793(98)00015-5;
RA Tanaka T., Ogura M.;
RT "A novel Bacillus natto plasmid pLS32 capable of replication in
RT Bacillus subtilis.";
RL FEBS Lett. 422:243-246(1998).
DR EMBL; D49467; BAA24874.1; -; Genomic_DNA.
DR GO; GO:0016301; F:kinase activity; IEA.
KW Kinase; Plasmid.
SQ SEQUENCE 71 AA; 8171 MW; B7DB456163C5AFDD CRC64;

Query Match 7.5%; Score 6; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 ETLKAI 34
DB 12 ETLKAI 17

RESULT 14
Q728A1_DESVH PRELIMINARY; PRT; 71 AA.
ID Q728A1;
AC Q728A1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=DVU2703;
OS Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB
OS 8303).

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OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
OC Desulfovibrionaceae; Desulfovibrio.
OX NCBI_TaxID=882;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15077118; DOI=10.1038/nbt959;
RA Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,
RA Kolonay J.F., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M.,
RA Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R.,
RA Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,
RA Peterson J.D., Davidse T.M., Zafar N., Zhou L., Radune D.,
RA Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R.,
RA Feldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.; Utterback T.R.,
RT "The genome sequence of the anaerobic, sulfate-reducing bacterium
RT Desulfovibrio vulgaris Hildenborough."
RL Nat. Biotechnol. 22:554-559(2004).
DR EMBL; AE017318; AAS97175.1; -; Genomic_DNA.
DR TIGR; DVU2703; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 71 AA; 7316 MW; A9450594FCA4C18 CRC64;

Query Match 7.5%; Score 6; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
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QY 42 GLAGGV 47
DB 52 GLAGGV 57

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AC QSEQ77;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
OS Schistosoma japonicum (blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Han Z.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY915878; AAX31099.1; -; mRNA.
DR InterPro; IPR000074; ApcA1_A4_E.
DR InterPro; IPR006121; HeavyMe_transpt.
DR Pfam; PF00403; HMA_1.
DR PROSITE; PS50846; HMA_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 73 AA; 8059 MW; 8510BE3AF5226877 CRC64;

Query Match 7.5%; Score 6; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 DAIKEV 76
DB 32 DAIKEV 37

Search completed: January 20, 2006, 17:50:49
Job time : 94 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2006, 17:50:54 ; Search time 73 Seconds  
(without alignments)  
144.453 Million cell updates/sec

Title: US-10-619-323-1\_COPY\_35\_58

Perfect score: 24

Sequence: 1 LRFDSQTKSIPFQETNNNSSPYT 24

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size : 0

Total number of hits satisfying chosen parameters: 939972

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Listing first 1000 summaries

Database : A\_Geneseq\_21.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*
- 9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	25.0	6	5	ABP51699 CD9 cell
2	6	25.0	22	9	ADV54659 G protein
3	6	25.0	22	9	ADV55655 G protein
4	6	25.0	23	2	AAW99457 C.albican
5	6	25.0	23	5	AAE19801 First cat
6	6	25.0	23	7	ADM33266 Candida a
7	5	20.8	5	2	AAW00431 Interleuk
8	5	20.8	7	1	AAW71426 Immunomod
9	5	20.8	8	2	AAW11529 Interleuk
10	5	20.8	8	2	AAW11528 Interleuk
11	5	20.8	9	2	AAW47083 Immunogen
12	5	20.8	9	4	ABP12131 HIV A02 s
13	5	20.8	9	5	ABW94781 CTL epit
14	5	20.8	9	5	ABW94700 CTL epit
15	5	20.8	9	5	ABW94890 CTL epit
16	5	20.8	9	5	ABW94512 CTL epit
17	5	20.8	9	5	ABW95000 CTL epit
18	5	20.8	9	5	ABW94602 CTL epit
19	5	20.8	9	5	ABW95087 CTL epit
20	5	20.8	9	5	AAE31350 Human tyr
21	5	20.8	9	5	AAE31351 Human tyr
22	5	20.8	9	5	AAE31352 Human tyr
23	5	20.8	9	6	ABJ20142 MHC bindi
24	5	20.8	9	8	ADP25771 Plasmodiu

25	5	20.8	9	8	ADP25547	Adp25547 Plasmodiu
26	5	20.8	9	8	ADT40166	Adt40166 HSARS vir
27	5	20.8	9	8	ADS79583	Ads79583 SARS viru
28	5	20.8	9	8	ADT37696	Adt37696 HSARS vir
29	5	20.8	9	9	ADZ50678	Adz50678 Y. pestis
30	5	20.8	10	4	AAAG8662	Aag8662 Saccharom
31	5	20.8	10	4	AAAG8680	Aag8680 Saccharom
32	5	20.8	10	4	ABP12285	Abp12285 HIV A02 s
33	5	20.8	10	5	ABW94839	Abw94839 CTL epit
34	5	20.8	10	5	ABW95132	Abw95132 CTL epit
35	5	20.8	12	5	ABG93666	Abg93666 Human Mit
36	5	20.8	12	5	ABG93725	Abg93725 Human Mit
37	5	20.8	14	7	ADF71051	Adf71051 Saccharom
38	5	20.8	15	8	ADM36120	Adm36120 RTN3 pept
39	5	20.8	16	4	AAW99487	Aaw99487 Vaccine r
40	5	20.8	16	5	AAE17169	Aae17169 Meningoco
41	5	20.8	17	2	AAW17549	Aaw17549 Beta-B2-C
42	5	20.8	17	5	AAU89944	Aau89944 Insulin/i
43	5	20.8	17	9	AEA43954	Aea43954 Anti-TPO
44	5	20.8	17	9	AEA43960	Aea43960 Anti-TPO
45	5	20.8	18	6	ABP82477	Abp82477 G protein
46	5	20.8	18	6	ABP82915	Abp82915 G protein
47	5	20.8	20	8	ADH16103	Adh16103 Gliadin r
48	5	20.8	20	8	ADH16104	Adh16104 Gliadin r
49	5	20.8	20	8	ADH15373	Adh15373 Gliadin r
50	5	20.8	20	8	ADH15374	Adh15374 Gliadin r
51	5	20.8	20	8	ADM36164	Adm36164 Human RTN
52	5	20.8	21	5	AAU89040	Aau89040 Insulin/i
53	5	20.8	21	6	ADA03870	Ada03870 Insulin r
54	5	20.8	21	7	ADH95083	Adh95083 Insulin r
55	5	20.8	21	7	ADM35382	Adm35382 HLA bindi
56	5	20.8	21	7	ADM34149	Adm34149 HLA bindi
57	5	20.8	21	8	ADL67774	Adl67774 IGF-IR/IR
58	5	20.8	21	8	ADM37619	Adm37619 Anti-IR f
59	5	20.8	21	9	ADX85960	Adx85960 HIV gp120
60	5	20.8	22	2	AAW06590	Aaw06590 Interleuk
61	5	20.8	22	9	ADV55048	Adv55048 G protein
62	5	20.8	22	9	ADV54935	Adv54935 G protein
63	5	20.8	22	9	ADV55154	Adv55154 G protein
64	5	20.8	23	2	AAW82478	Aaw82478 Neurospor
65	5	20.8	23	5	AAE22579	Aae22579 Drosophil
66	5	20.8	23	8	ADO55733	Ado55733 Neurospor
67	5	20.8	24	2	AAW06593	Aaw06593 Interleuk
68	5	20.8	25	2	AAW06594	Aaw06594 Interleuk
69	5	20.8	25	5	ABG62549	Abg62549 Rubacteri
70	4	16.7	4	2	AAW27137	Aaw27137 Fibronect
71	4	16.7	4	2	AAW44663	Aaw44663 Platelet
72	4	16.7	4	2	AAW44662	Aaw44662 Platelet
73	4	16.7	4	2	AAW00429	Aaw00429 Interleuk
74	4	16.7	4	2	AAW30984	Aaw30984 Non-cross
75	4	16.7	4	2	ABP55543	Abp55543 Hepatitis
76	4	16.7	4	6	ADA26528	Ada26528 Tobacco s
77	4	16.7	4	6	AAE32856	Aae32856 Hepatitis
78	4	16.7	4	8	ADH51741	Adh51741 Novel hum
79	4	16.7	4	9	ADV11616	Adv11616 RGD1 pept
80	4	16.7	5	2	AAW27143	Aaw27143 Fibronect
81	4	16.7	5	2	AAW54176	Aaw54176 CHA255 11
82	4	16.7	5	3	ABW19053	Abw19053 RGD pepti
83	4	16.7	5	4	ABW80034	Abw80034 Oligopept
84	4	16.7	5	4	ABW81904	Abw81904 Bag cell
85	4	16.7	5	5	AAU85943	Aau85943 Peptide #
86	4	16.7	5	8	ADN03333	Adn03333 Exemplary
87	4	16.7	5	8	ADR42168	Adr42168 gamma-Bag
88	4	16.7	5	8	ADQ95092	Adq95092 Synthetic
89	4	16.7	5	8	ADU48082	Adu48082 Peptide {
90	4	16.7	6	1	AAF71425	Aaf71425 Immunomod
91	4	16.7	6	2	AAW14820	Aaw14820 Bay thioe
92	4	16.7	6	3	AAW80540	Aaw80540 Bay C18:1
93	4	16.7	6	3	AAW83826	Aaw83826 Pyrrolobe
94	4	16.7	6	4	AAW88728	Aaw88728 Human int
95	4	16.7	6	4	AAW49582	Aaw49582 Rt-loop p
96	4	16.7	6	5	AAE21423	Aae21423 Saccharom
97	4	16.7	6	8	ADO26631	Ado26631 Synthetic

98	4	16.7	6	8	ADO26633	Synthetic	171	4	16.7	9	6	ABR06146	Human can
99	4	16.7	6	9	AE948702	Serine pr	172	4	16.7	9	6	ABR16846	Human can
100	4	16.7	7	2	AE86832	CD9 antiq	173	4	16.7	9	7	ADD88500	Influenza
101	4	16.7	7	2	AAW11530	Interleuk	174	4	16.7	9	7	ADG18265	Influenza
102	4	16.7	7	2	AAW25984	Hypervari	175	4	16.7	9	8	ADM73326	Human eur
103	4	16.7	7	2	AAW34373	PKB subat	176	4	16.7	9	8	ADN92001	Human 202
104	4	16.7	7	5	AB888727	Human int	177	4	16.7	9	8	ADN90431	Human 202
105	4	16.7	7	5	AB808575	Human HCC	178	4	16.7	9	8	ADN91112	Human 202
106	4	16.7	7	5	AB878367	Amino aci	179	4	16.7	9	8	ADN92316	Human 202
107	4	16.7	7	5	AAE14637	Human CD9	180	4	16.7	9	8	ADN93124	Human 202
108	4	16.7	7	6	AAO23188	Template-	181	4	16.7	9	8	ADN89811	Human 202
109	4	16.7	7	6	AAO23194	Template-	182	4	16.7	9	8	ADN90762	Human 202
110	4	16.7	7	6	AAO23193	Template-	183	4	16.7	9	8	ADN92237	Human 202
111	4	16.7	7	6	AAO23195	Template-	184	4	16.7	9	8	ADN92242	Human 202
112	4	16.7	7	7	ABR62643	Human pro	185	4	16.7	9	8	ADN92390	Human 202
113	4	16.7	7	7	ADK35697	Peptide e	186	4	16.7	9	8	ADN90152	Human 202
114	4	16.7	7	7	ABW00439	Human CD9	187	4	16.7	9	8	ADN91691	Human 202
115	4	16.7	7	7	ADK69863	Human CD9	188	4	16.7	9	8	ADN92934	Human 202
116	4	16.7	7	7	ADM08995	Canine im	189	4	16.7	9	8	ADN92778	Human 202
117	4	16.7	7	8	ADL19367	Human CD9	190	4	16.7	9	8	ADN92861	Human 202
118	4	16.7	7	8	ADL15613	N. mening	191	4	16.7	9	8	ADN90803	Human 202
119	4	16.7	7	8	ADN08516	Cotton te	192	4	16.7	9	8	ADN93006	Human 202
120	4	16.7	7	8	ADK68307	Androgen	193	4	16.7	9	8	ADN92214	Human 202
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122	4	16.7	7	9	AEA89006	Human CD9	195	4	16.7	9	8	ADP25484	Plasmodiu
123	4	16.7	8	2	AAE69615	MHC class	196	4	16.7	9	8	ADP25705	Plasmodiu
124	4	16.7	8	2	AAI40242	Amino aci	197	4	16.7	9	8	ADP25820	Plasmodiu
125	4	16.7	8	2	AAI40316	Amino aci	198	4	16.7	9	8	ADP25587	Plasmodiu
126	4	16.7	8	2	AAI53467	HIV-1 nef	199	4	16.7	9	8	ADP26040	Plasmodiu
127	4	16.7	8	2	AAI53393	HIV-1 nef	200	4	16.7	9	8	ADP25639	Plasmodiu
128	4	16.7	8	2	AAI26734	HIV-deriv	201	4	16.7	9	8	ADP25516	Plasmodiu
129	4	16.7	8	2	AAI26808	HIV-deriv	202	4	16.7	9	8	ADP25703	Plasmodiu
130	4	16.7	8	4	AA888726	Human int	203	4	16.7	9	8	ADR12491	Anti-canc
131	4	16.7	8	4	AAE52156	Mutant Pe	204	4	16.7	9	8	ADR47098	HLA-bindi
132	4	16.7	8	5	AB870259	Peptide #	205	4	16.7	9	8	ADT41381	hSARS vir
133	4	16.7	8	5	AB808570	Human HCC	206	4	16.7	9	8	ADS80796	SARS viru
134	4	16.7	8	7	ABW01593	Human TRL	207	4	16.7	9	8	ADT38911	hSARS vir
135	4	16.7	8	8	ADG94480	Human JNM	208	4	16.7	9	8	ADT02851	Human tum
136	4	16.7	8	8	ADI46879	Permeabil	209	4	16.7	9	8	ADT72523	Human RSV
137	4	16.7	8	8	ADI46862	Permeabil	210	4	16.7	9	8	ADT72889	Human RSV
138	4	16.7	8	8	ADN65659	HLA bindi	211	4	16.7	9	8	ADT72890	Human RSV
139	4	16.7	8	8	ADN65651	HLA bindi	212	4	16.7	9	8	ADT90910	Human eur
140	4	16.7	8	8	ADP87055	Junctiona	213	4	16.7	9	8	ADV29616	Human 109
141	4	16.7	8	8	ADP87039	Junctiona	214	4	16.7	9	8	ADV29229	Human 109
142	4	16.7	8	8	ADR05419	S39 subti	215	4	16.7	9	8	ADV30499	Human 109
143	4	16.7	8	8	ADT89656	Human TRL	216	4	16.7	9	8	ADV26688	Human 109
144	4	16.7	8	8	ADU08080	Heat choc	217	4	16.7	9	8	ADV30066	Human 109
145	4	16.7	9	2	AAW49512	Human leu	218	4	16.7	9	8	ADV26538	Human 109
146	4	16.7	9	2	AAW49266	Human leu	219	4	16.7	9	8	ADV29208	Human 109
147	4	16.7	9	2	AAW43849	Specific	220	4	16.7	9	9	ADW92427	hIN1 infl
148	4	16.7	9	2	AAW43845	Specific	221	4	16.7	9	9	ADZ00083	Cyclic pe
149	4	16.7	9	4	AA888725	Human int	222	4	16.7	9	9	ADZ86764	Cytotoxic
150	4	16.7	9	4	AAE63616	Complemen	223	4	16.7	10	1	AAE71431	Immunomod
151	4	16.7	9	4	AAJ02654	Hepatitis	224	4	16.7	10	1	AAE71430	Immunomod
152	4	16.7	9	4	AAJ00731	Hepatitis	225	4	16.7	10	2	AAE43942	Bovine Gl
153	4	16.7	9	4	AAJ02116	Hepatitis	226	4	16.7	10	2	AAE43939	Immunomod
154	4	16.7	9	5	ABE94604	CTL epito	227	4	16.7	10	2	AAW41459	Fragment
155	4	16.7	9	5	ABE95085	CTL epito	228	4	16.7	10	2	AAW10312	T cell ep
156	4	16.7	9	5	ABE95104	CTL epito	229	4	16.7	10	2	AAE40255	Amino aci
157	4	16.7	9	5	ABE94517	CTL epito	230	4	16.7	10	2	AAE53406	HIV-1 nef
158	4	16.7	9	5	ABE95006	CTL epito	231	4	16.7	10	2	AAE04359	Salmonell
159	4	16.7	9	5	ABE94503	CTL epito	232	4	16.7	10	2	AAE26747	HIV-deriv
160	4	16.7	9	5	ABE94921	CTL epito	233	4	16.7	10	3	AAE66452	HLA-A2-b1
161	4	16.7	9	5	ABE94618	CTL epito	234	4	16.7	10	4	AAE88724	Human int
162	4	16.7	9	5	ABG34115	Antigenic	235	4	16.7	10	4	AAE47551	Ag85B(110
163	4	16.7	9	5	ABG80675	Human tum	236	4	16.7	10	4	AAE94982	Human com
164	4	16.7	9	5	ABG80676	Human tum	237	4	16.7	10	4	AAE49023	IL-6R-der
165	4	16.7	9	6	ABR16010	Human can	238	4	16.7	10	4	AAE87012	Saccharom
166	4	16.7	9	6	ABR17207	Human can	239	4	16.7	10	4	AAE02254	Hepatitis
167	4	16.7	9	6	ABR17023	Human can	240	4	16.7	10	4	AAE02732	Hepatitis
168	4	16.7	9	6	ABR17056	Human can	241	4	16.7	10	5	ABE94634	CTL epito
169	4	16.7	9	6	ABR06295	Human can	242	4	16.7	10	5	ABE94837	CTL epito
170	4	16.7	9	6	ABR16253	Human can	243	4	16.7	10	5	ABE95058	CTL epito

244	4	16.7	10	5	ABB94760	Abb94760 CTL epitope	317	4	16.7	10	8	ADV26570	Adv26570 Human 109
245	4	16.7	10	5	ABU15234	Abj15234 Immunogen	318	4	16.7	10	9	ADW15724	Adw15724 Novel hum
246	4	16.7	10	5	ABU57443	Abu57443 HIV cytoto	319	4	16.7	10	9	ABW44901	Abw44901 M tuberc
247	4	16.7	10	5	ABG79994	Abg79994 MHC Class	320	4	16.7	11	2	AAR6031	Aar6031 Oligopept
248	4	16.7	10	6	AAE30016	Aae30016 Retinobla	321	4	16.7	11	2	AAR51276	Aar51276 Meningoco
249	4	16.7	10	6	ABP55431	Abp55431 Retinobla	322	4	16.7	11	2	AAR51277	Aar51277 Meningoco
250	4	16.7	10	6	ABRI6899	Abri6899 Human can	323	4	16.7	11	2	AAR83267	Aar83267 NPF motif
251	4	16.7	10	6	ABRI17105	Abri17105 Human can	324	4	16.7	11	2	AAW05147	Aaw05147 HIV Tat p
252	4	16.7	10	6	ABRI16364	Abri16364 Human can	325	4	16.7	11	2	AAW83026	Aaw83026 Synthetic
253	4	16.7	10	6	ABR06177	Abro6177 Human can	326	4	16.7	11	3	AAW98025	Aaw98025 Synthetic
254	4	16.7	10	6	ABRI17348	Abri17348 Human can	327	4	16.7	11	4	AAB88723	Aab88723 Human int
255	4	16.7	10	6	ABRI16092	Abri16092 Human can	328	4	16.7	11	4	AAM99178	Aam99178 Vaccine r
256	4	16.7	10	6	ABRI17291	Abri17291 Human can	329	4	16.7	11	4	AAU68099	Aau68099 Human Bre
257	4	16.7	10	6	ABR06813	Abro6813 Human can	330	4	16.7	11	4	AAB87985	Aab87985 Peptide a
258	4	16.7	10	6	ABRI17109	Abri17109 Human can	331	4	16.7	11	4	Aaj02241	Aaj02241 Hepatitis
259	4	16.7	10	6	ABR06633	Abro6633 Human can	332	4	16.7	11	4	Aaj00754	Aaj00754 Hepatitis
260	4	16.7	10	6	ABRI16934	Abri16934 Human can	333	4	16.7	11	4	AAJ00754	Aaj00754 Hepatitis
261	4	16.7	10	6	ABRI17275	Abri17275 Human can	334	4	16.7	11	4	AAJ02722	Aaj02722 Hepatitis
262	4	16.7	10	6	ABU70004	Abu70004 Human imm	335	4	16.7	11	6	ADA01464	Ada01464 Human ang
263	4	16.7	10	6	ABU70279	Abu70279 Human imm	336	4	16.7	11	6	ABJ20167	Abj20167 MHC bindi
264	4	16.7	10	7	ADD69231	Add69231 Human hea	337	4	16.7	11	6	ABP71065	Abp71065 TRAF2-bin
265	4	16.7	10	7	ADD23532	Add23532 Breast ca	338	4	16.7	11	6	AAO23202	Aao23202 Template-
266	4	16.7	10	7	ADD96812	Add96812 HIV-1 cro	339	4	16.7	11	7	ABO32492	Ab032492 HIV-1 mul
267	4	16.7	10	7	ADD96537	Add96537 HIV-1 cro	340	4	16.7	11	7	ABE71005	Abe71005 HIV-1 Tat
268	4	16.7	10	7	ADM08993	Adm08993 Canine im	341	4	16.7	11	7	ADL94498	Adl94498 HIV-1 Tat
269	4	16.7	10	8	ADG94420	Adg94420 Human JAM	342	4	16.7	11	8	ADG92153	Adg92153 Chemopene
270	4	16.7	10	8	ADG94434	Adg94434 Human JAM	343	4	16.7	11	8	ADS92210	Ads92210 Chemopene
271	4	16.7	10	8	ADG94442	Adg94442 Human JAM	344	4	16.7	11	8	ADT40637	Adt40637 hSARS vir
272	4	16.7	10	8	ADK68931	Adk68931 Epitope 1	345	4	16.7	11	8	ADT40544	Adt40544 hSARS vir
273	4	16.7	10	8	ADI46818	Adi46818 Permeabil	346	4	16.7	11	8	ADT40544	Adt40544 hSARS vir
274	4	16.7	10	8	ADI46853	Adi46853 Permeabil	347	4	16.7	11	8	ADT40544	Adt40544 hSARS vir
275	4	16.7	10	8	ADI46840	Adi46840 Permeabil	348	4	16.7	11	8	ADT38074	Adt38074 hSARS vir
276	4	16.7	10	8	ADI46832	Adi46832 Permeabil	349	4	16.7	11	8	ADT38167	Adt38167 hSARS vir
277	4	16.7	10	8	ADL27224	Adl27224 Peptide f	350	4	16.7	11	9	ADW03581	Adw03581 Human RIN
278	4	16.7	10	8	ADN90892	Adn90892 Human 202	351	4	16.7	12	1	AAP71428	Aap71428 Immunomod
279	4	16.7	10	8	ADN90592	Adn90592 Human 202	352	4	16.7	12	1	AAP71427	Aap71427 Immunomod
280	4	16.7	10	8	ADN93567	Adn93567 Human 202	353	4	16.7	12	1	AAR06818	Aar06818 Cell surf
281	4	16.7	10	8	ADN93693	Adn93693 Human 202	354	4	16.7	12	2	AAR06032	Aar06032 Oligopept
282	4	16.7	10	8	ADN89969	Adn89969 Human 202	355	4	16.7	12	2	AAR20117	Aar20117 MHC Class
283	4	16.7	10	8	ADN91826	Adn91826 Human 202	356	4	16.7	12	2	AAR49390	Aar49390 HLA-A2 po
284	4	16.7	10	8	ADN91529	Adn91529 Human 202	357	4	16.7	12	2	AAR49477	Aar49477 HLA-A2 po
285	4	16.7	10	8	ADN93757	Adn93757 Human 202	358	4	16.7	12	2	AAR49401	Aar49401 HLA-Cw9 p
286	4	16.7	10	8	ADN90237	Adn90237 Human 202	359	4	16.7	12	2	AAR69608	Aar69608 MHC Class
287	4	16.7	10	8	ADN90940	Adn90940 Human 202	360	4	16.7	12	2	AAW11838	Aaw11838 Peptide s
288	4	16.7	10	8	ADN93400	Adn93400 Human 202	361	4	16.7	12	2	AAV29652	Aav29652 H-ras com
289	4	16.7	10	8	ADN93430	Adn93430 Human 202	362	4	16.7	12	4	AAS88722	Aas88722 Human int
290	4	16.7	10	8	ADN90583	Adn90583 Human 202	363	4	16.7	12	4	AAV97744	Aav97744 Peroxidase
291	4	16.7	10	8	ADN93756	Adn93756 Human 202	364	4	16.7	12	5	AAU09443	Aau09443 Chlamydo
292	4	16.7	10	8	ADN93941	Adn93941 Human 202	365	4	16.7	12	5	ABU11918	Abu11918 Human HGP
293	4	16.7	10	8	ADO22326	Ado22326 Retinobla	366	4	16.7	12	6	ABU14073	Abu14073 Transadomi
294	4	16.7	10	8	ADP87030	Adp87030 Junctiona	367	4	16.7	12	6	ABU14073	Abu14073 Transadomi
295	4	16.7	10	8	ADP87017	Adp87017 Junctiona	368	4	16.7	12	7	ADD23761	Add23761 Breast ca
296	4	16.7	10	8	ADP87009	Adp87009 Junctiona	369	4	16.7	12	8	ADN65155	Adn65155 HLA bindi
297	4	16.7	10	8	ADP86995	Adp86995 Junctiona	370	4	16.7	12	8	ADN05491	Adn05491 Antipeori
298	4	16.7	10	8	ADQ10729	Adq10729 Human imm	371	4	16.7	12	8	ADQ15899	Adq15899 Human MDM
299	4	16.7	10	8	ADRI12499	Adri12499 Anti-canc	372	4	16.7	12	9	ADV59259	Adv59259 G protein
300	4	16.7	10	8	ADRI12506	Adri12506 Anti-canc	373	4	16.7	12	9	ADV59654	Adv59654 G protein
301	4	16.7	10	8	ADR12498	Adri12498 Anti-canc	374	4	16.7	12	9	ADV57523	Adv57523 G protein
302	4	16.7	10	8	ADR47105	Adri47105 HLA-bindi	375	4	16.7	12	9	ADV57112	Adv57112 G protein
303	4	16.7	10	8	ADR47106	Adri47106 HLA-bindi	376	4	16.7	12	9	ADV60057	Adv60057 G protein
304	4	16.7	10	8	ADR47113	Adri47113 HLA-bindi	377	4	16.7	12	9	ADV57896	Adv57896 G protein
305	4	16.7	10	8	ADS81209	Ads81209 Tumour-as	378	4	16.7	12	9	ADV58797	Adv58797 G protein
306	4	16.7	10	8	ADT90925	Adt90925 Human sur	379	4	16.7	12	9	ADV59934	Adv59934 G protein
307	4	16.7	10	8	ADT90917	Adt90917 Human sur	380	4	16.7	13	2	AAR06819	Aar06819 Cell surf
308	4	16.7	10	8	ADT90918	Adt90918 Human sur	381	4	16.7	13	2	AAR20118	Aar20118 MHC Class
309	4	16.7	10	8	ADV27455	Adv27455 Human 109	382	4	16.7	13	2	AAR69609	Aar69609 MHC Class
310	4	16.7	10	8	ADV31299	Adv31299 Human 109	383	4	16.7	13	2	AAR96474	Aar96474 Hepatitis
311	4	16.7	10	8	ADV30878	Adv30878 Human 109	384	4	16.7	13	2	AAR94321	Aar94321 Anti-thro
312	4	16.7	10	8	ADV27261	Adv27261 Human 109	385	4	16.7	13	2	AAW76600	Aaw76600 Simian im
313	4	16.7	10	8	ADV27264	Adv27264 Human 109	386	4	16.7	13	2	AAW76599	Aaw76599 Simian im
314	4	16.7	10	8	ADV30663	Adv30663 Human 109	387	4	16.7	13	2	AAW54569	Aaw54569 Peptide 8
315	4	16.7	10	8	ADV27014	Adv27014 Human 109	388	4	16.7	13	2	AAW44131	Aaw44131 HLA-A2 pe
316	4	16.7	10	8	ADV27793	Adv27793 Human 109	389	4	16.7	13	2	AAW79341	Aaw79341 Staphyloc

390	4	16.7	13	4	AAB88721	Aab88721 Human int	463	4	16.7	14	8	ADI56797	Adi56797 Melanoma
391	4	16.7	13	4	AAB87209	Aae07209 Human LIV	464	4	16.7	14	8	ADI56772	Adi56772 Flu virus
392	4	16.7	13	4	AAB85938	Aab85938 Lima bean	465	4	16.7	14	8	ADP73498	Adp73498 Neisseria
393	4	16.7	13	4	AAB85937	Aab85937 Chick pea	466	4	16.7	14	8	ADQ94315	Adq94315 Human pre
394	4	16.7	13	5	ABP72103	Abp72103 Beta 1,2-	467	4	16.7	14	8	ADR12790	Adr12790 N. mening
395	4	16.7	13	5	ADG66697	Adg66697 B. lichen	468	4	16.7	14	8	ADU49898	Adu49898 Human glu
396	4	16.7	13	5	ADG66700	Adg66700 B. lichen	469	4	16.7	14	9	ADM80714	Adm80714 Human pro
397	4	16.7	13	5	ADG66699	Adg66699 B. lichen	470	4	16.7	14	9	ADY53789	Ady53789 Human Ig
398	4	16.7	13	5	ADG66698	Adg66698 B. lichen	471	4	16.7	14	9	ADY53788	Ady53788 Human Ig
399	4	16.7	13	6	ABU08282	Abu08282 Prostate	472	4	16.7	14	9	ADZ00084	Adz00084 Cyclic pe
400	4	16.7	13	6	ADA43109	Ada43109 HLA-DR be	473	4	16.7	14	9	AEA64487	Aea64487 Cyclic pe
401	4	16.7	13	6	ADA43111	Ada43111 HLA-DR be	474	4	16.7	14	9	AEA64482	Aea64482 Cyclic pe
402	4	16.7	13	6	ADA43113	Ada43113 HLA-DR be	475	4	16.7	14	9	AEA64483	Aea64483 Cyclic pe
403	4	16.7	13	6	ADA43110	Ada43110 HLA-DR be	476	4	16.7	14	9	AEA64486	Aea64486 Cyclic pe
404	4	16.7	13	6	ADA43112	Ada43112 HLA-DR be	477	4	16.7	14	9	AEA64485	Aea64485 Cyclic pe
405	4	16.7	13	7	ADD18064	Add18064 Human G-p	478	4	16.7	14	9	AEA64484	Aea64484 Cyclic pe
406	4	16.7	13	8	ADI00496	Adi00496 Influenza	479	4	16.7	14	9	AEA64481	Aea64481 Cyclic pe
407	4	16.7	13	8	ADI56771	Adi56771 Flu virus	480	4	16.7	14	9	AEA49389	Aea49389 HLA-A2 po
408	4	16.7	13	8	ADH89766	Adh89766 Cell pene	481	4	16.7	15	2	AAR49633	Aar49633 Camel imm
409	4	16.7	13	8	ADK69701	Adk69701 Novel fus	482	4	16.7	15	2	AAW75601	Aaw75601 M. tuberc
410	4	16.7	13	8	ADK68462	Adk68462 Peptide s	483	4	16.7	15	2	AAW75656	Aaw75656 M. tuberc
411	4	16.7	13	8	ADO21581	Ado21581 Chickpea	484	4	16.7	15	2	AAW75602	Aaw75602 M. tuberc
412	4	16.7	13	8	ADO21582	Ado21582 Lima bean	485	4	16.7	15	2	AAW75600	Aaw75600 M. tuberc
413	4	16.7	13	8	ADO06903	Ado06903 PRRSV gp5	486	4	16.7	15	2	AAW75655	Aaw75655 M. tuberc
414	4	16.7	13	8	ADO06902	Ado06902 PRRSV gp5	487	4	16.7	15	2	AAW75657	Aaw75657 M. tuberc
415	4	16.7	13	8	ADM5154	Adm5154 HLA bindi	488	4	16.7	15	2	AAW92585	Aaw92585 Mouse bet
416	4	16.7	13	9	ADY27605	Ady27605 Alpha-1-3	489	4	16.7	15	3	AAW92584	Aaw92584 Mouse bet
417	4	16.7	13	9	ADY14192	Ady14192 Soluble p	490	4	16.7	15	3	AAW00051	Aaw00051 Cartilage
418	4	16.7	13	9	ADY27630	Ady27630 Alpha-2-3	491	4	16.7	15	4	AAH88719	Aah88719 Human int
419	4	16.7	13	9	ADZ38302	Adz38302 Human kin	492	4	16.7	15	4	AAH88718	Aah88718 Rb derive
420	4	16.7	13	9	ADZ38302	Adz38302 Human kin	493	4	16.7	15	4	ABH51033	Abh51033 Human sec
421	4	16.7	14	2	AAR33244	Aar33244 HIV-NJ-33	494	4	16.7	15	4	AAH78795	Aah78795 Human myo
422	4	16.7	14	2	AAR49400	Aar49400 HLA-Cw9 p	495	4	16.7	15	4	ABP24631	Abp24631 HIV DR su
423	4	16.7	14	2	AAW77226	Aaw77226 Hamster i	496	4	16.7	15	4	AAJ03358	Aaj03358 Hepatitis
424	4	16.7	14	2	AAW30030	Aaw30030 Mutant hu	497	4	16.7	15	5	ABP58871	Abp58871 Follicle
425	4	16.7	14	2	AAW41922	Aaw41922 Peptide u	498	4	16.7	15	5	ABB07889	Abb07889 Phosphoen
426	4	16.7	14	2	AAW62008	Aaw62008 SEQ ID NO	499	4	16.7	15	5	ABG62749	Abg62749 Eubacteri
427	4	16.7	14	2	AAW66136	Aaw66136 Prosaposi	500	4	16.7	15	5	ABG62484	Abg62484 Eubacteri
428	4	16.7	14	2	AAI36479	Aai36479 Fragment	501	4	16.7	15	5	AAE18792	Aae18792 Streptoco
429	4	16.7	14	3	AAI999143	Aai999143 HLA class	502	4	16.7	15	5	ABP60052	Abp60052 Motor pro
430	4	16.7	14	3	AAI998021	Aai998021 Sunflower	503	4	16.7	15	5	ABU11944	Abu11944 Human HGP
431	4	16.7	14	4	AAI98714	Aai98714 Human pep	504	4	16.7	15	6	ABU11956	Abu11956 Human HGP
432	4	16.7	14	4	AAI97761	Aai97761 Human pep	505	4	16.7	15	6	ABP59317	Abp59317 Human neu
433	4	16.7	14	4	AAI988720	Aai988720 Human int	506	4	16.7	15	6	ABR32307	AbR32307 Human can
434	4	16.7	14	4	AAI999335	Aai999335 Vaccine r	507	4	16.7	15	6	ABR34213	AbR34213 Human can
435	4	16.7	14	4	AAU68411	Aau68411 Human Bre	508	4	16.7	15	6	ABR31673	AbR31673 Human can
436	4	16.7	14	4	AAU68411	Aau68411 Human Bre	509	4	16.7	15	6	ABR34163	AbR34163 Human can
437	4	16.7	14	5	ABR05878	AbR05878 Retinobla	510	4	16.7	15	6	ABR31911	AbR31911 Human can
438	4	16.7	14	5	ABR05878	AbR05878 Amb a I r	511	4	16.7	15	6	ABR34228	AbR34228 Human can
439	4	16.7	14	5	ABR05950	AbR05950 Amb a I r	512	4	16.7	15	6	ABR31842	AbR31842 Human can
440	4	16.7	14	6	ABP72984	Abp72984 Membrane	513	4	16.7	15	6	ABR32082	AbR32082 Human can
441	4	16.7	14	6	ABU11935	Abu11935 Human HGP	514	4	16.7	15	6	ABR34096	AbR34096 Human can
442	4	16.7	14	6	ABU11936	Abu11936 Human HGP	515	4	16.7	15	6	ABR34203	AbR34203 Human can
443	4	16.7	14	6	ABU11919	Abu11919 Human HGP	516	4	16.7	15	6	ABR34131	AbR34131 Human can
444	4	16.7	14	6	ABU11920	Abu11920 Human HGP	517	4	16.7	15	6	ABR33779	AbR33779 Human can
445	4	16.7	14	6	ABU11937	Abu11937 Human HGP	518	4	16.7	15	6	ABR31750	AbR31750 Human can
446	4	16.7	14	6	ABU38788	AbJ38788 Human G-p	519	4	16.7	15	6	ABR32083	AbR32083 Human can
447	4	16.7	14	6	ABJ38718	AbJ38718 Human G-p	520	4	16.7	15	6	ABR34153	AbR34153 Human can
448	4	16.7	14	6	ABJ38764	AbJ38764 Human G-p	521	4	16.7	15	6	ABR34131	AbR34131 Human can
449	4	16.7	14	6	ABJ38765	AbJ38765 Human G-p	522	4	16.7	15	6	ABR83373	AbR83373 G protein
450	4	16.7	14	6	ABJ38787	AbJ38787 Human G-p	523	4	16.7	15	6	ABU08065	AbU08065 N-termina
451	4	16.7	14	6	ABJ38719	AbJ38719 Human G-p	524	4	16.7	15	6	ABU56365	AbU56365 Mycobacte
452	4	16.7	14	6	ADD12025	Add12025 Human nov	525	4	16.7	15	6	ABU56364	AbU56364 Mycobacte
453	4	16.7	14	7	ADD18065	Add18065 Human G-p	526	4	16.7	15	6	ABO45290	AbO45290 Novel hum
454	4	16.7	14	7	ADD18066	Add18066 Human G-p	527	4	16.7	15	6	ABO26770	AbO26770 Protein a
455	4	16.7	14	7	ADE10863	Adel0863 Chimeric	528	4	16.7	15	7	AAE39310	Aae39310 M. tuberc
456	4	16.7	14	7	ADG44360	Adg44360 Anti-path	529	4	16.7	15	7	AAE39311	Aae39311 M. tuberc
457	4	16.7	14	7	ADM39768	Adm39768 Neisseria	530	4	16.7	15	7	AAE39309	Aae39309 M. tuberc
458	4	16.7	14	7	ADM40850	Adm40850 Neisseria	531	4	16.7	15	7	AAE39311	Aae39311 M. tuberc
459	4	16.7	14	7	ADM36522	Adm36522 Soybean l	532	4	16.7	15	7	ADE45025	Ade45025 Human p95
460	4	16.7	14	8	ADG63963	Adg63963 Recombina	533	4	16.7	15	7	ADP32542	AdP32542 Clostridi
461	4	16.7	14	8	ADI00497	Adi00497 Influenza	534	4	16.7	15	7	ADP45151	AdP45151 M. tuberc
462	4	16.7	14	8	ADI00522	Adi00522 Melanoma-	535	4	16.7	15	7	ADP45152	AdP45152 M. tuberc

536	4	16.7	15	7	ADP45153	Adf45153 M. tuberc	609	4	16.7	16	7	ABO27244	Abo27244 Self-anti
537	4	16.7	15	7	ADF70981	Adf70981 Subtielli	610	4	16.7	16	7	ADD88732	Add88732 Malarial
538	4	16.7	15	7	ADF70982	Adf70982 Subtielli	611	4	16.7	16	7	ADG18497	Adg18497 P. falcip
539	4	16.7	15	7	ADF70980	Adf70980 Subtielli	612	4	16.7	16	7	ADG68018	Adg68018 Human TRP
540	4	16.7	15	7	ADF70979	Adf70979 Subtielli	613	4	16.7	16	7	ADG68004	Adg68004 Human TRP
541	4	16.7	15	7	ADL96063	Adl96063 Human neu	614	4	16.7	16	7	ADJ46091	Adj46091 CS3 subun
542	4	16.7	15	8	ADI35018	Adi35018 Hepatitis	615	4	16.7	16	8	ADH62685	Adh62685 E. coli p
543	4	16.7	15	8	ADI35021	Adi35021 Hepatitis	616	4	16.7	16	8	ADK69565	Adk69565 Epitope l
544	4	16.7	15	8	ADI35020	Adi35020 Hepatitis	617	4	16.7	16	8	ADP69105	Adp69105 Human NOV
545	4	16.7	15	8	ADN94442	Adn94442 Human 202	618	4	16.7	16	8	ADP69105	Adp69105 Human NOV
546	4	16.7	15	8	ADN94444	Adn94444 Human 202	619	4	16.7	16	8	ADP69105	Adp69105 Human NOV
547	4	16.7	15	8	ADN94328	Adn94328 Human 202	620	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
548	4	16.7	15	8	ADN94443	Adn94443 Human 202	621	4	16.7	16	9	ADW92659	Adw92659 Malaria b
549	4	16.7	15	8	ADN94405	Adn94405 Human 202	622	4	16.7	16	9	ADZ03645	Adz03645 CS3 pilin
550	4	16.7	15	8	ADN94207	Adn94207 Human 202	623	4	16.7	16	9	AEA53623	Aea53623 Novel hum
551	4	16.7	15	8	ADN94137	Adn94137 Human 202	624	4	16.7	16	9	AEA08145	Aea08145 CS3 pilus
552	4	16.7	15	8	ADN94272	Adn94272 Human 202	625	4	16.7	16	9	AEA08144	Aea08144 CS3 pilus
553	4	16.7	15	8	ADN94640	Adn94640 Human 202	626	4	16.7	16	9	AEA08110	Aea08110 CS3 pilus
554	4	16.7	15	8	ADN94487	Adn94487 Human 202	627	4	16.7	16	9	AE48707	Aeb48707 Serine pr
555	4	16.7	15	8	ADO36837	Ado36837 Majorly a	628	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
556	4	16.7	15	8	ADO36838	Ado36838 Majorly a	629	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
557	4	16.7	15	8	ADO36836	Ado36836 Majorly a	630	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
558	4	16.7	15	8	ADP26542	Adp26542 Plasmodiu	631	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
559	4	16.7	15	8	ADQ81257	Adq81257 GW182 pep	632	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
560	4	16.7	15	8	ADT91833	Adt91833 SIV varia	633	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
561	4	16.7	15	8	ADV31616	Adv31616 Human 109	634	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
562	4	16.7	15	8	ADV31524	Adv31524 Human 109	635	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
563	4	16.7	15	8	ADV31553	Adv31553 Human 109	636	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
564	4	16.7	15	8	ADV31447	Adv31447 Human 109	637	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
565	4	16.7	15	8	ADV31856	Adv31856 Human 109	638	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
566	4	16.7	15	8	ADV31685	Adv31685 Human 109	639	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
567	4	16.7	15	8	ADV32081	Adv32081 Human 109	640	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
568	4	16.7	15	8	ADV31857	Adv31857 Human 109	641	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
569	4	16.7	15	8	ADU64212	Adu64212 30 KD pro	642	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
570	4	16.7	15	8	ADU64211	Adu64211 30 KD pro	643	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
571	4	16.7	15	8	ADU64213	Adu64213 30 KD pro	644	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
572	4	16.7	15	8	ADU64270	Adu64270 32 KD pro	645	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
573	4	16.7	15	8	ADU64272	Adu64272 32 KD pro	646	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
574	4	16.7	15	8	ADU64271	Adu64271 32 KD pro	647	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
575	4	16.7	15	9	ADV14736	Adv14736 Protein r	648	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
576	4	16.7	15	9	ADV22664	Adv22664 HIV-1 Tat	649	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
577	4	16.7	15	9	ADV22662	Adv22662 HIV-1 Tat	650	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
578	4	16.7	15	9	ADV22663	Adv22663 HIV-1 Tat	651	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
579	4	16.7	15	9	ADV23401	Adv23401 HBV immun	652	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
580	4	16.7	15	9	ADV23399	Adv23399 HBV immun	653	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
581	4	16.7	15	9	ADV23400	Adv23400 HBV immun	654	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
582	4	16.7	15	9	ADW64465	Adw64465 Wild type	655	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
583	4	16.7	15	9	ADX02678	Adx02678 Neural th	656	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
584	4	16.7	15	9	ADX69408	Adx69408 CDK 2 or	657	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
585	4	16.7	15	9	ADY84962	Ady84962 Nef 218 p	658	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
586	4	16.7	15	9	ADZ17849	Adz17849 p21-deriv	659	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
587	4	16.7	16	2	AAR49461	Aar49461 HLA-A30 p	660	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
588	4	16.7	16	2	AAR88364	Aar88364 CS3 pilus	661	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
589	4	16.7	16	2	AAR85697	Aar85697 HCV-J NG3	662	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
590	4	16.7	16	2	AAW17877	Aaw17877 Phototab	663	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
591	4	16.7	16	2	AAW75331	Aaw75331 Adenoviru	664	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
592	4	16.7	16	2	AAW75331	Aaw75331 Adenoviru	665	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
593	4	16.7	16	2	AAW85349	Aaw85349 Helper T-	666	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
594	4	16.7	16	2	AAW71002	Aaw71002 Epitope f	667	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
595	4	16.7	16	3	AAV59337	Aav59337 Tyrosine	668	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
596	4	16.7	16	4	AAB88718	Aab88718 Human int	669	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
597	4	16.7	16	4	AAM99214	Aam99214 Vaccine r	670	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
598	4	16.7	16	4	AAE12235	Aae12235 Mycobacte	671	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
599	4	16.7	16	4	AAB57228	Aab57228 Maltose b	672	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
600	4	16.7	16	4	AAB29011	Aab29011 Vector pm	673	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
601	4	16.7	16	5	ABO08039	Abo08039 Amino aci	674	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
602	4	16.7	16	5	AAE17168	Aae17168 Meningoco	675	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
603	4	16.7	16	5	AAU77202	Aau77202 Polyspar	676	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
604	4	16.7	16	6	ABO23259	Abo23259 Light cha	677	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
605	4	16.7	16	6	ABP82420	Abp82420 G protein	678	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
606	4	16.7	16	6	ABP82331	Abp82331 G protein	679	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
607	4	16.7	16	6	ABO01417	Abo01417 Single ch	680	4	16.7	16	9	AE93665	Aeb93665 Abetak pe
608	4	16.7	16	7	ABO01256	Abo01256 Single ch	681	4	16.7	16	9	AE93665	Aeb93665 Abetak pe

682	4	16.7	18	2	Aaw06613	Aaw06613	HIV-1 mat	755	4	16.7	19	8	ADR68311	Adr68311	Androgen
683	4	16.7	18	2	Aaw06615	Aaw06615	HIV-1 mat	756	4	16.7	19	8	ADU15798	AdU15798	PDZ domain
684	4	16.7	18	2	Aaw06616	Aaw06616	HIV-1 mat	757	4	16.7	19	9	ADV14076	Adv14076	Yeast N-t
685	4	16.7	18	2	Aaw46687	Aaw46687	Biotinyl	758	4	16.7	19	9	ADV14103	Adv14103	Yeast N-t
686	4	16.7	18	2	Aay24541	Aay24541	Biotinyl	759	4	16.7	19	9	ADW52277	AdW52277	Human PL
687	4	16.7	18	3	Aay99046	Aay99046	HLA class	760	4	16.7	19	9	AEBO7936	AeBO7936	Peptide b
688	4	16.7	18	3	Aay99045	Aay99045	HLA class	761	4	16.7	20	2	AR07710	Ar07710	Rb-15 ant
689	4	16.7	18	3	Aay99043	Aay99043	HLA class	762	4	16.7	20	2	AA27685	Aa27685	Anticocci
690	4	16.7	18	3	Aay99041	Aay99041	HLA class	763	4	16.7	20	2	AA47009	Aa47009	Interleuk
691	4	16.7	18	3	Aay99044	Aay99044	HLA class	764	4	16.7	20	2	AA49383	Aa49383	HLA-A2 po
692	4	16.7	18	3	AA88716	AA88716	Human int	765	4	16.7	20	2	AA49394	Aa49394	HLA-C pos
693	4	16.7	18	4	AAE09921	AAE09921	Human int	766	4	16.7	20	2	AAW99451	AaW99451	Human par
694	4	16.7	18	5	ABP52503	ABP52503	Fusion pr	767	4	16.7	20	2	AAW71357	AaW71357	Wild type
695	4	16.7	18	5	ABG32409	ABG32409	Peptide #	768	4	16.7	20	2	AAW71358	AaW71358	Conserved
696	4	16.7	18	5	ABG32404	ABG32404	Peptide #	769	4	16.7	20	2	AAW03008	AaW03008	Peptide f
697	4	16.7	18	6	ABP74746	ABP74746	Proteome	770	4	16.7	20	2	AAW08022	AaW08022	HIV pep1
698	4	16.7	18	7	AD810872	AD810872	Chimeric	771	4	16.7	20	2	AAW41658	AaW41658	Immunomod
699	4	16.7	18	7	ADD88730	ADD88730	Malarial	772	4	16.7	20	2	ABP71216	AbP71216	DRBeta1*0
700	4	16.7	18	7	ADG18495	ADG18495	P. falcip	773	4	16.7	20	2	AAW22209	AaW22209	Endogenou
701	4	16.7	18	7	ADM39777	ADM39777	N. meningi	774	4	16.7	20	2	AAW37480	AaW37480	Brevibact
702	4	16.7	18	7	ADM40859	ADM40859	Neisseria	775	4	16.7	20	2	AAW54559	AaW54559	Peptide f
703	4	16.7	18	8	ADG63972	ADG63972	Recombina	776	4	16.7	20	2	AAW31907	AaW31907	Spider ve
704	4	16.7	18	8	ADL26438	ADL26438	Synthetic	777	4	16.7	20	2	AAV31909	AaV31909	Spider ve
705	4	16.7	18	8	ADP73507	ADP73507	Neisseria	778	4	16.7	20	3	AAV92062	AaV92062	Drosophil
706	4	16.7	18	8	ADR12799	ADR12799	N. mening	779	4	16.7	20	4	AAW88714	AaW88714	Human int
707	4	16.7	18	8	ADS84937	ADS84937	Beta-site	780	4	16.7	20	4	AAW91128	AaW91128	Parathyro
708	4	16.7	18	8	ADU76760	ADU76760	HIV promo	781	4	16.7	20	4	AAE03101	AaE03101	Human gen
709	4	16.7	18	8	ADU76761	ADU76761	HIV promo	782	4	16.7	20	4	AAU01420	AaU01420	Peptide #
710	4	16.7	18	8	ADU76761	ADU76761	HIV promo	783	4	16.7	20	4	AAU01419	AaU01419	Peptide #
711	4	16.7	18	8	ADU76762	ADU76762	HIV promo	784	4	16.7	20	4	AAW74641	AaW74641	Wild-type
712	4	16.7	18	8	ADU76766	ADU76766	HIV promo	785	4	16.7	20	4	AAW74640	AaW74640	Mutant m8
713	4	16.7	18	9	ADV22987	ADV22987	HCV H77 i	786	4	16.7	20	4	AAO05387	AaO05387	Human pol
714	4	16.7	18	9	ADW22986	ADW22986	HCV H77 i	787	4	16.7	20	5	ABG63650	ABG63650	Human alb
715	4	16.7	18	9	ADM64466	ADM64466	Truncated	788	4	16.7	20	5	ABG63278	ABG63278	Human pro
716	4	16.7	18	9	ADW92657	ADW92657	Malaria b	789	4	16.7	20	5	AAO18726	AAO18726	Heparitis
717	4	16.7	19	2	AA49395	AA49395	HLA-A2 pos	790	4	16.7	20	5	ABW84377	ABW84377	H. brasili
718	4	16.7	19	2	AA49384	AA49384	HLA-A2 po	791	4	16.7	20	5	AAU89680	AaU89680	Insulin/i
719	4	16.7	19	2	AA49385	AA49385	HLA-A2 po	792	4	16.7	20	6	AAU89680	AaU89680	Insulin/i
720	4	16.7	19	2	AA49386	AA49386	HLA-A2 po	793	4	16.7	20	6	ADA41361	ADa41361	Human sec
721	4	16.7	19	2	AA49384	AA49384	Peptide f	794	4	16.7	20	6	ADW67719	ADW67719	HIV-1 nef
722	4	16.7	19	3	AAV04437	AAV04437	Oestrogen	795	4	16.7	20	7	ADW67720	ADW67720	HIV-1 nef
723	4	16.7	19	3	AAV69298	AAV69298	Expressed	796	4	16.7	20	7	ADW67720	ADW67720	HIV-1 nef
724	4	16.7	19	4	AAW21526	AAW21526	Peptide #	797	4	16.7	20	7	ADW67720	ADW67720	HIV-1 nef
725	4	16.7	19	4	AAW88715	AAW88715	Human int	798	4	16.7	20	7	ADW67720	ADW67720	HIV-1 nef
726	4	16.7	19	4	ABW43871	ABW43871	Peptide #	799	4	16.7	20	7	ADW67720	ADW67720	HIV-1 nef
727	4	16.7	19	4	AAW37788	AAW37788	Peptide #	800	4	16.7	20	7	ADG17820	ADG17820	Binding a
728	4	16.7	19	4	AAW57678	AAW57678	KV.1 PL p	801	4	16.7	20	7	ADG17862	ADG17862	Binding a
729	4	16.7	19	4	AAW374654	AAW374654	Wild type	802	4	16.7	20	7	ADG17862	ADG17862	Binding a
730	4	16.7	19	4	AAW374655	AAW374655	Mutant P5	803	4	16.7	20	7	ADG17862	ADG17862	Binding a
731	4	16.7	19	4	AAW58088	AAW58088	KV.1 PL p	804	4	16.7	20	7	ADG17862	ADG17862	Binding a
732	4	16.7	19	4	ABW26797	ABW26797	Protein #	805	4	16.7	20	7	ADW33877	ADW33877	HLA bindi
733	4	16.7	19	4	AAW7598	AAW7598	Human bon	806	4	16.7	20	7	ADW33877	ADW33877	HLA bindi
734	4	16.7	19	4	AAW55816	AAW55816	PL peptid	807	4	16.7	20	8	ADW35110	ADW35110	HLA bindi
735	4	16.7	19	4	AAW64858	AAW64858	Human bra	808	4	16.7	20	8	ADW15375	ADW15375	Gladiin r
736	4	16.7	19	4	ABG59250	ABG59250	Human liv	809	4	16.7	20	8	ADH16105	ADH16105	Gladiin r
737	4	16.7	19	5	AAU75837	AAU75837	Wheat xyl	810	4	16.7	20	8	ADH15372	ADH15372	Gladiin r
738	4	16.7	19	5	ABU05208	ABU05208	C-termina	811	4	16.7	20	8	ADH16102	ADH16102	Gladiin r
739	4	16.7	19	5	ABP63231	ABP63231	KV1.3 PL	812	4	16.7	20	8	ADL76915	ADL76915	Albumin f
740	4	16.7	19	6	ABP72985	ABP72985	Membrane	813	4	16.7	20	8	ADL95977	ADL95977	Prostate
741	4	16.7	19	7	ADG61117	ADG61117	Human CD4	814	4	16.7	20	8	ADL95980	ADL95980	Prostate
742	4	16.7	19	7	ADP26606	ADP26606	BGS-19 pe	815	4	16.7	20	8	ADM29147	ADM29147	Hepatitis
743	4	16.7	19	7	ADP14807	ADP14807	SLE/sjogr	816	4	16.7	20	8	ADM29148	ADM29148	Hepatitis
744	4	16.7	19	8	ADQ06898	ADQ06898	PRRSV gp5	817	4	16.7	20	8	ADO08701	ADO08701	HCV epito
745	4	16.7	19	8	ADQ06899	ADQ06899	PRRSV gp5	818	4	16.7	20	8	ADP71365	ADP71365	Sequence
746	4	16.7	19	8	ADQ06897	ADQ06897	PRRSV gp5	819	4	16.7	20	8	ADP71205	ADP71205	HCV E1 pr
747	4	16.7	19	8	ADQ020647	ADQ020647	rNOS PDZ	820	4	16.7	20	8	ADP71339	ADP71339	HIV-1 tat
748	4	16.7	19	8	ADQ20687	ADQ20687	PSD-95 PD	821	4	16.7	20	8	ADQ31345	ADQ31345	HIV-1 tat
749	4	16.7	19	8	ADQ20751	ADQ20751	PSD-95 PD	822	4	16.7	20	8	ADP71365	ADP71365	Sequence
750	4	16.7	19	8	ADQ20775	ADQ20775	PSD-95 PD	823	4	16.7	20	8	ADP71365	ADP71365	Sequence
751	4	16.7	19	8	ADQ20704	ADQ20704	PSD-95 PD	824	4	16.7	20	8	ADP71362	ADP71362	Sequence
752	4	16.7	19	8	ADP71362	ADP71362	Sequence	825	4	16.7	20	9	ADU12429	ADU12429	Human pho
753	4	16.7	19	8	ADP71364	ADP71364	Sequence	826	4	16.7	20	9	ADY38344	ADY38344	Antigenic
754	4	16.7	19	8	ADP71363	ADP71363	Sequence	827	4	16.7	20	9	ADZ98096	ADZ98096	Human ami

828	4	16.7	20	9	AD298544	Human aml	901	4	16.7	21	8	ADL69019	IGF-1R/IR
829	4	16.7	20	9	AEB42994	Circumspo	902	4	16.7	21	8	ADL67835	IGF-1R/IR
830	4	16.7	20	9	AEB42993	Circumspo	903	4	16.7	21	8	ADK82488	Human vol
831	4	16.7	20	9	AEB48204	Amino aci	904	4	16.7	21	8	ADM37680	Anti-IR f
832	4	16.7	20	1	AAP71422	Immunomod	905	4	16.7	21	8	ADM37761	Anti-IGF-
833	4	16.7	21	1	AAP71423	Immunomod	906	4	16.7	21	8	ADM38864	Site 1 pe
834	4	16.7	21	1	AAP71424	Immunomod	907	4	16.7	21	8	ADM37768	Anti-IGF-
835	4	16.7	21	1	AAR49393	HLA-C pos	908	4	16.7	21	8	ADP71368	Sequence
836	4	16.7	21	2	AAR49382	HLA-A2 po	909	4	16.7	21	8	ADP71366	Sequence
837	4	16.7	21	2	AAR49382	HLA-A2 po	910	4	16.7	21	8	ADP71367	Sequence
838	4	16.7	21	2	AAR49382	HLA-A2 po	911	4	16.7	21	8	ADT40385	hsARS vir
839	4	16.7	21	2	AAR49382	HLA-A2 po	912	4	16.7	21	8	ADT40385	hsARS vir
840	4	16.7	21	2	AAR49382	HLA-A2 po	913	4	16.7	21	8	ADT40385	hsARS vir
841	4	16.7	21	4	AAB88758	Human int	914	4	16.7	21	9	ADW92656	Malaria b
842	4	16.7	21	4	AAB88758	Human int	915	4	16.7	22	2	AAR49392	HLA-C pos
843	4	16.7	21	4	AAB88758	Human int	916	4	16.7	22	2	AAR49392	HLA-C pos
844	4	16.7	21	4	AAB88758	Human int	917	4	16.7	22	2	AAR49392	HLA-C pos
845	4	16.7	21	4	AAB88758	Human int	918	4	16.7	22	2	AAR49392	HLA-C pos
846	4	16.7	21	4	AAB88758	Human int	919	4	16.7	22	2	AAR49392	HLA-C pos
847	4	16.7	21	4	AAB88758	Human int	920	4	16.7	22	2	AAR49392	HLA-C pos
848	4	16.7	21	4	AAB88758	Human int	921	4	16.7	22	3	AAV78370	H. pylori
849	4	16.7	21	4	AAB88758	Human int	922	4	16.7	22	3	AAV78370	H. pylori
850	4	16.7	21	4	AAB88758	Human int	923	4	16.7	22	5	AAU78030	Mung bean
851	4	16.7	21	4	AAB88758	Human int	924	4	16.7	22	5	AAU78030	Mung bean
852	4	16.7	21	4	AAB88758	Human int	925	4	16.7	22	7	ADM57801	Human T c
853	4	16.7	21	4	AAB88758	Human int	926	4	16.7	23	2	AAU78030	Human T c
854	4	16.7	21	4	AAB88758	Human int	927	4	16.7	23	2	AAU78030	Human T c
855	4	16.7	21	4	AAB88758	Human int	928	4	16.7	23	2	AAU78030	Human T c
856	4	16.7	21	4	AAB88758	Human int	929	4	16.7	23	2	AAU78030	Human T c
857	4	16.7	21	4	AAB88758	Human int	930	4	16.7	23	2	AAU78030	Human T c
858	4	16.7	21	4	AAB88758	Human int	931	4	16.7	23	2	AAU78030	Human T c
859	4	16.7	21	4	AAB88758	Human int	932	4	16.7	23	2	AAU78030	Human T c
860	4	16.7	21	4	AAB88758	Human int	933	4	16.7	23	2	AAU78030	Human T c
861	4	16.7	21	4	AAB88758	Human int	934	4	16.7	23	2	AAU78030	Human T c
862	4	16.7	21	4	AAB88758	Human int	935	4	16.7	23	3	AAU78030	Human T c
863	4	16.7	21	4	AAB88758	Human int	936	4	16.7	23	4	AAU78030	Human T c
864	4	16.7	21	4	AAB88758	Human int	937	4	16.7	23	4	AAU78030	Human T c
865	4	16.7	21	4	AAB88758	Human int	938	4	16.7	23	4	AAU78030	Human T c
866	4	16.7	21	4	AAB88758	Human int	939	4	16.7	23	4	AAU78030	Human T c
867	4	16.7	21	4	AAB88758	Human int	940	4	16.7	23	4	AAU78030	Human T c
868	4	16.7	21	4	AAB88758	Human int	941	4	16.7	23	4	AAU78030	Human T c
869	4	16.7	21	4	AAB88758	Human int	942	4	16.7	23	4	AAU78030	Human T c
870	4	16.7	21	4	AAB88758	Human int	943	4	16.7	23	4	AAU78030	Human T c
871	4	16.7	21	4	AAB88758	Human int	944	4	16.7	23	4	AAU78030	Human T c
872	4	16.7	21	4	AAB88758	Human int	945	4	16.7	23	4	AAU78030	Human T c
873	4	16.7	21	4	AAB88758	Human int	946	4	16.7	23	4	AAU78030	Human T c
874	4	16.7	21	4	AAB88758	Human int	947	4	16.7	23	4	AAU78030	Human T c
875	4	16.7	21	4	AAB88758	Human int	948	4	16.7	23	4	AAU78030	Human T c
876	4	16.7	21	4	AAB88758	Human int	949	4	16.7	23	4	AAU78030	Human T c
877	4	16.7	21	4	AAB88758	Human int	950	4	16.7	23	4	AAU78030	Human T c
878	4	16.7	21	4	AAB88758	Human int	951	4	16.7	23	4	AAU78030	Human T c
879	4	16.7	21	4	AAB88758	Human int	952	4	16.7	23	4	AAU78030	Human T c
880	4	16.7	21	4	AAB88758	Human int	953	4	16.7	23	4	AAU78030	Human T c
881	4	16.7	21	4	AAB88758	Human int	954	4	16.7	23	4	AAU78030	Human T c
882	4	16.7	21	4	AAB88758	Human int	955	4	16.7	23	4	AAU78030	Human T c
883	4	16.7	21	4	AAB88758	Human int	956	4	16.7	23	4	AAU78030	Human T c
884	4	16.7	21	4	AAB88758	Human int	957	4	16.7	23	4	AAU78030	Human T c
885	4	16.7	21	4	AAB88758	Human int	958	4	16.7	23	4	AAU78030	Human T c
886	4	16.7	21	4	AAB88758	Human int	959	4	16.7	23	4	AAU78030	Human T c
887	4	16.7	21	4	AAB88758	Human int	960	4	16.7	23	4	AAU78030	Human T c
888	4	16.7	21	4	AAB88758	Human int	961	4	16.7	23	4	AAU78030	Human T c
889	4	16.7	21	4	AAB88758	Human int	962	4	16.7	23	4	AAU78030	Human T c
890	4	16.7	21	4	AAB88758	Human int	963	4	16.7	23	4	AAU78030	Human T c
891	4	16.7	21	4	AAB88758	Human int	964	4	16.7	23	4	AAU78030	Human T c
892	4	16.7	21	4	AAB88758	Human int	965	4	16.7	23	4	AAU78030	Human T c
893	4	16.7	21	4	AAB88758	Human int	966	4	16.7	23	4	AAU78030	Human T c
894	4	16.7	21	4	AAB88758	Human int	967	4	16.7	23	4	AAU78030	Human T c
895	4	16.7	21	4	AAB88758	Human int	968	4	16.7	23	4	AAU78030	Human T c
896	4	16.7	21	4	AAB88758	Human int	969	4	16.7	23	4	AAU78030	Human T c
897	4	16.7	21	4	AAB88758	Human int	970	4	16.7	23	4	AAU78030	Human T c
898	4	16.7	21	4	AAB88758	Human int	971	4	16.7	23	4	AAU78030	Human T c
899	4	16.7	21	4	AAB88758	Human int	972	4	16.7	23	4	AAU78030	Human T c
900	4	16.7	21	4	AAB88758	Human int	973	4	16.7	23	4	AAU78030	Human T c



974 4 16.7 25 4 AAm99189  
 975 4 16.7 25 4 AAm99592  
 976 4 16.7 25 4 ABb38475  
 977 4 16.7 25 4 AAm31917  
 978 4 16.7 25 4 ABb23631  
 979 4 16.7 25 4 AAm71620  
 980 4 16.7 25 4 AAm59087  
 981 4 16.7 25 4 ABg53302  
 982 4 16.7 25 5 ABg41432  
 983 4 16.7 25 5 ABg62214  
 984 4 16.7 25 5 ABg62627  
 985 4 16.7 25 5 ABg62526  
 986 4 16.7 25 5 ABg96124  
 987 4 16.7 25 7 ADM08232  
 988 4 16.7 25 7 ADM08239  
 989 4 16.7 25 7 ADM08240  
 990 4 16.7 25 7 ADM08247  
 991 4 16.7 25 7 ADM08208  
 992 4 16.7 25 7 ADM08206  
 993 4 16.7 25 7 ADM08211  
 994 4 16.7 25 7 ADM08236  
 995 4 16.7 25 7 ADM08210  
 996 4 16.7 25 7 ADM08245  
 997 4 16.7 25 7 ADM08241  
 998 4 16.7 25 7 ADM08243  
 999 4 16.7 25 7 ADM09203  
 1000 4 16.7 25 7 ADM08246

## ALIGNMENTS

RESULT 1  
 ABP51699  
 ID ABP51699 standard; peptide; 6 AA.  
 AC ABP51699;  
 XX  
 DT 01-OCT-2002 (first entry)  
 XX  
 DE CD9 cell surface protein peptide.  
 XX  
 KW Human; epidermal growth factor receptor; EGFR; immunogenic; cancer;  
 KW apoptosis; cytostatic; cell surface protein.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 PN WO200247613-A2.  
 XX  
 PD 20-JUN-2002.  
 XX  
 PF 13-NOV-2001; 2001WO-US047734.  
 XX  
 PR 27-NOV-2000; 2000US-00723307.  
 XX  
 PA (NOUN ) UNIV NORTHWESTERN.  
 XX  
 PI Calenoff E, Ditlow CC;  
 XX  
 DR WPI; 2002-566624/60.  
 XX  
 PT Candidates for cancer-specific or cancer-associated antigens useful for  
 PT diagnosis and treatment of cancer comprise synthetic peptides.  
 XX  
 PS Disclosure; Page 16; 53pp; English.  
 XX  
 CC The present invention describes a method for identifying candidates that  
 CC are cancer-specific or cancer-associated antigens. The method involves:  
 CC (1) mapping hydrophilic regions of amino acid sequences; (2) identifying  
 CC hydrophilic peptide regions that are glycosylated in non-cancerous cells,  
 CC but deglycosylated in cancer cells; and (3) synthesizing, labeling and  
 CC testing peptides. The cancer-specific/associated antigen sequences have

CC cytostatic activity, and can be used for promoting cancer cell apoptosis.  
 CC The method can be used for identifying candidates that are cancer-  
 CC specific or cancer-associated antigens for use in the diagnosis and  
 CC treatment of cancer. The method involves the use of a site of  
 CC deglycosylated amino acids in the cancer cells, and so confers a cancer-  
 CC specific or highly cancer-associated immunogenicity or marker function to  
 CC the peptide and avoiding self-recognition. The peptides are further not  
 CC intracellularly expressed, but are located on the cell surfaces  
 CC (predictably secreted or released into pericellular fluids) in sufficient  
 CC numbers, and so are sufficiently accessible for targeting T cells; and  
 CC are present at the earlier stages of cancer progression as well as during  
 CC later stages; and are retained on the surface of the cancer cells for a  
 CC time sufficient for the therapeutic T cells to find their target and  
 CC retain the bound T cells for a time sufficient to affect cancer cell  
 CC death. ABP51697 to ABP51771 represent amino acid sequence used in the  
 CC exemplification of the present invention  
 XX  
 SQ Sequence 6 AA;  
 Query Match 25.0%; Score 6; DB 5; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 16 NNNSS 21  
 Db 1 NNNSS 6  
 RESULT 2  
 ADV54659  
 ID ADV54659 standard; peptide; 22 AA.  
 XX  
 AC ADV54659;  
 XX  
 DT 10-MAR-2005 (first entry)  
 XX  
 DE G protein coupled receptor peptide SEQ ID NO 2156.  
 XX  
 KW diagnosis; cancer; obesity; diabetes; diabetes; asthma; inflammation; depression;  
 KW food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.  
 XX  
 OS Unidentified.  
 XX  
 PN WO2004111636-A2.  
 XX  
 PD 23-DEC-2004.  
 XX  
 PF 17-JUN-2004; 2004WO-EP051158.  
 XX  
 PR 17-JUN-2003; 2003EP-00101775.  
 PR 17-JUN-2003; 2003US-0479061P.  
 XX  
 PA (VIRV-) VTB VZW.  
 PA (UYGE-) UNIV GENT.  
 XX  
 PI Kas K, Vandekerckhove J, Krols L;  
 XX  
 DR WPI; 2005-057893/06.  
 XX  
 PT Identifying a peptide combo which corresponds with a family of proteins,  
 PT useful for diagnosing a variety of diseases, drug development or in  
 PT agriculture, comprises generating peptides by applying a digest on the  
 PT family of protein.  
 XX  
 PS Example; SEQ ID NO 2156; 265pp; English.  
 XX  
 CC The invention relates to a method of identifying a peptide combo which  
 CC corresponds with a family of proteins where each of the members of the  
 CC peptide combo is derived from a unique protein from the family. The  
 CC peptide combo is useful for quantifying specific known splice variants of  
 CC one or more particular proteins in a sample, for diagnosing complex  
 CC genetic diseases such as cancer, obesity, diabetes, asthma and  
 CC inflammation, neuropsychiatric disorders such as depression, for



CC quantifying one to several hundreds of protein disease markers  
 CC simultaneously leading to a more accurate diagnostic sub-classification,  
 CC for determining the extent of protein modification in a particular sample  
 CC of proteins, for tissue-typing analysis, for prenatal testing to detect  
 CC the presence of a congenital disease or for quantitating protein levels  
 CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases  
 CC or neurological diseases, as biomarkers preclinical drug development,  
 CC development of improved animal models, biomarkers related with  
 CC toxicology, clinical drug development, guidance marketed drugs,  
 CC prognostic or diagnostic disease markers, drug target validation and  
 CC selection, monitoring protein splicing, drug lead profiling, pathway  
 CC analysis, answering basic disease biology questions, and in the fields of  
 CC food and feed, cosmetics, agriculture and animal breeding. The present  
 CC sequence represents a peptide from a G-protein coupled receptor peptide  
 CC combo.

XX  
 XX Sequence 22 AA;  
 SQ  
 Query Match 25.0%; Score 6; DB 9; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 46;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 NNNNS 21  
 DB 8 NNNNS 13

## RESULT 3

ADV55655  
 ID ADV55655 standard; peptide; 22 AA.

XX  
 AC ADV55655;

XX  
 DT 10-MAR-2005 (first entry)

XX  
 DE G protein coupled receptor peptide SEQ ID NO 3153.

XX  
 KW diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;  
 food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.

XX  
 OS Unidentified.

XX  
 PN WO2004111636-A2.

XX  
 PD 23-DEC-2004.

XX  
 PF 17-JUN-2004; 2004WO-EP051158.

XX  
 PR 17-JUN-2003; 2003EP-00101775.

XX  
 PR 17-JUN-2003; 2003US-0479061P.

XX  
 PA (VIBV-) VIB VZW

XX  
 PA (UYGB-) UNIV GENT.

XX  
 PI Kas K, Vandekerckhove J, Krols L;

XX  
 WPI; 2005-057893/06.

XX  
 PT Identifying a peptide combo which corresponds with a family of proteins,  
 useful for diagnosing a variety of diseases, drug development or in  
 PT agriculture, comprises generating peptides by applying a digest on the  
 PT family of protein.

XX  
 PS Example; SEQ ID NO 3153; 265pp; English.

XX  
 CC The invention relates to a method of identifying a peptide combo which  
 CC corresponds with a family of proteins where each of the members of the  
 CC peptide combo is derived from a unique protein from the family. The  
 CC peptide combo is useful for quantifying specific known splice variants of  
 CC one or more particular proteins in a sample, for diagnosing complex  
 CC genetic diseases such as cancer, obesity, diabetes, asthma and  
 CC inflammation, neuropsychiatric disorders such as depression, for  
 CC quantifying one to several hundreds of protein disease markers

CC simultaneously leading to a more accurate diagnostic sub-classification,  
 CC for determining the extent of protein modification in a particular sample  
 CC of proteins, for tissue-typing analysis, for prenatal testing to detect  
 CC the presence of a congenital disease or for quantitating protein levels  
 CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases  
 CC or neurological diseases, as biomarkers preclinical drug development,  
 CC development of improved animal models, biomarkers related with  
 CC toxicology, clinical drug development, guidance marketed drugs,  
 CC prognostic or diagnostic disease markers, drug target validation and  
 CC selection, monitoring protein splicing, drug lead profiling, pathway  
 CC analysis, answering basic disease biology questions, and in the fields of  
 CC food and feed, cosmetics, agriculture and animal breeding. The present  
 CC sequence represents a peptide from a G-protein coupled receptor peptide  
 CC combo.

XX  
 XX Sequence 22 AA;

Query Match 25.0%; Score 6; DB 9; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 46;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 NNNNS 21  
 DB 8 NNNNS 13

## RESULT 4

AAW99457  
 ID AAW99457 standard; protein; 23 AA.

XX  
 AC AAW99457;

XX  
 DT 08-JUN-1999 (first entry)

XX  
 DE C.albicans alpha-INTip 1st cation binding site-derived peptide.

XX  
 KW Integrin-like motif; vaccine; immune response; antibody; inhibition;  
 adhesion; endothelial cell; pathogenesis; infection.

XX  
 OS Synthetic.

XX  
 OS Candida albicans.

XX  
 PN US5886151-A.

XX  
 PD 23-MAR-1999.

XX  
 PF 03-MAY-1996; 96US-00642846.

XX  
 PR 03-MAY-1996; 96US-00642846.

XX  
 PA (MINU ) UNIV MINNESOTA.

XX  
 PI Tao N, Kendrick K, Gale CA, Hostetter MK, Bendel CW;

XX  
 WPI; 1999-242618/20.

XX  
 PT New isolated Candida albicans protein with integrin-like motifs.

XX  
 PS Claim 1; Col 33; 21pp; English.

XX  
 CC Peptides AAW99456-W99461 are derived from a Candida albicans protein with  
 CC integrin-like motifs, alpha-INP1. This sequence represents a peptide  
 CC derived from the first cation binding site of alpha-INP1. The peptides  
 CC can be used for producing vaccines for stimulating an immune response.  
 CC The antibodies can inhibit the adhesion of C.albicans to cells,  
 CC particularly endothelial cells. This blocking activity of the adhesion to  
 CC cells can reduce or prevent subsequent events in the pathogenesis of  
 CC invasive candidal infection

XX  
 XX Sequence 23 AA;

Query Match 25.0%; Score 6; DB 2; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 48;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TNNNS 20  
Db 5 TNNNS 10  
|||||

RESULT 5  
AAE19801  
ID AAE19801 standard; peptide; 23 AA.  
AC AAE19801;  
XX  
DT 18-JUN-2002 (first entry)  
XX  
DE First cation-binding site peptide.  
XX  
KW Integrin-like protein; alphaIntlp; gene; fungicide; contraceptive; HIV;  
KW human immunodeficiency virus; vaccine; cholera.  
XX  
OS Unidentified.  
XX  
PN US6346411-B1.  
XX  
PD 12-FEB-2002.  
XX  
PF 08-MAR-1999; 99US-00264604.  
XX  
PR 03-MAY-1996; 96US-00642846.  
XX  
PA (MINU ) UNIV MINNESOTA.  
XX  
PI Hostetter MK, Gale CA, Bendel CM, Tao N;  
XX  
DR WPI; 2002-224995/28.  
XX  
PT Polynucleotide encoding Candida albicans protein with integrin-like  
PT motifs and protein, useful as vaccines and for raising antibodies for  
PT inhibiting adhesion of pathogen to cells preferably epithelial cells.  
XX  
PS Example; Col 17; 25pp; English.  
XX  
CC The present invention relates to an isolated polynucleotide encoding  
CC Candida albicans protein with integrin-like motifs. Candida albicans  
CC protein is utilised in vaccines (for gastrointestinal pathogens like  
CC cholera) and as antigens to prepare anti-peptide antibodies, which are  
CC utilised in inhibiting adhesion of C. albicans to cells preferably  
CC epithelial cells. In the genitourinary tract, expression of spermicides  
CC by S. cerevisiae transformed with the C. albicans integrin-like gene on  
CC an extrachromosomal plasmid could provide a cheap and infrequent method  
CC of contraception. Also, synthesis of protein-based antiretroviral agents  
CC could help to reduce transmission of human immunodeficiency virus (HIV)  
CC in the birth canal. The present sequence is first cation-binding site  
CC peptide used in the exemplification of the invention  
XX  
SQ Sequence 23 AA;

Query Match 25.0%; Score 6; DB 5; Length 23;  
Best Local Similarity 100.0%; Pred. No. 48;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TNNNS 20  
Db 5 TNNNS 10  
|||||

RESULT 6  
ADM33266  
ID ADM33266 standard; peptide; 23 AA.  
XX  
AC ADM33266;  
XX  
DT 03-JUN-2004 (first entry)

XX  
DE Candida albicans integrin-like protein epitope seqid 4.  
XX  
KW fungicide; vaccine; cell adhesion inhibitor; integrin-like motif;  
KW integrin-like protein; alphaIntlp; EF-hand divalent cation binding site;  
KW transmembrane domain; RGD tripeptide; I domain;  
KW gastrointestinal pathogen; cholera; epitope.  
XX  
OS Candida albicans.  
XX  
PN US2003082680-A1.  
XX  
PD 01-MAY-2003.  
XX  
PF 15-OCT-2001; 2001US-00978343.  
XX  
PR 03-MAY-1996; 96US-00642846.  
PR 08-MAR-1999; 99US-00264604.  
XX  
PA (MINU ) UNIV MINNESOTA.  
XX  
PI Hostetter MK, Gale CA, Kendrick K;  
XX  
DR WPI; 2003-743894/70.  
XX  
PT New isolated and purified integrin-like protein of Candida albicans,  
PT alpha Intlp, useful for raising antibodies to alpha Intlp protein for  
PT inhibiting adhesion of C. albicans to epithelial cells.  
XX  
PS Claim 16; SEQ ID NO 4; 25pp; English.  
XX  
CC The invention describes an isolated and purified Candida albicans protein  
CC (I) with integrin-like motifs (alphaIntlp) comprising an I domain, two EF  
CC -hand divalent cation binding sites, a sequence sufficient to encode a  
CC transmembrane domain, an internal RGD tripeptide, and a carboxy-terminal  
CC sequence with a single tyrosine residue. Antibodies to (I) are useful for  
CC inhibiting adhesion of C. albicans to cells, e.g. human epithelial cells,  
CC which comprises contacting the C. albicans blastospores with antibodies  
CC to (I) or its fragments or by contacting the cells with antibodies to a  
CC peptide comprising integrin-like motifs containing an I domain, two EF-  
CC hand divalent cation binding sites, a sequence sufficient to form a  
CC transmembrane domain, an internal RGD tripeptide and a carboxy-terminal  
CC sequence having a single tyrosine residue. An extrachromosomal plasmid of  
CC Saccharomyces cerevisiae containing non-native DNA encoding (I) is useful  
CC for delivering a gene product to a subject. A vaccine comprising (I) or a  
CC (I) peptide may be used to provide a source of vaccine antigen for  
CC gastrointestinal pathogens, e.g. cholera. This is the amino acid sequence  
CC of a Candida albicans integrin-like protein (alphaIntlp) epitope  
CC encompassing the first cation binding site.  
XX  
SQ Sequence 23 AA;

Query Match 25.0%; Score 6; DB 7; Length 23;  
Best Local Similarity 100.0%; Pred. No. 48;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TNNNS 20  
Db 5 TNNNS 10  
|||||

RESULT 7  
AAW00431  
ID AAW00431 standard; peptide; 5 AA.  
XX  
AC AAW00431;  
XX  
DT 29-AUG-1996 (first entry)  
XX  
DE Interleukin-6 antagonist peptide.  
XX  
KW IL-6; antagonist; autoimmune disease.  
XX

OS Synthetic.  
 XX JP07324097-A.  
 XX  
 XX 12-DEC-1995.  
 XX  
 XX 30-MAY-1994; 94JP-00117259.  
 XX  
 XX 30-MAY-1994; 94JP-00117259.  
 XX  
 XX (DAIL ) DAICEL CHEM IND LTD.  
 XX (FUJI ) FUJISAWA PHARM CO LTD.  
 XX  
 XX WPI; 1996-065476/07.  
 XX  
 XX Interleukin 6 antagonist - useful for treating autoimmune diseases.  
 XX  
 XX Claim 4, 6; Page 2, 3; 19pp; Japanese.  
 XX  
 CC New IL-6 antagonists are provided which are of formula X-W-Y, in which X is H or an amino-protecting group, Y is OH or a carboxy-protecting group, and W is a peptide containing all or part of the sequence as given in AA000401, AA000402, AA000403 or AA000404, where any free mercapto groups in the sequence are optionally protected. The present sequence is a specifically preferred partial sequence of AA000403 and is itself claimed as a new chemical entity. The IL-6 antagonists are useful for treating autoimmune diseases  
 XX  
 XX Sequence 5 AA;  
 SQ  
 Query Match 20.8%; Score 5; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 19 NSSFY 23  
 DB 1 NSSFY 5  
 |||||  
 RESULT 8  
 AAP71426  
 ID AAP71426 standard; protein; 7 AA.  
 AC  
 XX AAP71426;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 03-MAY-1991 (first entry)  
 XX  
 XX Immunomodulator peptide DR-7 inhibits HIV-T4 interaction.  
 DE  
 XX AIDS; T4 cell receptor; immunomodulation.  
 KW  
 XX Synthetic.  
 OS  
 XX WO8703601-A.  
 PN  
 XX 18-JUN-1987.  
 PD  
 XX 08-DEC-1986; 86WO-FR000425.  
 PF  
 XX 06-DEC-1985; 85FR-00018155.  
 PR  
 XX (INSP ) INST PASTEUR.  
 PA (AUFR/) AUFRAY C.  
 PA (CNRS ) CENT NAT RECH SCI.  
 XX  
 XX Auffray C, Montagnier L, Klatzmann D, Charron D;  
 PI  
 XX WPI; 1987-177935/25.  
 DR  
 XX New peptide derivs. contg. specified exposed tetrapeptide sequences -  
 FT inhibiting interaction of AIDS virus with T4 cell receptors.  
 XX

PS Claim 8; Page 49; 57pp; French.  
 XX  
 CC The peptide is a specific example of a peptide comprising the tetrapeptide motif RFDS preceded by either Ala, Val or Leu and followed by an Asp residue. The peptide comprises 6-30 amino acid residues. It interferes with interaction between the AIDS virus and T4 receptors on lymphocytes. The peptide also has immuno-modulatory activity. It is useful in diagnosis to detect antibodies to the region of the viral genome containing the RFDS sequence. See also AAP71422-5 and AAP71427-P71437. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PA field.)  
 CC  
 XX Sequence 7 AA;  
 SQ  
 Query Match 20.8%; Score 5; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LRFDS 5  
 DB 1 LRFDS 5  
 |||||  
 RESULT 9  
 AAW11529  
 ID AAW11529 standard; peptide; 8 AA.  
 XX  
 XX AAW11529;  
 AC  
 XX 22-APR-1997 (first entry)  
 DT  
 XX Interleukin-6 antagonist 2.  
 DE  
 XX Interleukin-6; IL-6; antagonist; inhibitor; autoimmune disease; skin;  
 KW intestine; systemic lupus erythematosus; chronic rheumatism.  
 XX  
 XX Synthetic.  
 OS  
 XX Key Location/Qualifiers  
 FH Modified-site 8  
 FT /note= "amidated"  
 FT  
 XX JP08311098-A.  
 PN  
 XX 26-NOV-1996.  
 PD  
 XX 22-MAY-1995; 95JP-00146742.  
 PF  
 XX 22-MAY-1995; 95JP-00146742.  
 PR  
 XX (DAIL ) DAICEL CHEM IND LTD.  
 PA (FUJI ) FUJISAWA PHARM CO LTD.  
 XX  
 XX WPI; 1997-061811/06.  
 DR  
 XX Interleukin-6 antagonistic peptide(s) comprising arginine - useful for treating autoimmune, renal, skin and intestinal diseases.  
 PT  
 XX Example 2; Page 11; 20pp; Japanese.  
 PS  
 XX The present peptide is a specific example of new interleukin-6 antagonists of the general formula X-A-B-D-Y, where X is 1-10 amino acids or an amino group protecting group; Y is 1-5 amino acids, a carboxyl group protecting group or an amide; A is preferably Arg having an opt. protected guanidino group but can be any amino acid; D is Arg having an opt. protected guanidino group and B is preferably a Leu residue but can be any amino acid, including non-natural amino acids, opt. having a protected side-chain. The peptides are useful for treating autoimmune diseases (e.g. systemic lupus erythematosus or chronic rheumatism), renal, skin and intestinal diseases  
 CC  
 XX Sequence 8 AA;  
 SQ

```

Query Match      20.8%; Score 5; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 NSSFY 23
Db 1 NSSFY 5

RESULT 10
AAW11528
ID AAW11528 standard; peptide; 9 AA.
XX
AC AAW11528;
XX
DT 22-APR-1997 (first entry)
XX
DE Interleukin-6 antagonist 1.
XX
KW Interleukin-6; IL-6; antagonist; inhibitor; autoimmune disease; skin;
KW intestine; systemic lupus erythematosus; chronic rheumatism.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 9 /note= "amidated"
FT
XX
PN JP08311098-A.
XX
PD 26-NOV-1996.
XX
PF 22-MAY-1995; 95JP-00146742.
XX
PR 22-MAY-1995; 95JP-00146742.
XX
PA (DAIL ) DAICEL CHEM IND LTD.
PA (FUJI ) FUJISAWA PHARM CO LTD.
XX
DR WPI; 1997-061811/06.
XX
PT Interleukin-6 antagonistic peptide(s) comprising arginine - useful for
PT treating autoimmune, renal, skin and intestinal diseases.
XX
PS Example 1; Page 11; 20pp; Japanese.
XX
CC The present peptide is a specific example of new interleukin-6
CC antagonists of the general formula X-A-B-D-Y, where X is 1-10 amino acids
CC or an amino group protecting group; Y is 1-5 amino acids, a carboxyl
CC group protecting group or an amide; A is preferably Arg having an opt.
CC protected guanidino group but can be any amino acid; D is Arg having an
CC opt. protected guanidino group and B is preferably a Leu residue but can
CC be any amino acid, including non-natural amino acids, opt. having a
CC protected side-chain. The peptides are useful for treating autoimmune
CC diseases (e.g. systemic lupus erythematosus or chronic rheumatism),
CC renal, skin and intestinal diseases
XX
SQ Sequence 9 AA;
Query Match      20.8%; Score 5; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 NSSFY 23
Db 2 NSSFY 6

RESULT 11
AAY47083
ID AAY47083 standard; peptide; 9 AA.
XX
AC AAY47083;

Query Match      20.8%; Score 5; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SIFEQ 13
Db 1 SIFEQ 5

RESULT 12
ABP12131
ID ABP12131 standard; peptide; 9 AA.
XX
AC ABP12131;
XX
DT 11-SEP-2003 (revised)
DT 15-JUL-2002 (first entry)

```

XX 01-DEC-1999 (first entry)

DT Immunogenic peptide having a human leukocyte antigen binding motif #1694.

DE Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;

XX immune response; T cell activation; major histocompatibility complex;

KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;

KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;

KW vaccine; immunisation.

XX Synthetic.

OS Homo sapiens.

XX WO9945954-A1.

PN 16-SEP-1999.

PD 13-MAR-1998; 98WO-US005039.

PF 13-MAR-1998; 98WO-US005039.

PR (EPIM-) EPIMUNE INC.

XX Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;

PI WPI; 1999-551214/46.

DR New immunogenic peptides with HLA binding motif, useful in treatment and

PT diagnosis of cancers and viral diseases.

XX Claim 1; Page 93; 150pp; English.

XX AAY45390 to AAY48214 represent specifically claimed immunogenic peptides

CC having a human major histocompatibility complex (MHC) Class I (also known

CC as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides

CC can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2

CC or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against

CC the antigen from which the peptide is derived. Cytotoxic T lymphocytes

CC (CTLs) which destroy antigen-bearing cells are normally induced by an

CC antigen in the form of a peptide fragment bound to a HLA molecule, rather

CC than the intact foreign antigen itself, and are particularly important in

CC tumour rejection and in fighting viral infections. The peptides are

CC therefore useful therapeutically to treat or prevent viral infections and

CC cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B

CC and C, AIDS, and renal carcinoma. They can be administered as vaccines to

CC elicit an immune response in individuals susceptible or otherwise at risk

CC of viral infection or cancer, or used to treat chronic or acute

CC conditions. They are also useful diagnostically, and can be used to

CC induce a cytotoxic T cell response, by contacting a cytotoxic T cell with

CC the peptide e.g. to produce CTLs ex vivo for infusion back into a

CC patient. The polynucleotides encoding the immunogenic peptides are also

CC useful therapeutically and for immunisation as above

XX Sequence 9 AA;

SQ Query Match 20.8%; Score 5; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SIFEQ 13

Db 1 SIFEQ 5

RESULT 12

ABP12131

ID ABP12131 standard; peptide; 9 AA.

XX

AC ABP12131;

XX

DT 11-SEP-2003 (revised)

DT 15-JUL-2002 (first entry)

XX HIV A02 super motif env peptide #188.  
XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vif; vpr; vpu;  
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;  
KW vaccine; HIV infection; immunisation; virucide.  
XX  
OS Human immunodeficiency virus 1.  
XX  
XX WO200124810-A1.  
XX  
XX 12-APR-2001.  
XX  
XX 05-OCT-2000; 2000WO-US027766.  
PF  
XX 05-OCT-1999; 99US-00412863.  
PR  
XX (EPIM-) EPIMUNE INC.  
PA  
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
PI Baker DM, Cellis E, Kubo RT, Grey HM;  
PI  
XX WPI; 2001-354887/37.  
DR  
XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
XX peptide groups, useful for vaccinating against HIV-1.  
PT  
XX  
XX Claim 32; Page 117; 448pp; English.  
XX  
XX The present invention describes a composition (I) comprising a prepared  
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
CC sequence selected from 51 defined amino acid sequences (ABP25347 to  
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may  
CC be used for immunising subjects against HIV-1 infections. The use of  
CC group-based vaccines has several advantages over traditional vaccines,  
CC particularly when compared to the use of whole antigens in vaccine  
CC compositions. There is evidence that the immune response to whole  
CC antigens is directed largely toward variable regions of the antigen,  
CC allowing for immune escape due to mutations. The groups for inclusion in  
CC an group-based vaccine may be selected from conserved regions of viral or  
CC tumour-associated antigens, which therefore reduces the likelihood of  
CC escape mutants. Furthermore, immunosuppressive groups that may be present  
CC in whole antigens can be avoided with the use of group-based vaccines. An  
CC additional advantage of an group-based vaccine approach is the ability to  
CC combine selected groups (CTL and HTL), and further, to modify the  
CC composition of the groups, achieving, for example, enhanced  
CC immunogenicity. Accordingly, the immune response can be modulated, as  
CC appropriate, for the target disease. Similar engineering of the response  
CC is not possible with traditional approaches. ABP11501 to ABP25412  
CC represent peptide sequences used in the exemplification of the present  
CC invention. (Updated on 11-SEP-2003 to standardise OS field)  
XX  
XX Sequence 9 AA;  
SQ  
Query Match 20.8%; Score 5; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 16 NNNS 20  
DB 3 NNNS 7  
RESULT 13  
ABB94781  
ID ABB94781 standard; peptide; 9 AA.  
XX  
AC ABB94781;  
XX  
XX 17-JUN-2002 (first entry)  
DT  
XX CTL epitope HLA peptide SEQ ID NO:310.  
DE  
XX

KW Human; 158P1H4; chromosome 8q22q23, 158P1F4; chromosome 8q23; cancer;  
KW bladder cancer; immune response; cytotoxic T lymphocyte; CTL; HLA;  
KW human leukocyte antigen; helper T lymphocyte; HTL.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
XX WO200216598-A2.  
XX  
XX 28-FEB-2002.  
XX  
XX 22-AUG-2001; 2001WO-US026411.  
PF  
XX 22-AUG-2000; 2000US-0227098P.  
PR  
XX 10-APR-2001; 2001US-0282739P.  
PR  
XX (AGEN-) AGENSYS INC.  
PA  
XX Challita-Eid PM, Hubert RS, Raitano AB, Afar DEH, Levin E;  
PI Paris M, Ge W, Jakobovits A;  
PI  
XX WPI; 2002-269357/31.  
DR  
XX Monitoring 158P1H4 gene products in biological sample from patient who  
XX has or is suspected of having cancer, useful for treating cancer,  
PT comprises identifying presence of aberrant 158P1H4 gene products in  
PT biological sample.  
XX  
XX Claim 64; Page 152; 209pp; English.  
XX  
XX The present invention describes a method for monitoring 158P1H4 gene  
CC products in a biological sample from a patient who has or is suspected of  
CC having cancer. The method comprises determining the status of 158P1H4  
CC gene products in a tissue sample from an individual, comparing the status  
CC to the status of 158P1H4 gene products in a normal sample, and  
CC identifying the presence of aberrant 158P1H4 gene products in the sample.  
CC 158P1H4 sequences have cytototoxic activity and can be used in vaccine  
CC production. 158P1H4 polynucleotides may be used in monitoring genetic  
CC abnormalities. The 158P1H4 proteins may be used in assessing the status  
CC of 158P1H4 gene products in normal versus cancerous tissues and so  
CC elucidating the malignant phenotype, in generating and characterising  
CC domain-specific antibodies, for identifying agents or cellular factors  
CC that bind to 158P1H4 or its particular domain, and for generating cancer  
CC vaccines. Antibodies against 158P1H4 are useful in diagnostic and  
CC prognostic assays, in treating patients with cancer, in generating  
CC cytotoxic T lymphocyte (CTL) or helper T lymphocyte (HTL) responses, and  
CC as immunological reagents for detecting 158P1H4-expressing cells. The  
CC antibodies are particularly useful in bladder cancer diagnostic and  
CC prognostic assays, and imaging methodologies. The 158P1H4 gene has been  
CC located to chromosome 8q22-q23, and the 158P1F4 gene also described in  
CC the present invention has been located to chromosome 8q23. ABL50400 to  
CC ABL50429 and ABB94468 to ABB95188 represent sequences used in the  
CC exemplification of the present invention  
XX  
XX Sequence 9 AA;  
SQ  
Query Match 20.8%; Score 5; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 DSQTK 8  
DB 5 DSQTK 9  
RESULT 14  
ABB94700  
ID ABB94700 standard; peptide; 9 AA.  
XX  
XX ABB94700;  
AC  
XX  
XX 17-JUN-2002 (first entry)  
DT  
XX

DE CTL epitope HLA peptide SEQ ID NO:229.  
XX Human; 158PIH4; chromosome 8q220q23, 158PIF4; chromosome 8q23; cancer;  
KW bladder cancer; immune response; cytotoxic T lymphocyte; CTL; HLA;  
KW human leukocyte antigen; helper T lymphocyte; HTL.  
XX Homo sapiens.  
OS Synthetic.  
XX WO200216598-A2.  
XX 28-FEB-2002.  
XX 22-AUG-2001; 2001WO-US026411.  
XX 22-AUG-2000; 2000US-0227098P.  
PR 10-APR-2001; 2001US-0282739P.  
XX (AGEN-) AGENSYS INC.  
XX Challita-Eid PM, Hubert RS, Raitano AB, Afar DEH, Levin E;  
PI Faris M, Ge W, Jakobovits A;  
XX WPI; 2002-269357/31.  
XX Monitoring 158PIH4 gene products in biological sample from patient who  
PT has or is suspected of having cancer, useful for treating cancer,  
PT comprises identifying presence of aberrant 158PIH4 gene products in  
PT biological sample.  
PS Claim 64; Page 149; 209pp; English.  
XX The present invention describes a method for monitoring 158PIH4 gene  
CC products in a biological sample from a patient who has or is suspected of  
CC having cancer. The method comprises determining the status of 158PIH4  
CC gene products in a tissue sample from an individual, comparing the status  
CC to the status of 158PIH4 gene products in a normal sample, and  
CC identifying the presence of aberrant 158PIH4 gene products in the sample.  
CC 158PIH4 sequences have cytostatic activity and can be used in vaccine  
CC production. 158PIH4 polynucleotides may be used in monitoring genetic  
CC abnormalities. The 158PIH4 proteins may be used in assessing the status  
CC of 158PIH4 gene products in normal versus cancerous tissues and so  
CC elucidating the malignant phenotype, in generating and characterising  
CC domain-specific antibodies, for identifying agents or cellular factors  
CC that bind to 158PIH4 or its particular domain, and for generating cancer  
CC vaccines. Antibodies against 158PIH4 are useful in diagnostic and  
CC cytotoxic T lymphocyte (CTL) or helper T lymphocyte (HTL) responses, and  
CC as immunological reagents for detecting 158PIH4-expressing cells. The  
CC antibodies are particularly useful in bladder cancer diagnostic and  
CC prognostic assays, and imaging methodologies. The 158PIH4 gene has been  
CC located to chromosome 8q22-q23, and the 158PIF4 gene also described in  
CC the present invention has been located to chromosome 8q23. ABL50400 to  
CC ABL50429 and ABB94468 to ABB95188 represent sequences used in the  
CC exemplification of the present invention  
XX Sequence 9 AA;  
SQ Query Match 20.8%; Score 5; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 DSQTK 8  
|||||  
DB 5 DSQTK 9  
RESULT 15  
ABB94890  
ID ABB94890 standard; peptide; 9 AA.  
XX  
AC ABB94890;  
XX

DT 17-JUN-2002 (first entry)  
XX CTL epitope HLA peptide SEQ ID NO:419.  
DE Human; 158PIH4; chromosome 8q220q23, 158PIF4; chromosome 8q23; cancer;  
XX bladder cancer; immune response; cytotoxic T lymphocyte; CTL; HLA;  
KW human leukocyte antigen; helper T lymphocyte; HTL.  
XX Homo sapiens.  
OS Synthetic.  
XX WO200216598-A2.  
XX 28-FEB-2002.  
XX 22-AUG-2001; 2001WO-US026411.  
XX 22-AUG-2000; 2000US-0227098P.  
PR 10-APR-2001; 2001US-0282739P.  
XX (AGEN-) AGENSYS INC.  
XX Challita-Eid PM, Hubert RS, Raitano AB, Afar DEH, Levin E;  
PI Faris M, Ge W, Jakobovits A;  
XX WPI; 2002-269357/31.  
XX Monitoring 158PIH4 gene products in biological sample from patient who  
PT has or is suspected of having cancer, useful for treating cancer,  
PT comprises identifying presence of aberrant 158PIH4 gene products in  
PT biological sample.  
XX Claim 64; Page 156; 209pp; English.  
XX The present invention describes a method for monitoring 158PIH4 gene  
CC products in a biological sample from a patient who has or is suspected of  
CC having cancer. The method comprises determining the status of 158PIH4  
CC gene products in a tissue sample from an individual, comparing the status  
CC to the status of 158PIH4 gene products in a normal sample, and  
CC identifying the presence of aberrant 158PIH4 gene products in the sample.  
CC 158PIH4 sequences have cytostatic activity and can be used in vaccine  
CC production. 158PIH4 polynucleotides may be used in monitoring genetic  
CC abnormalities. The 158PIH4 proteins may be used in assessing the status  
CC of 158PIH4 gene products in normal versus cancerous tissues and so  
CC elucidating the malignant phenotype, in generating and characterising  
CC domain-specific antibodies, for identifying agents or cellular factors  
CC that bind to 158PIH4 or its particular domain, and for generating cancer  
CC vaccines. Antibodies against 158PIH4 are useful in diagnostic and  
CC prognostic assays, in treating patients with cancer, in generating  
CC cytotoxic T lymphocyte (CTL) or helper T lymphocyte (HTL) responses, and  
CC as immunological reagents for detecting 158PIH4-expressing cells. The  
CC antibodies are particularly useful in bladder cancer diagnostic and  
CC prognostic assays, and imaging methodologies. The 158PIH4 gene has been  
CC located to chromosome 8q22-q23, and the 158PIF4 gene also described in  
CC the present invention has been located to chromosome 8q23. ABL50400 to  
CC ABL50429 and ABB94468 to ABB95188 represent sequences used in the  
CC exemplification of the present invention  
XX Sequence 9 AA;  
SQ Query Match 20.8%; Score 5; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 DSQTK 8  
|||||  
DB 1 DSQTK 5  
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Job time : 101 secs

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OM protein - protein search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	6	25.0	23	2	US-09-378-343-4
4	6	25.0	23	5	US-09-599-652-4
5	5	20.8	17	1	US-08-729-152-32
6	5	20.8	21	2	US-09-962-756-501
7	5	20.8	23	1	US-08-486-953A-48
8	5	20.8	23	2	US-08-204-052-48
9	5	20.8	23	2	US-09-967-869A-1
10	4	16.7	4	1	US-07-834-848-3
11	4	16.7	4	1	US-08-251-027-10
12	4	16.7	4	1	US-08-747-137-33
13	4	16.7	4	2	US-10-353-174-33
14	4	16.7	5	1	US-07-834-848-7
15	4	16.7	5	1	US-07-834-848-10
16	4	16.7	5	2	US-09-164-021-11
17	4	16.7	5	2	US-09-608-892-68
18	4	16.7	5	2	US-09-519-703-11
19	4	16.7	5	2	US-09-623-548A-1080
20	4	16.7	5	2	US-09-657-276-1080
21	4	16.7	6	1	US-07-620-426B-18
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26	4	16.7	6	2	US-09-579-894-20
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					Sequence 1080, Ap
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					Sequence 133, App
					Sequence 20, Appl
					Sequence 7, Appli

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Sequence 51, Appl	7	2	US-09-019-793A-51	4	16.7
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Sequence 132, App	7	2	US-09-721-108-132	4	16.7
Sequence 61, Appl	7	2	US-09-192-854-61	4	16.7
Sequence 92, Appl	7	2	US-09-601-326-92	4	16.7
Sequence 99, Appl	7	2	US-09-511-933-99	4	16.7
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Sequence 503, App	8	2	US-09-303-518D-503	4	16.7
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Sequence 130, App	9	2	US-09-721-108-130	4	16.7
Sequence 131, App	9	2	US-09-285-912A-131	4	16.7
Sequence 132, App	9	2	US-09-285-912A-132	4	16.7
Sequence 8, Appli	10	1	US-08-045-261-8	4	16.7
Sequence 149, App	10	1	US-08-480-190-149	4	16.7
Sequence 149, App	10	1	US-08-488-379-149	4	16.7
Sequence 26, Appl	10	1	US-08-428-257A-26	4	16.7
Sequence 149, App	10	2	US-08-475-399A-149	4	16.7
Sequence 129, App	10	2	US-09-721-108-129	4	16.7
Sequence 157, App	10	2	US-09-601-729-157	4	16.7
Sequence 149, App	10	2	US-08-077-255A-149	4	16.7
Sequence 55, Appl	10	2	US-09-644-456B-55	4	16.7
Sequence 1, Appli	10	2	US-10-101-812-1	4	16.7
Sequence 149, App	10	4	PCT-US93-07545-149	4	16.7
Sequence 10, Appl	11	1	US-08-411-727-10	4	16.7
Sequence 18, Appl	11	1	US-08-411-727-18	4	16.7
Sequence 43, Appl	11	1	US-08-040-548-43	4	16.7
Sequence 43, Appl	11	1	US-08-466-344-43	4	16.7
Sequence 58, Appl	11	1	US-08-893-853-58	4	16.7
Sequence 93, Appl	11	2	US-08-491-954-93	4	16.7
Sequence 109, App	11	2	US-09-113-921-109	4	16.7
Sequence 109, App	11	2	US-09-451-067-109	4	16.7
Sequence 128, App	11	2	US-09-721-108-128	4	16.7
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Sequence 111, App	12	1	US-08-480-190-111	4	16.7
Sequence 187, App	12	1	US-08-480-190-187	4	16.7
Sequence 100, App	12	1	US-08-488-379-100	4	16.7
Sequence 111, App	12	1	US-08-488-379-111	4	16.7
Sequence 187, App	12	1	US-08-488-379-187	4	16.7
Sequence 13, Appl	12	2	US-09-003-903-13	4	16.7
Sequence 27, Appl	12	2	US-08-481-968A-27	4	16.7
Sequence 27, Appl	12	2	US-08-154-712B-27	4	16.7
Sequence 100, App	12	2	US-08-475-399A-100	4	16.7
Sequence 111, App	12	2	US-08-475-399A-111	4	16.7
Sequence 187, App	12	2	US-08-475-399A-187	4	16.7
Sequence 3, Appli	12	2	US-09-744-900-3	4	16.7
Sequence 100, App	12	2	US-09-721-108-127	4	16.7
Sequence 127, App	12	2	US-08-077-255A-100	4	16.7
Sequence 111, App	12	2	US-08-077-255A-111	4	16.7
Sequence 187, App	12	2	US-08-077-255A-187	4	16.7
Sequence 27, Appl	12	2	PCT-US93-07545-27	4	16.7
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Sequence 111, App	12	4	PCT-US93-07545-111	4	16.7
Sequence 187, App	12	4	PCT-US93-07545-187	4	16.7



101	4	16.7	13	1	US-08-057-184-2	Sequence 2, Appli	174	4	16.7	17	1	US-08-488-379-98	Sequence 98, Appl
102	4	16.7	13	1	US-08-346-293-16	Sequence 16, Appl	175	4	16.7	17	1	US-08-488-379-108	Sequence 108, App
103	4	16.7	13	1	US-08-248-839C-45	Sequence 45, Appl	176	4	16.7	17	1	US-08-488-379-109	Sequence 109, App
104	4	16.7	13	1	US-08-321-670-10	Sequence 10, Appl	177	4	16.7	17	2	US-09-556-877-143	Sequence 143, App
105	4	16.7	13	2	US-08-836-075A-157	Sequence 157, App	178	4	16.7	17	2	US-09-620-412C-143	Sequence 143, App
106	4	16.7	13	2	US-09-194-285-56	Sequence 56, Appl	179	4	16.7	17	2	US-08-475-399A-97	Sequence 97, Appl
107	4	16.7	13	2	US-09-721-108-126	Sequence 126, App	180	4	16.7	17	2	US-08-475-399A-98	Sequence 98, Appl
108	4	16.7	13	2	US-09-519-959-2	Sequence 2, Appli	181	4	16.7	17	2	US-08-475-399A-108	Sequence 108, App
109	4	16.7	14	1	US-08-346-293-17	Sequence 17, Appl	182	4	16.7	17	2	US-08-475-399A-109	Sequence 109, App
110	4	16.7	14	1	US-08-176-126B-5	Sequence 5, Appli	183	4	16.7	17	2	US-09-598-419-143	Sequence 143, App
111	4	16.7	14	1	US-08-290-448A-92	Sequence 92, Appl	184	4	16.7	17	2	US-09-721-108-122	Sequence 122, App
112	4	16.7	14	1	US-08-290-448A-92	Sequence 92, Appl	185	4	16.7	17	2	US-08-077-255A-97	Sequence 97, Appl
113	4	16.7	14	1	US-08-175-069A-92	Sequence 92, Appl	186	4	16.7	17	2	US-08-077-255A-98	Sequence 98, Appl
114	4	16.7	14	1	US-08-480-190-110	Sequence 110, App	187	4	16.7	17	2	US-08-077-255A-108	Sequence 108, App
115	4	16.7	14	1	US-08-669-435-5	Sequence 5, Appli	188	4	16.7	17	2	US-08-077-255A-109	Sequence 109, App
116	4	16.7	14	1	US-08-488-379-110	Sequence 110, App	189	4	16.7	17	2	US-10-204-664A-3	Sequence 3, Appli
117	4	16.7	14	1	US-08-372-100C-8	Sequence 8, Appli	190	4	16.7	17	4	PCT-US93-07545-97	Sequence 97, Appl
118	4	16.7	14	2	US-08-331-625A-33	Sequence 33, Appl	191	4	16.7	17	4	PCT-US93-07545-98	Sequence 98, Appl
119	4	16.7	14	2	US-08-865-511B-8	Sequence 8, Appli	192	4	16.7	17	4	PCT-US93-07545-108	Sequence 108, App
120	4	16.7	14	2	US-09-231-159-10	Sequence 10, Appl	193	4	16.7	17	4	PCT-US93-07545-109	Sequence 109, App
121	4	16.7	14	2	US-08-611-307-10	Sequence 10, Appl	194	4	16.7	18	1	US-08-383-753-66	Sequence 66, Appl
122	4	16.7	14	2	US-08-461-939B-92	Sequence 92, Appl	195	4	16.7	18	1	US-08-480-190-106	Sequence 106, App
123	4	16.7	14	2	US-08-464-000-92	Sequence 92, Appl	196	4	16.7	18	1	US-08-480-190-107	Sequence 107, App
124	4	16.7	14	2	US-09-494-151-33	Sequence 33, Appl	197	4	16.7	18	1	US-08-586-772-66	Sequence 66, Appl
125	4	16.7	14	2	US-08-475-399A-110	Sequence 110, App	198	4	16.7	18	1	US-08-488-379-106	Sequence 106, App
126	4	16.7	14	2	US-08-506-436-8	Sequence 8, Appli	199	4	16.7	18	1	US-08-488-379-107	Sequence 107, App
127	4	16.7	14	2	US-09-972-484-33	Sequence 33, Appl	200	4	16.7	18	1	US-08-649-991-48	Sequence 48, Appl
128	4	16.7	14	2	US-09-721-108-125	Sequence 125, App	201	4	16.7	18	1	US-08-649-991-50	Sequence 50, Appl
129	4	16.7	14	2	US-08-077-255A-110	Sequence 110, App	202	4	16.7	18	1	US-08-649-991-51	Sequence 51, Appl
130	4	16.7	14	2	US-08-928-074-10	Sequence 10, Appl	203	4	16.7	18	1	US-08-959-512-66	Sequence 66, Appl
131	4	16.7	14	4	PCT-US93-07545-110	Sequence 110, App	204	4	16.7	18	2	US-09-513-983-66	Sequence 66, Appl
132	4	16.7	14	4	PCT-US94-14431A-5	Sequence 5, Appli	205	4	16.7	18	2	US-08-630-95A-172	Sequence 172, App
133	4	16.7	14	4	PCT-US95-17085-8	Sequence 8, Appli	206	4	16.7	18	2	US-08-475-399A-106	Sequence 106, App
134	4	16.7	15	1	US-08-471-780C-73	Sequence 73, Appl	207	4	16.7	18	2	US-08-475-399A-107	Sequence 107, App
135	4	16.7	15	1	US-08-467-282B-73	Sequence 73, Appl	208	4	16.7	18	2	US-09-721-108-121	Sequence 121, App
136	4	16.7	15	1	US-08-480-190-99	Sequence 99, Appl	209	4	16.7	18	2	US-08-077-255A-106	Sequence 106, App
137	4	16.7	15	1	US-08-471-282A-73	Sequence 73, Appl	210	4	16.7	18	2	US-08-077-255A-107	Sequence 107, App
138	4	16.7	15	1	US-08-466-710C-73	Sequence 73, Appl	211	4	16.7	18	2	US-09-879-937-172	Sequence 172, App
139	4	16.7	15	1	US-08-488-379-99	Sequence 99, Appl	212	4	16.7	18	2	US-10-394-980-29	Sequence 29, Appl
140	4	16.7	15	2	US-08-468-739C-73	Sequence 73, Appl	213	4	16.7	18	2	US-09-869-003-20	Sequence 20, Appl
141	4	16.7	15	2	US-08-481-968A-17	Sequence 17, Appl	214	4	16.7	18	4	PCT-US93-07545-106	Sequence 106, App
142	4	16.7	15	2	US-08-154-712B-17	Sequence 17, Appl	215	4	16.7	18	4	PCT-US93-07545-107	Sequence 107, App
143	4	16.7	15	2	US-08-475-399A-99	Sequence 99, Appl	216	4	16.7	19	1	US-08-480-190-94	Sequence 94, Appl
144	4	16.7	15	2	US-09-205-258-986	Sequence 986, App	217	4	16.7	19	1	US-08-480-190-95	Sequence 95, Appl
145	4	16.7	15	2	US-09-157-689-50	Sequence 50, Appl	218	4	16.7	19	1	US-08-480-190-96	Sequence 96, Appl
146	4	16.7	15	2	US-09-157-689-51	Sequence 51, Appl	219	4	16.7	19	1	US-08-480-190-105	Sequence 105, App
147	4	16.7	15	2	US-09-157-689-52	Sequence 52, Appl	220	4	16.7	19	1	US-08-488-379-94	Sequence 94, Appl
148	4	16.7	15	2	US-09-721-108-124	Sequence 124, App	221	4	16.7	19	1	US-08-488-379-95	Sequence 95, Appl
149	4	16.7	15	2	US-08-077-255A-99	Sequence 99, Appl	222	4	16.7	19	1	US-08-488-379-96	Sequence 96, Appl
150	4	16.7	15	2	US-09-947-925A-17	Sequence 17, Appl	223	4	16.7	19	1	US-08-488-379-105	Sequence 105, App
151	4	16.7	15	2	US-09-293-769A-73	Sequence 73, Appl	224	4	16.7	19	2	US-08-865-511B-22	Sequence 23, Appl
152	4	16.7	15	2	US-09-953-510-50	Sequence 50, Appl	225	4	16.7	19	2	US-08-865-511B-23	Sequence 24, Appl
153	4	16.7	15	2	US-09-953-510-51	Sequence 51, Appl	226	4	16.7	19	2	US-08-475-399A-94	Sequence 94, Appl
154	4	16.7	15	2	US-09-953-510-52	Sequence 52, Appl	227	4	16.7	19	2	US-08-475-399A-95	Sequence 95, Appl
155	4	16.7	15	2	US-10-004-860-986	Sequence 986, App	228	4	16.7	19	2	US-08-475-399A-96	Sequence 96, Appl
156	4	16.7	15	4	PCT-US93-07545-99	Sequence 99, Appl	229	4	16.7	19	2	US-08-475-399A-105	Sequence 105, App
157	4	16.7	16	1	US-07-794-288D-204	Sequence 204, App	230	4	16.7	19	2	US-09-721-108-120	Sequence 120, App
158	4	16.7	16	1	US-08-480-190-171	Sequence 171, App	231	4	16.7	19	2	US-08-077-255A-94	Sequence 94, Appl
159	4	16.7	16	1	US-08-488-379-171	Sequence 171, App	232	4	16.7	19	2	US-08-077-255A-95	Sequence 95, Appl
160	4	16.7	16	2	US-09-155-613A-9	Sequence 9, Appli	233	4	16.7	19	2	US-08-077-255A-96	Sequence 96, Appl
161	4	16.7	16	2	US-08-475-399A-171	Sequence 171, App	234	4	16.7	19	2	US-08-077-255A-105	Sequence 105, App
162	4	16.7	16	2	US-08-851-567B-18	Sequence 18, Appl	235	4	16.7	19	2	US-09-688-017-203	Sequence 203, App
163	4	16.7	16	2	US-09-721-108-123	Sequence 123, App	236	4	16.7	19	4	PCT-US93-07545-94	Sequence 94, Appl
164	4	16.7	16	2	US-08-077-255A-171	Sequence 171, App	237	4	16.7	19	4	PCT-US93-07545-95	Sequence 95, Appl
165	4	16.7	16	2	US-09-618-577-33	Sequence 33, Appl	238	4	16.7	19	4	PCT-US93-07545-96	Sequence 96, Appl
166	4	16.7	16	2	US-09-055-505-33	Sequence 33, Appl	239	4	16.7	19	4	PCT-US93-07545-105	Sequence 105, App
167	4	16.7	16	2	US-09-013-077A-3	Sequence 3, Appli	240	4	16.7	20	1	US-08-043-760-1	Sequence 1, Appli
168	4	16.7	16	4	PCT-US93-07545-171	Sequence 171, App	241	4	16.7	20	1	US-07-798-776-10	Sequence 10, Appl
169	4	16.7	17	1	US-08-480-190-97	Sequence 97, Appl	242	4	16.7	20	1	US-08-218-025A-41	Sequence 41, Appl
170	4	16.7	17	1	US-08-480-190-98	Sequence 98, Appl	243	4	16.7	20	1	US-08-218-025A-42	Sequence 42, Appl
171	4	16.7	17	1	US-08-480-190-108	Sequence 108, App	244	4	16.7	20	1	US-08-360-049-1	Sequence 1, Appli
172	4	16.7	17	1	US-08-480-190-109	Sequence 109, App	245	4	16.7	20	1	US-08-480-190-93	Sequence 93, Appl
173	4	16.7	17	1	US-08-488-379-97	Sequence 97, Appl	246	4	16.7	20	1	US-08-480-190-104	Sequence 104, App



247	4	16.7	20	1	US-08-480-190-244	Sequence 244, App	320	4	16.7	22	2	US-08-470-106-30	Sequence 30, Appl
248	4	16.7	20	1	US-08-411-726-4	Sequence 4, Appli	321	4	16.7	22	2	US-09-028-937-30	Sequence 30, Appl
249	4	16.7	20	1	US-08-488-379-93	Sequence 93, Appl	322	4	16.7	22	2	US-08-912-931-92	Sequence 92, Appl
250	4	16.7	20	1	US-08-488-379-104	Sequence 104, App	323	4	16.7	22	2	US-08-475-399A-43	Sequence 43, Appl
251	4	16.7	20	1	US-08-488-379-244	Sequence 244, App	324	4	16.7	22	2	US-08-475-399A-102	Sequence 102, App
252	4	16.7	20	1	US-08-934-915-89	Sequence 89, Appl	325	4	16.7	22	2	US-08-851-567B-70	Sequence 70, Appl
253	4	16.7	20	1	US-08-934-915-153	Sequence 153, App	326	4	16.7	22	2	US-09-402-181B-92	Sequence 92, Appl
254	4	16.7	20	1	US-08-372-100C-2	Sequence 2, Appli	327	4	16.7	22	2	US-09-721-456-92	Sequence 92, Appl
255	4	16.7	20	1	US-08-372-100C-3	Sequence 3, Appli	328	4	16.7	22	2	US-08-077-255A-43	Sequence 43, Appl
256	4	16.7	20	2	US-08-251-288A-10	Sequence 10, Appl	329	4	16.7	22	2	US-08-077-255A-102	Sequence 102, App
257	4	16.7	20	2	US-09-298-819A-10	Sequence 10, Appl	330	4	16.7	22	2	US-08-187-873-8	Sequence 8, Appli
258	4	16.7	20	2	US-08-865-511B-2	Sequence 2, Appli	331	4	16.7	22	4	PCT-US93-07545-43	Sequence 43, Appl
259	4	16.7	20	2	US-08-865-511B-3	Sequence 3, Appli	332	4	16.7	22	4	PCT-US93-07545-102	Sequence 102, App
260	4	16.7	20	2	US-09-586-563C-10	Sequence 10, Appl	333	4	16.7	23	1	US-08-480-190-101	Sequence 101, App
261	4	16.7	20	2	US-09-586-562C-10	Sequence 10, Appl	334	4	16.7	23	1	US-08-480-190-195	Sequence 195, App
262	4	16.7	20	2	US-08-475-399A-93	Sequence 93, Appl	335	4	16.7	23	1	US-08-493-235-37	Sequence 37, Appl
263	4	16.7	20	2	US-08-475-399A-104	Sequence 104, App	336	4	16.7	23	1	US-08-528-057-29	Sequence 29, Appl
264	4	16.7	20	2	US-08-475-399A-244	Sequence 244, App	337	4	16.7	23	1	US-08-486-953A-43	Sequence 43, Appl
265	4	16.7	20	2	US-08-506-436-2	Sequence 2, Appli	338	4	16.7	23	1	US-08-486-953A-44	Sequence 44, Appl
266	4	16.7	20	2	US-08-506-436-3	Sequence 3, Appli	339	4	16.7	23	1	US-08-679-405-7	Sequence 7, Appli
267	4	16.7	20	2	US-09-721-108-119	Sequence 119, App	340	4	16.7	23	1	US-08-488-379-101	Sequence 101, App
268	4	16.7	20	2	US-08-077-255A-93	Sequence 93, Appl	341	4	16.7	23	1	US-08-488-379-195	Sequence 195, App
269	4	16.7	20	2	US-08-077-255A-104	Sequence 104, App	342	4	16.7	23	1	US-08-842-793-7	Sequence 7, Appli
270	4	16.7	20	2	US-08-077-255A-244	Sequence 244, App	343	4	16.7	23	1	US-08-031-538-55	Sequence 55, Appl
271	4	16.7	20	2	US-09-623-548A-302	Sequence 302, App	344	4	16.7	23	2	US-08-609-236-3	Sequence 3, Appli
272	4	16.7	20	2	US-09-657-276-302	Sequence 302, App	345	4	16.7	23	2	US-08-475-399A-101	Sequence 101, App
273	4	16.7	20	4	PCT-US93-07545-93	Sequence 93, Appl	346	4	16.7	23	2	US-08-475-399A-195	Sequence 195, App
274	4	16.7	20	4	PCT-US93-07545-104	Sequence 104, App	347	4	16.7	23	2	US-08-077-255A-101	Sequence 101, App
275	4	16.7	20	4	PCT-US93-07545-244	Sequence 244, App	348	4	16.7	23	2	US-08-077-255A-195	Sequence 195, App
276	4	16.7	20	4	PCT-US95-17085-2	Sequence 2, Appli	349	4	16.7	23	2	US-09-285-912A-65	Sequence 65, Appl
277	4	16.7	20	4	PCT-US95-17085-3	Sequence 3, Appli	350	4	16.7	23	2	US-09-285-912A-109	Sequence 109, App
278	4	16.7	21	1	US-08-480-190-92	Sequence 92, Appl	351	4	16.7	23	2	US-08-204-052-43	Sequence 43, Appl
279	4	16.7	21	1	US-08-480-190-103	Sequence 103, App	352	4	16.7	23	2	US-08-204-052-44	Sequence 44, Appl
280	4	16.7	21	1	US-08-488-379-92	Sequence 92, Appl	353	4	16.7	23	2	PCT-US93-07545-101	Sequence 101, App
281	4	16.7	21	1	US-08-488-379-103	Sequence 103, App	354	4	16.7	23	4	PCT-US93-07545-195	Sequence 195, App
282	4	16.7	21	2	US-08-423-646A-34	Sequence 34, Appl	355	4	16.7	23	4	PCT-US96-11458-7	Sequence 7, Appli
283	4	16.7	21	2	US-08-423-646A-35	Sequence 35, Appl	356	4	16.7	24	2	US-08-725-459B-34	Sequence 34, Appl
284	4	16.7	21	2	US-08-423-646A-36	Sequence 36, Appl	357	4	16.7	24	2	US-09-270-767-36880	Sequence 36880, A
285	4	16.7	21	2	US-08-475-399A-92	Sequence 92, Appl	358	4	16.7	24	2	US-09-270-767-52097	Sequence 52097, A
286	4	16.7	21	2	US-08-475-399A-103	Sequence 103, App	359	4	16.7	25	1	US-08-145-708A-20	Sequence 20, Appl
287	4	16.7	21	2	US-09-721-108-118	Sequence 118, App	360	4	16.7	25	1	US-08-406-347A-12	Sequence 12, Appl
288	4	16.7	21	2	US-09-721-108-119	Sequence 119, App	361	4	16.7	25	1	US-08-331-454-20	Sequence 20, Appl
289	4	16.7	21	2	US-09-721-108-150	Sequence 150, App	362	4	16.7	25	2	US-09-314-268-4	Sequence 4, Appli
290	4	16.7	21	2	US-09-721-108-151	Sequence 151, App	363	4	16.7	25	2	US-08-905-054B-10	Sequence 10, Appl
291	4	16.7	21	2	US-09-721-108-152	Sequence 152, App	364	4	16.7	25	2	US-09-716-129-133	Sequence 133, App
292	4	16.7	21	2	US-09-721-108-153	Sequence 153, App	365	4	16.7	25	2	US-09-258-031C-1	Sequence 1, Appli
293	4	16.7	21	2	US-09-721-108-154	Sequence 154, App	366	4	16.7	25	4	PCT-US92-07813-10	Sequence 10, Appl
294	4	16.7	21	2	US-09-721-108-155	Sequence 155, App	367	3	12.5	3	1	US-08-251-027-4	Sequence 4, Appli
295	4	16.7	21	2	US-09-721-108-156	Sequence 156, App	368	3	12.5	3	1	US-08-305-768-26	Sequence 26, Appl
296	4	16.7	21	2	US-09-721-108-157	Sequence 157, App	369	3	12.5	3	1	US-08-871-163-26	Sequence 26, Appl
297	4	16.7	21	2	US-09-721-108-158	Sequence 158, App	370	3	12.5	3	1	US-08-767-903-26	Sequence 26, Appl
298	4	16.7	21	2	US-09-721-108-159	Sequence 159, App	371	3	12.5	3	4	PCT-US95-11724-26	Sequence 26, Appl
299	4	16.7	21	2	US-09-721-108-160	Sequence 160, App	372	3	12.5	4	1	US-08-285-777-2	Sequence 2, Appli
300	4	16.7	21	2	US-09-721-108-161	Sequence 161, App	373	3	12.5	4	1	US-08-457-605-2	Sequence 2, Appli
301	4	16.7	21	2	US-09-721-108-162	Sequence 162, App	374	3	12.5	4	1	US-08-305-768-30	Sequence 30, Appl
302	4	16.7	21	2	US-08-077-255A-92	Sequence 92, Appl	375	3	12.5	4	1	US-08-305-768-29	Sequence 29, Appl
303	4	16.7	21	2	US-08-077-255A-103	Sequence 103, App	376	3	12.5	4	1	US-08-372-262-4	Sequence 4, Appli
304	4	16.7	21	2	US-09-270-767-58351	Sequence 58351, A	377	3	12.5	4	1	US-08-456-424-8	Sequence 8, Appli
305	4	16.7	21	2	US-09-270-767-59315	Sequence 59315, A	378	3	12.5	4	1	US-08-456-424-9	Sequence 9, Appli
306	4	16.7	21	2	US-09-962-756-562	Sequence 562, App	379	3	12.5	4	1	US-08-456-424-13	Sequence 13, Appl
307	4	16.7	21	2	US-09-962-756-643	Sequence 643, App	380	3	12.5	4	1	US-08-456-424-14	Sequence 14, Appl
308	4	16.7	21	2	US-09-962-756-650	Sequence 650, App	381	3	12.5	4	1	US-08-456-424-24	Sequence 24, Appl
309	4	16.7	21	2	US-09-962-756-1746	Sequence 1746, App	382	3	12.5	4	1	US-08-456-424-25	Sequence 25, Appl
310	4	16.7	21	4	PCT-US93-07545-92	Sequence 92, Appl	383	3	12.5	4	1	US-08-456-424-95	Sequence 95, Appl
311	4	16.7	21	4	PCT-US93-07545-103	Sequence 103, App	384	3	12.5	4	1	US-08-456-424-96	Sequence 96, Appl
312	4	16.7	22	1	US-07-681-701-3	Sequence 3, Appli	385	3	12.5	4	1	US-08-871-163-29	Sequence 29, Appl
313	4	16.7	22	1	US-08-480-190-43	Sequence 43, Appl	386	3	12.5	4	1	US-08-871-163-30	Sequence 30, Appl
314	4	16.7	22	1	US-08-480-190-102	Sequence 102, App	387	3	12.5	4	2	US-08-947-965-63	Sequence 63, Appl
315	4	16.7	22	1	US-08-493-235-36	Sequence 36, Appl	388	3	12.5	4	2	US-08-767-903-29	Sequence 29, Appl
316	4	16.7	22	1	US-08-488-379-43	Sequence 43, Appl	389	3	12.5	4	2	US-08-767-903-30	Sequence 30, Appl
317	4	16.7	22	1	US-08-488-379-102	Sequence 102, App	390	3	12.5	4	2	US-08-974-549A-169	Sequence 169, App
318	4	16.7	22	2	US-08-318-794-30	Sequence 30, Appl	391	3	12.5	4	2	US-09-066-481-14	Sequence 14, Appl
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590	3	12.5	6	1	US-08-482-228-90	Sequence 90, Appl	663	3	12.5	6	2	US-09-721-870-163	Sequence 163, App
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593	3	12.5	6	1	US-09-127-574-48	Sequence 48, Appl	666	3	12.5	6	2	US-09-387-671-24	Sequence 24, Appl
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597	3	12.5	6	2	US-08-482-528-18	Sequence 18, Appl	670	3	12.5	6	2	US-09-305-928-256	Sequence 256, App
598	3	12.5	6	2	US-08-482-528-90	Sequence 90, Appl	671	3	12.5	6	2	US-09-802-096-61	Sequence 61, Appl
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603	3	12.5	6	2	US-08-767-903-16	Sequence 16, Appl	676	3	12.5	6	2	US-09-693-746-66	Sequence 66, Appl
604	3	12.5	6	2	US-08-767-903-17	Sequence 17, Appl	677	3	12.5	6	2	US-09-912-414-1	Sequence 1, Appli
605	3	12.5	6	2	US-08-767-903-18	Sequence 18, Appl	678	3	12.5	6	2	US-09-623-548A-1180	Sequence 1180, Ap
606	3	12.5	6	2	US-08-767-903-19	Sequence 19, Appl	679	3	12.5	6	2	US-09-623-548A-1186	Sequence 13, Appl
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608	3	12.5	6	2	US-08-767-903-21	Sequence 21, Appl	681	3	12.5	6	2	US-10-054-968-14	Sequence 14, Appl
609	3	12.5	6	2	US-08-767-903-22	Sequence 22, Appl	682	3	12.5	6	2	US-09-657-276-1180	Sequence 1180, Ap
610	3	12.5	6	2	US-08-767-903-23	Sequence 23, Appl	683	3	12.5	6	2	US-09-657-276-1186	Sequence 1186, Ap
611	3	12.5	6	2	US-08-767-903-24	Sequence 24, Appl	684	3	12.5	6	2	US-09-641-801-13	Sequence 13, Appl

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686	3	12.5	6	2	US-09-791-524A-101	Sequence 101, App	759	3	12.5	7	2	US-08-974-549A-130	Sequence 130, App
687	3	12.5	6	2	US-09-925-179-61	Sequence 61, App	760	3	12.5	7	2	US-08-974-549A-133	Sequence 133, App
688	3	12.5	6	2	US-10-281-652-13	Sequence 13, Appl	761	3	12.5	7	2	US-09-147-933-14	Sequence 14, Appl
689	3	12.5	6	2	US-09-688-017-36	Sequence 36, Appl	762	3	12.5	7	2	US-09-147-933-18	Sequence 18, Appl
690	3	12.5	6	2	US-10-006-865-855	Sequence 855, App	763	3	12.5	7	2	US-09-147-933-26	Sequence 26, Appl
691	3	12.5	6	2	US-10-006-865-870	Sequence 870, App	764	3	12.5	7	2	US-09-258-754-236	Sequence 236, App
692	3	12.5	6	4	PCT-US94-02629-6	Sequence 6, Appl	765	3	12.5	7	2	US-09-258-754-384	Sequence 384, App
693	3	12.5	6	4	PCT-US95-03236-28	Sequence 28, Appl	766	3	12.5	7	2	US-08-826-133-1	Sequence 1, Appl
694	3	12.5	6	4	PCT-US95-11724-9	Sequence 9, Appl	767	3	12.5	7	2	US-09-562-897-16	Sequence 16, Appl
695	3	12.5	6	4	PCT-US95-11724-14	Sequence 14, Appl	768	3	12.5	7	2	US-09-042-107-236	Sequence 236, App
696	3	12.5	6	4	PCT-US95-11724-15	Sequence 15, Appl	769	3	12.5	7	2	US-09-042-107-384	Sequence 384, App
697	3	12.5	6	4	PCT-US95-11724-16	Sequence 16, Appl	770	3	12.5	7	2	US-08-706-344C-16	Sequence 16, Appl
698	3	12.5	6	4	PCT-US95-11724-17	Sequence 17, Appl	771	3	12.5	7	2	US-08-478-316-47	Sequence 47, Appl
699	3	12.5	6	4	PCT-US95-11724-18	Sequence 18, Appl	772	3	12.5	7	2	US-08-478-316-48	Sequence 48, Appl
700	3	12.5	6	4	PCT-US95-11724-19	Sequence 19, Appl	773	3	12.5	7	2	US-08-478-316-49	Sequence 49, Appl
701	3	12.5	6	4	PCT-US95-11724-20	Sequence 20, Appl	774	3	12.5	7	2	US-08-478-316-50	Sequence 50, Appl
702	3	12.5	6	4	PCT-US95-11724-21	Sequence 21, Appl	775	3	12.5	7	2	US-09-410-025-11	Sequence 11, Appl
703	3	12.5	6	4	PCT-US95-11724-22	Sequence 22, Appl	776	3	12.5	7	2	US-08-932-082-8	Sequence 8, Appl
704	3	12.5	6	4	PCT-US95-11724-23	Sequence 23, Appl	777	3	12.5	7	2	US-09-323-571-22	Sequence 22, Appl
705	3	12.5	6	4	PCT-US95-11724-24	Sequence 24, Appl	778	3	12.5	7	2	US-09-081-707-13	Sequence 13, Appl
706	3	12.5	6	6	5169835-47	Patent No. 5169835	779	3	12.5	7	2	US-09-214-095D-32	Sequence 32, Appl
707	3	12.5	7	1	US-07-715-183C-14	Sequence 14, Appl	780	3	12.5	7	2	US-09-214-095D-35	Sequence 35, Appl
708	3	12.5	7	1	US-07-945-982-7	Sequence 7, Appl	781	3	12.5	7	2	US-09-045-920-10	Sequence 10, Appl
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710	3	12.5	7	1	US-08-285-777-22	Sequence 22, Appl	783	3	12.5	7	2	US-08-486-673B-8	Sequence 8, Appl
711	3	12.5	7	1	US-08-092-110A-4	Sequence 4, Appl	784	3	12.5	7	2	US-09-069-821-18	Sequence 18, Appl
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713	3	12.5	7	1	US-08-279-906A-1	Sequence 1, Appl	786	3	12.5	7	2	US-09-227-357-366	Sequence 366, App
714	3	12.5	7	1	US-08-097-938-8	Sequence 8, Appl	787	3	12.5	7	2	US-09-400-653A-2	Sequence 2, Appl
715	3	12.5	7	1	US-08-200-900A-30	Sequence 30, Appl	788	3	12.5	7	2	US-09-187-859-857	Sequence 857, App
716	3	12.5	7	1	US-08-537-069-14	Sequence 14, Appl	789	3	12.5	7	2	US-09-187-859-872	Sequence 872, App
717	3	12.5	7	1	US-08-273-474-4	Sequence 4, Appl	790	3	12.5	7	2	US-09-187-859-1833	Sequence 1833, Ap
718	3	12.5	7	1	US-08-273-474-35	Sequence 35, Appl	791	3	12.5	7	2	US-09-187-859-1863	Sequence 1863, Ap
719	3	12.5	7	1	US-08-405-200-33	Sequence 33, Appl	792	3	12.5	7	2	US-09-187-859-2121	Sequence 2121, Ap
720	3	12.5	7	1	US-08-476-000-8	Sequence 8, Appl	793	3	12.5	7	2	US-09-187-859-2141	Sequence 2141, Ap
721	3	12.5	7	1	US-08-486-721A-5	Sequence 5, Appl	794	3	12.5	7	2	US-09-187-859-2189	Sequence 2189, Ap
722	3	12.5	7	1	US-08-486-721A-8	Sequence 8, Appl	795	3	12.5	7	2	US-09-187-859-2219	Sequence 2219, Ap
723	3	12.5	7	1	US-08-486-721A-11	Sequence 11, Appl	796	3	12.5	7	2	US-09-187-859-2863	Sequence 2863, Ap
724	3	12.5	7	1	US-08-486-721A-12	Sequence 12, Appl	797	3	12.5	7	2	US-09-187-859-2926	Sequence 2926, Ap
725	3	12.5	7	1	US-08-486-721A-13	Sequence 13, Appl	798	3	12.5	7	2	US-09-187-859-3805	Sequence 3805, Ap
726	3	12.5	7	1	US-08-486-721A-14	Sequence 14, Appl	799	3	12.5	7	2	US-09-110-822-7	Sequence 7, Appl
727	3	12.5	7	1	US-08-299-567-2	Sequence 2, Appl	800	3	12.5	7	2	US-09-019-793A-47	Sequence 47, Appl
728	3	12.5	7	1	US-08-472-840-8	Sequence 8, Appl	801	3	12.5	7	2	US-09-013-793A-48	Sequence 48, Appl
729	3	12.5	7	1	US-08-392-973A-34	Sequence 34, Appl	802	3	12.5	7	2	US-09-019-793A-49	Sequence 49, Appl
730	3	12.5	7	1	US-08-377-432-29	Sequence 29, Appl	803	3	12.5	7	2	US-09-019-793A-50	Sequence 50, Appl
731	3	12.5	7	1	US-08-866-845-1	Sequence 1, Appl	804	3	12.5	7	2	US-09-248-061B-2	Sequence 2, Appl
732	3	12.5	7	1	US-08-340-283-183	Sequence 183, App	805	3	12.5	7	2	US-09-588-921-13	Sequence 13, Appl
733	3	12.5	7	1	US-08-476-976-8	Sequence 8, Appl	806	3	12.5	7	2	US-09-479-479-5	Sequence 5, Appl
734	3	12.5	7	1	US-08-871-163-39	Sequence 39, Appl	807	3	12.5	7	2	US-09-297-851-5	Sequence 5, Appl
735	3	12.5	7	1	US-08-871-163-40	Sequence 40, Appl	808	3	12.5	7	2	US-09-305-927-267	Sequence 267, App
736	3	12.5	7	1	US-08-702-105A-22	Sequence 22, Appl	809	3	12.5	7	2	US-09-305-927-282	Sequence 282, App
737	3	12.5	7	1	US-08-968-676-68	Sequence 68, Appl	810	3	12.5	7	2	US-09-212-868-1	Sequence 1, Appl
738	3	12.5	7	1	US-08-946-241B-11	Sequence 11, Appl	811	3	12.5	7	2	US-09-430-702-11	Sequence 11, Appl
739	3	12.5	7	1	US-08-672-345C-32	Sequence 32, Appl	812	3	12.5	7	2	US-09-496-118B-10	Sequence 10, Appl
740	3	12.5	7	1	US-08-672-345C-35	Sequence 35, Appl	813	3	12.5	7	2	US-09-588-822-13	Sequence 13, Appl
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742	3	12.5	7	1	US-08-482-228-30	Sequence 30, Appl	815	3	12.5	7	2	US-08-900-241-29	Sequence 29, Appl
743	3	12.5	7	1	US-08-814-806-5	Sequence 5, Appl	816	3	12.5	7	2	US-09-394-455-36	Sequence 36, Appl
744	3	12.5	7	2	US-09-071-877-10	Sequence 10, Appl	817	3	12.5	7	2	US-09-281-495-5	Sequence 5, Appl
745	3	12.5	7	2	US-08-482-528-30	Sequence 30, Appl	818	3	12.5	7	2	US-09-627-851B-13	Sequence 13, Appl
746	3	12.5	7	2	US-08-767-903-39	Sequence 39, Appl	819	3	12.5	7	2	US-09-326-806-7	Sequence 7, Appl
747	3	12.5	7	2	US-08-767-903-40	Sequence 40, Appl	820	3	12.5	7	2	US-09-293-854-5	Sequence 5, Appl
748	3	12.5	7	2	US-08-702-110A-22	Sequence 22, Appl	821	3	12.5	7	2	US-09-822-270-4	Sequence 4, Appl
749	3	12.5	7	2	US-08-474-410-8	Sequence 8, Appl	822	3	12.5	7	2	US-09-552-802B-48	Sequence 48, Appl
750	3	12.5	7	2	US-09-309-053-11	Sequence 11, Appl	823	3	12.5	7	2	US-08-407-620A-5	Sequence 5, Appl
751	3	12.5	7	2	US-08-836-480-16	Sequence 16, Appl	824	3	12.5	7	2	US-09-839-542B-857	Sequence 857, App
752	3	12.5	7	2	US-08-377-781A-16	Sequence 16, Appl	825	3	12.5	7	2	US-09-839-542B-872	Sequence 872, App
753	3	12.5	7	2	US-09-173-941-48	Sequence 48, Appl	826	3	12.5	7	2	US-09-839-542B-1833	Sequence 1833, Ap
754	3	12.5	7	2	US-09-173-941-51	Sequence 51, Appl	827	3	12.5	7	2	US-09-839-542B-1863	Sequence 1863, Ap
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756	3	12.5	7	2	US-08-435-568A-20	Sequence 20, Appl	829	3	12.5	7	2	US-09-839-542B-2141	Sequence 2141, Ap
757	3	12.5	7	2	US-08-935-100-4	Sequence 4, Appl	830	3	12.5	7	2		

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832	3	12.5	7	2	US-09-839-542B-2219	Sequence 2219, Ap	905	3	12.5	7	2	US-09-693-746-99	Sequence 99, Appl
833	3	12.5	7	2	US-09-839-542B-2863	Sequence 2863, Ap	906	3	12.5	7	2	US-09-693-746-136	Sequence 136, App
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835	3	12.5	7	2	US-09-839-542B-3805	Sequence 3805, Ap	908	3	12.5	7	2	US-09-693-746-168	Sequence 168, App
836	3	12.5	7	2	US-09-839-932-7	Sequence 7, Appli	909	3	12.5	7	2	US-09-511-939-15	Sequence 15, Appl
837	3	12.5	7	2	US-09-499-203-6	Sequence 6, Appli	910	3	12.5	7	2	US-09-511-939-39	Sequence 39, Appl
838	3	12.5	7	2	US-09-620-249-1	Sequence 1, Appli	911	3	12.5	7	2	US-09-511-939-57	Sequence 57, Appl
839	3	12.5	7	2	US-09-975-413A-20	Sequence 20, Appl	912	3	12.5	7	2	US-09-511-939-60	Sequence 60, Appl
840	3	12.5	7	2	US-09-264-516A-267	Sequence 267, App	913	3	12.5	7	2	US-09-511-939-75	Sequence 75, Appl
841	3	12.5	7	2	US-09-494-190-48	Sequence 48, App	914	3	12.5	7	2	US-09-511-939-135	Sequence 135, App
842	3	12.5	7	2	US-09-494-190-51	Sequence 51, Appl	915	3	12.5	7	2	US-09-511-939-171	Sequence 171, App
843	3	12.5	7	2	US-09-494-190-52	Sequence 52, Appl	916	3	12.5	7	2	US-09-511-939-189	Sequence 189, App
844	3	12.5	7	2	US-09-722-250D-296	Sequence 296, App	917	3	12.5	7	2	US-09-511-939-261	Sequence 261, App
845	3	12.5	7	2	US-09-722-250D-384	Sequence 384, App	918	3	12.5	7	2	US-09-511-939-273	Sequence 273, App
846	3	12.5	7	2	US-09-402-181B-130	Sequence 130, App	919	3	12.5	7	2	US-09-511-939-303	Sequence 303, App
847	3	12.5	7	2	US-09-402-181B-133	Sequence 133, App	920	3	12.5	7	2	US-09-623-548A-810	Sequence 810, App
848	3	12.5	7	2	US-09-721-456-130	Sequence 130, App	921	3	12.5	7	2	US-09-623-548A-811	Sequence 811, App
849	3	12.5	7	2	US-09-721-456-133	Sequence 133, App	922	3	12.5	7	2	US-09-623-548A-1078	Sequence 1078, Ap
850	3	12.5	7	2	US-09-861-687-8	Sequence 8, Appli	923	3	12.5	7	2	US-09-051-395-2	Sequence 2, Appli
851	3	12.5	7	2	US-09-721-870-88	Sequence 88, Appl	924	3	12.5	7	2	US-09-051-395-3	Sequence 3, Appli
852	3	12.5	7	2	US-09-721-870-91	Sequence 91, Appl	925	3	12.5	7	2	US-09-051-395-8	Sequence 8, Appli
853	3	12.5	7	2	US-09-721-870-131	Sequence 131, App	926	3	12.5	7	2	US-08-765-837-7	Sequence 7, Appli
854	3	12.5	7	2	US-09-721-870-141	Sequence 141, App	927	3	12.5	7	2	US-09-962-756-2014	Sequence 2014, Ap
855	3	12.5	7	2	US-09-721-870-156	Sequence 156, App	928	3	12.5	7	2	US-10-062-623B-19	Sequence 19, Appl
856	3	12.5	7	2	US-09-721-870-157	Sequence 157, App	929	3	12.5	7	2	US-10-062-623B-20	Sequence 20, Appl
857	3	12.5	7	2	US-09-721-870-161	Sequence 161, App	930	3	12.5	7	2	US-09-657-276-810	Sequence 810, App
858	3	12.5	7	2	US-09-721-870-162	Sequence 162, App	931	3	12.5	7	2	US-09-657-276-811	Sequence 811, App
859	3	12.5	7	2	US-09-848-585-22	Sequence 22, Appl	932	3	12.5	7	2	US-09-657-276-1078	Sequence 1078, Ap
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862	3	12.5	7	2	US-09-721-108-22	Sequence 22, Appl	935	3	12.5	7	2	US-09-940-727B-35	Sequence 35, Appl
863	3	12.5	7	2	US-09-721-108-202	Sequence 202, App	936	3	12.5	7	2	US-09-973-278-521	Sequence 521, App
864	3	12.5	7	2	US-09-721-108-218	Sequence 218, App	937	3	12.5	7	2	US-10-726-555-10	Sequence 10, Appl
865	3	12.5	7	2	US-09-865-483-10	Sequence 10, Appl	938	3	12.5	7	2	US-10-607-595-296	Sequence 296, App
866	3	12.5	7	2	US-09-234-395-243	Sequence 243, App	939	3	12.5	7	2	US-10-392-970-7	Sequence 7, Appli
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868	3	12.5	7	2	US-09-305-928-258	Sequence 258, App	941	3	12.5	7	2	US-09-688-017-57	Sequence 57, Appl
869	3	12.5	7	2	US-09-192-854-11	Sequence 11, Appl	942	3	12.5	7	2	US-10-296-624A-1	Sequence 1, Appli
870	3	12.5	7	2	US-09-192-854-27	Sequence 27, Appl	943	3	12.5	7	2	US-10-006-869-857	Sequence 857, App
871	3	12.5	7	2	US-09-192-854-38	Sequence 38, Appl	944	3	12.5	7	2	US-10-006-869-872	Sequence 872, App
872	3	12.5	7	2	US-09-192-854-40	Sequence 40, Appl	945	3	12.5	7	2	US-10-006-869-1833	Sequence 1833, Ap
873	3	12.5	7	2	US-09-192-854-50	Sequence 50, Appl	946	3	12.5	7	2	US-10-006-869-1863	Sequence 1863, Ap
874	3	12.5	7	2	US-09-192-854-80	Sequence 80, Appl	947	3	12.5	7	2	US-10-006-869-2121	Sequence 2121, Ap
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877	3	12.5	7	2	US-09-192-854-148	Sequence 148, App	950	3	12.5	7	2	US-10-006-869-2219	Sequence 2219, Ap
878	3	12.5	7	2	US-09-192-854-155	Sequence 155, App	951	3	12.5	7	2	US-10-006-869-2263	Sequence 2263, Ap
879	3	12.5	7	2	US-09-192-854-172	Sequence 172, App	952	3	12.5	7	2	US-10-006-869-2826	Sequence 2826, Ap
880	3	12.5	7	2	US-09-563-222C-53	Sequence 53, Appl	953	3	12.5	7	2	US-10-006-869-3805	Sequence 3805, Ap
881	3	12.5	7	2	US-09-830-428A-21	Sequence 21, Appl	954	3	12.5	7	2	PCT-US94-07881-30	Sequence 30, Appl
882	3	12.5	7	2	US-09-995-973-20	Sequence 20, Appl	955	3	12.5	7	2	PCT-US94-07881-35	Sequence 35, Appl
883	3	12.5	7	2	US-09-995-973-24	Sequence 24, Appl	956	3	12.5	7	4	Patent No. 5208144	Patent No. 5208144
884	3	12.5	7	2	US-09-995-973-27	Sequence 27, Appl	957	3	12.5	7	4	Patent No. 5210075	Patent No. 5210075
885	3	12.5	7	2	US-09-285-912A-37	Sequence 37, Appl	958	3	12.5	7	6	Sequence 15, Appl	Sequence 15, Appl
886	3	12.5	7	2	US-09-285-912A-13	Sequence 13, Appl	959	3	12.5	7	6	Sequence 4, Appli	Sequence 4, Appli
887	3	12.5	7	2	US-09-956-086-18	Sequence 18, Appl	960	3	12.5	7	6	Sequence 23, Appl	Sequence 23, Appl
888	3	12.5	7	2	US-09-956-087-18	Sequence 18, Appl	961	3	12.5	8	1	Sequence 24, Appl	Sequence 24, Appl
889	3	12.5	7	2	US-08-794-042-30	Sequence 30, Appl	962	3	12.5	8	1	Sequence 25, Appl	Sequence 25, Appl
890	3	12.5	7	2	US-09-674-973A-311	Sequence 311, App	963	3	12.5	8	1	Sequence 26, Appl	Sequence 26, Appl
891	3	12.5	7	2	US-09-211-715-15	Sequence 15, Appl	964	3	12.5	8	1	Sequence 17, Appl	Sequence 17, Appl
892	3	12.5	7	2	US-09-211-715-21	Sequence 21, Appl	965	3	12.5	8	1	Sequence 7, Appli	Sequence 7, Appli
893	3	12.5	7	2	US-09-211-715-22	Sequence 22, Appl	966	3	12.5	8	1	Sequence 19, Appl	Sequence 19, Appl
894	3	12.5	7	2	US-09-211-715-23	Sequence 23, Appl	967	3	12.5	8	1	Sequence 18, Appl	Sequence 18, Appl
895	3	12.5	7	2	US-09-601-326-88	Sequence 88, Appl	968	3	12.5	8	1	Sequence 6, Appli	Sequence 6, Appli
896	3	12.5	7	2	US-09-601-326-89	Sequence 89, Appl	969	3	12.5	8	1	Sequence 7, Appli	Sequence 7, Appli
897	3	12.5	7	2	US-09-601-326-90	Sequence 90, Appl	970	3	12.5	8	1	Sequence 19, Appl	Sequence 19, Appl
898	3	12.5	7	2	US-09-601-326-91	Sequence 91, Appl	971	3	12.5	8	1	Sequence 18, Appl	Sequence 18, Appl
899	3	12.5	7	2	US-09-676-475A-296	Sequence 296, App	972	3	12.5	8	1	Sequence 7, Appli	Sequence 7, Appli
900	3	12.5	7	2	US-09-676-475A-384	Sequence 384, App	973	3	12.5	8	1	Sequence 6, Appli	Sequence 6, Appli
901	3	12.5	7	2	US-09-261-894A-68	Sequence 68, Appl	974	3	12.5	8	1	Sequence 7, Appli	Sequence 7, Appli
902	3	12.5	7	2			975	3	12.5	8	1	Sequence 9, Appli	Sequence 9, Appli
903	3	12.5	7	2			976	3	12.5	8	1	Sequence 10, Appl	Sequence 10, Appl

977 3 12.5 8 1 US-08-279-906A-11 Sequence 11, Appl  
978 3 12.5 8 1 US-08-032-846-36 Sequence 36, Appl  
979 3 12.5 8 1 US-08-405-200-32 Sequence 32, Appl  
980 3 12.5 8 1 US-08-406-347A-11 Sequence 11, Appl  
981 3 12.5 8 1 US-08-688-675-7 Sequence 7, Appl  
982 3 12.5 8 1 US-08-040-548-42 Sequence 42, Appl  
983 3 12.5 8 1 US-08-466-344-42 Sequence 42, Appl  
984 3 12.5 8 1 US-08-259-550A-51 Sequence 51, Appl  
985 3 12.5 8 1 US-08-475-213-4 Sequence 4, Appl  
986 3 12.5 8 1 US-08-676-125A-1 Sequence 1, Appl  
987 3 12.5 8 1 US-08-508-664-20 Sequence 20, Appl  
988 3 12.5 8 1 US-08-922-267A-70 Sequence 70, Appl  
989 3 12.5 8 1 US-08-704-655-13 Sequence 13, Appl  
990 3 12.5 8 1 US-08-906-925-3 Sequence 3, Appl  
991 3 12.5 8 1 US-08-541-780-17 Sequence 17, Appl  
992 3 12.5 8 1 US-08-630-645-5 Sequence 5, Appl  
993 3 12.5 8 1 US-09-016-366A-65 Sequence 65, Appl  
994 3 12.5 8 1 US-08-350-260A-467 Sequence 467, App  
995 3 12.5 8 1 US-08-350-260A-468 Sequence 468, App  
996 3 12.5 8 1 US-08-350-260A-478 Sequence 478, App  
997 3 12.5 8 1 US-08-350-260A-526 Sequence 526, App  
998 3 12.5 8 1 US-08-978-404B-57 Sequence 57, Appl  
999 3 12.5 8 1 US-08-978-404B-67 Sequence 67, Appl  
1000 3 12.5 8 1 US-08-837-593-10 Sequence 10, Appl

## ALIGNMENTS

RESULT 1  
US-08-642-846-4  
; Sequence 4, Application US/08642846  
; Patent No. 586151  
; GENERAL INFORMATION:  
; APPLICANT: HOSTETTER, MARGARET K.  
; APPLICANT: GALE, CHERYL A.  
; APPLICANT: BENDEL, CATHERINE M.  
; APPLICANT: TAO, NIAN-JUN  
; APPLICANT: KENDRICK, KATHLEEN  
; TITLE OF INVENTION: CANDIDA ALBICANS GENE, INTEGRIN-LIKE  
; TITLE OF INVENTION: PROTEIN, ANTIBODIES, AND METHODS OF USE  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MUEITING, RAASCH, GEBHARDT & SCHWAPPACH, P.A.  
; STREET: 119 NORTH FOURTH STREET, SUITE 203  
; CITY: MINNEAPOLIS  
; STATE: MINNESOTA  
; COUNTRY: USA  
; ZIP: 55401  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/642,846  
; FILING DATE: 03-MAY-1996  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MUEITING, ANN M.  
; REGISTRATION NUMBER: 33,977  
; REFERENCE/DOCKET NUMBER: 110.00280101  
; TELEPHONE: 612-305-1217  
; TELEFAX: 612-305-1228  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 23 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-642-846-4

Query Match 25.0%; Score 6; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TNNNNS 20  
Db 5 TNNNNS 10  
|||||

RESULT 2  
US-09-264-604-4  
; Sequence 4, Application US/09264604  
; Patent No. 6346411  
; GENERAL INFORMATION:  
; APPLICANT: HOSTETTER, MARGARET K.  
; APPLICANT: GALE, CHERYL A.  
; APPLICANT: BENDEL, CATHERINE M.  
; APPLICANT: TAO, NIAN-JUN  
; APPLICANT: KENDRICK, KATHLEEN  
; TITLE OF INVENTION: CANDIDA ALBICANS GENE, INTEGRIN-LIKE  
; TITLE OF INVENTION: PROTEIN, ANTIBODIES, AND METHODS OF USE  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MUEITING, RAASCH, GEBHARDT & SCHWAPPACH, P.A.  
; STREET: 119 NORTH FOURTH STREET, SUITE 203  
; CITY: MINNEAPOLIS  
; STATE: MINNESOTA  
; COUNTRY: USA  
; ZIP: 55401  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/264,604  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/642,846  
; FILING DATE: 03-MAY-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MUEITING, ANN M.  
; REGISTRATION NUMBER: 33,977  
; REFERENCE/DOCKET NUMBER: 110.00280101  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612-305-1217  
; TELEFAX: 612-305-1228  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 23 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-264-604-4

Query Match 25.0%; Score 6; DB 2; Length 23;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TNNNNS 20  
Db 5 TNNNNS 10  
|||||

RESULT 3  
US-09-978-343-4  
; Sequence 4, Application US/09978343  
; Patent No. 6774219  
; GENERAL INFORMATION:  
; APPLICANT: HOSTETTER, MARGARET K.

GALE, CHERYL A.  
BENDEL, CATHERINE M.  
TAO, NIAN-JUN  
KENDRICK, KATHLEEN  
TITLE OF INVENTION: CANDIDA ALBICANS GENE, INTEGRIN-LIKE  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MUETING, RAASCH, GEBHARDT & SCHWAPPACH, P.A.  
STREET: 119 NORTH FOURTH STREET, SUITE 203  
CITY: MINNEAPOLIS  
STATE: MINNESOTA  
COUNTRY: USA  
ZIP: 55401

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/978,343  
FILING DATE: 15-Oct-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/642,846  
FILING DATE: 03-MAY-1996

ATTORNEY/AGENT INFORMATION:  
NAME: MUETING, ANN M.  
REGISTRATION NUMBER: 33,977

REFERENCE/DOCKET NUMBER: 110.00280101  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-305-1217  
TELEFAX: 612-305-1228

INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-978-343-4  
Query Match 25.0%; Score 6; DB 2; Length 23;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TNNNS 20  
|||||  
DB 5 TNNNS 10

RESULT 4  
US-09-599-652-4  
Sequence 4, Application US/09599652  
Patent No. RE37741

GENERAL INFORMATION:  
APPLICANT: HOSTETTER, MARGARET K.  
APPLICANT: GALE, CHERYL A.

APPLICANT: BENDEL, CATHERINE M.  
APPLICANT: TAO, NIAN-JUN  
APPLICANT: KENDRICK, KATHLEEN

TITLE OF INVENTION: CANDIDA ALBICANS GENE, INTEGRIN-LIKE  
TITLE OF INVENTION: PROTEIN, ANTIBODIES, AND METHODS OF USE  
NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:  
ADDRESSEE: MUETING, RAASCH, GEBHARDT & SCHWAPPACH, P.A.  
STREET: 119 NORTH FOURTH STREET, SUITE 203  
CITY: MINNEAPOLIS  
STATE: MINNESOTA  
COUNTRY: USA  
ZIP: 55401

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE:  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/729,152  
FILING DATE: 11-OCT-1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 291993/1995  
FILING DATE: 13-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 32:

US-09-599-652-4  
Query Match 25.0%; Score 6; DB 5; Length 23;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TNNNS 20  
|||||  
DB 5 TNNNS 10

RESULT 5  
US-08-729-152-32  
Sequence 32, Application US/08729152  
Patent No. 5871739

GENERAL INFORMATION:  
APPLICANT: Incue, Eri  
TITLE OF INVENTION: Pharmaceutical Composition  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: Southern Building, Suite 700, 805 Fifteenth  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE:  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/729,152  
FILING DATE: 11-OCT-1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 291993/1995  
FILING DATE: 13-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 32:

US-09-599-652-4  
Query Match 25.0%; Score 6; DB 5; Length 23;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TNNNS 20  
|||||  
DB 5 TNNNS 10

RESULT 4  
US-09-599-652-4  
Sequence 4, Application US/09599652  
Patent No. RE37741

GENERAL INFORMATION:  
APPLICANT: HOSTETTER, MARGARET K.  
APPLICANT: GALE, CHERYL A.

APPLICANT: BENDEL, CATHERINE M.  
APPLICANT: TAO, NIAN-JUN  
APPLICANT: KENDRICK, KATHLEEN

TITLE OF INVENTION: CANDIDA ALBICANS GENE, INTEGRIN-LIKE  
TITLE OF INVENTION: PROTEIN, ANTIBODIES, AND METHODS OF USE  
NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:  
ADDRESSEE: MUETING, RAASCH, GEBHARDT & SCHWAPPACH, P.A.  
STREET: 119 NORTH FOURTH STREET, SUITE 203  
CITY: MINNEAPOLIS  
STATE: MINNESOTA  
COUNTRY: USA  
ZIP: 55401

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE:  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/729,152  
FILING DATE: 11-OCT-1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 291993/1995  
FILING DATE: 13-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 32:

US-09-599-652-4  
Query Match 25.0%; Score 6; DB 5; Length 23;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TNNNS 20  
|||||  
DB 5 TNNNS 10

RESULT 4  
US-09-599-652-4  
Sequence 4, Application US/09599652  
Patent No. RE37741

GENERAL INFORMATION:  
APPLICANT: HOSTETTER, MARGARET K.  
APPLICANT: GALE, CHERYL A.

APPLICANT: BENDEL, CATHERINE M.  
APPLICANT: TAO, NIAN-JUN  
APPLICANT: KENDRICK, KATHLEEN

TITLE OF INVENTION: CANDIDA ALBICANS GENE, INTEGRIN-LIKE  
TITLE OF INVENTION: PROTEIN, ANTIBODIES, AND METHODS OF USE  
NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:  
ADDRESSEE: MUETING, RAASCH, GEBHARDT & SCHWAPPACH, P.A.  
STREET: 119 NORTH FOURTH STREET, SUITE 203  
CITY: MINNEAPOLIS  
STATE: MINNESOTA  
COUNTRY: USA  
ZIP: 55401

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE:  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/729,152  
FILING DATE: 11-OCT-1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 291993/1995  
FILING DATE: 13-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 32:

US-09-599-652-4  
Query Match 25.0%; Score 6; DB 5; Length 23;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TNNNS 20  
|||||  
DB 5 TNNNS 10

RESULT 4  
US-09-599-652-4  
Sequence 4, Application US/09599652  
Patent No. RE37741

GENERAL INFORMATION:  
APPLICANT: HOSTETTER, MARGARET K.  
APPLICANT: GALE, CHERYL A.

APPLICANT: BENDEL, CATHERINE M.  
APPLICANT: TAO, NIAN-JUN  
APPLICANT: KENDRICK, KATHLEEN

TITLE OF INVENTION: CANDIDA ALBICANS GENE, INTEGRIN-LIKE  
TITLE OF INVENTION: PROTEIN, ANTIBODIES, AND METHODS OF USE  
NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:  
ADDRESSEE: MUETING, RAASCH, GEBHARDT & SCHWAPPACH, P.A.  
STREET: 119 NORTH FOURTH STREET, SUITE 203  
CITY: MINNEAPOLIS  
STATE: MINNESOTA  
COUNTRY: USA  
ZIP: 55401

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE:  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/729,152  
FILING DATE: 11-OCT-1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 291993/1995  
FILING DATE: 13-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 32:

US-09-599-652-4  
Query Match 25.0%; Score 6; DB 5; Length 23;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TNNNS 20  
|||||  
DB 5 TNNNS 10

RESULT 4  
US-09-599-652-4  
Sequence 4, Application US/09599652  
Patent No. RE37741

GENERAL INFORMATION:  
APPLICANT: HOSTETTER, MARGARET K.  
APPLICANT: GALE, CHERYL A.

APPLICANT: BENDEL, CATHERINE M.  
APPLICANT: TAO, NIAN-JUN  
APPLICANT: KENDRICK, KATHLEEN

TITLE OF INVENTION: CANDIDA ALBICANS GENE, INTEGRIN-LIKE  
TITLE OF INVENTION: PROTEIN, ANTIBODIES, AND METHODS OF USE  
NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:  
ADDRESSEE: MUETING, RAASCH, GEBHARDT & SCHWAPPACH, P.A.  
STREET: 119 NORTH FOURTH STREET, SUITE 203  
CITY: MINNEAPOLIS  
STATE: MINNESOTA  
COUNTRY: USA  
ZIP: 55401

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE:  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/729,152  
FILING DATE: 11-OCT-1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 291993/1995  
FILING DATE: 13-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 32:



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;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: peptide
US-08-729-152-32

Query Match 20.8%; Score 5; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 IFEQE 14
DB 9 IFEQE 13

RESULT 6
US-09-962-756-501
; Sequence 501, Application US/09962756
; Patent No. 6875741
; GENERAL INFORMATION:
; APPLICANT: PILLUTLA, RENUKA
; APPLICANT: BRISSETTE, RENEE
; APPLICANT: BLUME, ARTHUR J.
; APPLICANT: SCHAFER, LAUGE
; APPLICANT: BRANDT, JAKOB
; APPLICANT: GOLDSTEIN, NEIL I.
; APPLICANT: SPETZLER, JANE
; APPLICANT: OSTERGAARD, SOREN
; APPLICANT: HANSEN, PER HERTZ
; TITLE OF INVENTION: INSULIN AND IGP-1 RECEPTOR AGONISTS AND ANTAGONISTS
; FILE REFERENCE: 1878-4051US1
; CURRENT APPLICATION NUMBER: US/09/962,756
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/538,038
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/146,127
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 501
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-962-756-501

Query Match 20.8%; Score 5; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 NSSFY 23
DB 8 NSSFY 12

RESULT 7
US-08-486-953A-48
; Sequence 48, Application US/08486953A
; Patent No. 5849290
; GENERAL INFORMATION:
; APPLICANT: Brown, Robert
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Rosen, Daniel R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS,
; TREATMENT AND PREVENTION OF DISEASES OF CELL DEATH
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Clark & Elbing LLP

;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FastSeq
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,953A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/204,052
; FILING DATE: 28-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/223002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/428-0200
; TELEFAX: 617/428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-486-953A-48

Query Match 20.8%; Score 5; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 IFEQE 14
DB 19 IFEQE 23

RESULT 8
US-08-204-052-48
; Sequence 48, Application US/08204052
; Patent No. 6723893
; GENERAL INFORMATION:
; APPLICANT: Brown, Robert
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Rosen, Daniel R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS,
; TREATMENT AND PREVENTION OF DISEASES OF CELL DEATH
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,052
; FILING DATE: 28-FEB-1994
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/023,980
; FILING DATE: 26-FEB-1993
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ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00786/223001  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 48:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-204-052-48

Query Match 20.8%; Score 5; DB 2; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 IFEQE 14  
Db 19 IFEQE 23

RESULT 9  
US-09-967-869A-1  
Sequence 1, Application US/09967869A  
Patent No. 6919204  
GENERAL INFORMATION:  
APPLICANT: WOLFFE, Alan P.  
APPLICANT: URNOV, Evdodor  
APPLICANT: LAI, Albert  
APPLICANT: RASCHKE, Eva  
TITLE OF INVENTION: MODULATION OF GENE EXPRESSION USING LOCALIZATION  
FILE REFERENCE: 8325-0019 / S19  
CURRENT APPLICATION NUMBER: US/09/967,869A  
CURRENT FILING DATE: 2001-09-28  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 23  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: segment from  
OTHER INFORMATION: Drosophila MBD-like sequence  
US-09-967-869A-1

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Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 NNNSS 21  
Db 7 NNNSS 11

RESULT 10  
US-07-834-848-3  
Sequence 3, Application US/07834848  
Patent No. 5436221  
GENERAL INFORMATION:  
APPLICANT: KITAGUCHI, HIROSHI  
APPLICANT: KOMAZAWA, HIROYUKI  
APPLICANT: KOJIMA, MASAYOSHI  
APPLICANT: MORI, HIDETO  
APPLICANT: NISHIKAWA, NAOYUKI  
APPLICANT: SATOH, HIDEAKI  
APPLICANT: ORIKASA, ATSUSHI  
APPLICANT: ONO, MITSUNORI

APPLICANT: AZUMA, ICHIRO  
APPLICANT: SAIKI, IKUO  
TITLE OF INVENTION: PEPTIDE DERIVATIVES AND APPLICATION  
TITLE OF INVENTION: THEREOF  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sughrue, Mion, Zinn, Macpeak, & Seas  
STREET: 2100 Pennsylvania Ave., NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20037-3202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/834,848  
FILING DATE: 19920213  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Biggart, Waddell A.  
REGISTRATION NUMBER: 24,961  
REFERENCE/DOCKET NUMBER: Q28480  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)293-7060  
TELEFAX: (202)293-7860  
TELEX: 6491103  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-834-848-3

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Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RFDS 5  
Db 1 RFDS 4

RESULT 11  
US-08-251-027-10  
Sequence 10, Application US/08251027  
Patent No. 5519005  
GENERAL INFORMATION:  
APPLICANT: Lider, Ofer  
APPLICANT: Greenspoon, No. 5519005m  
APPLICANT: Hershkoviz, Rami  
APPLICANT: Alon, Ronen  
TITLE OF INVENTION: A METHOD OF INHIBITION OF CELLULAR AND  
TITLE OF INVENTION: MOLECULAR LEVEL BIOLOGICAL INTERACTIONS UTILIZING  
TITLE OF INVENTION: NON-PEPTIDIC SURROGATES OF THE ARG-GLY-ASP SEQUENCE  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kohn & Associates  
STREET: 30500 No. 5519005thwestern Highway, Suite 410  
CITY: Farmington Hills  
STATE: Michigan  
COUNTRY: U.S.  
ZIP: 48334  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/251,027

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; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 539-5050
; TELEFAX: (810) 539-5055
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-251-027-10

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Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RFDS 5
Db 1 RFDS 4

RESULT 13
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; Sequence 33, Application US/10353174
; Patent No. 6858716
; GENERAL INFORMATION:
; APPLICANT: EISEN, ANDREW
; TITLE OF INVENTION: DROSOPHILA RECOMBINATION-ASSOCIATED PROTEIN AND METHODS FOR USE
; FILE REFERENCE: 2567/1f496-US3
; CURRENT APPLICATION NUMBER: US/10/353,174
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/144,736
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: US 09/621,377
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: Potential N-glycosylation site
US-10-353-174-33

Query Match 16.7%; Score 4; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 NNSS 21
Db 1 NNSS 4

RESULT 14
US-07-834-848-7
; Sequence 7, Application US/07834848
; Patent No. 5436221
; GENERAL INFORMATION:
; APPLICANT: KITAGUCHI, HIROSHI
; APPLICANT: KOMAZAWA, HIROYUKI
; APPLICANT: KOJIMA, MASAYOSHI
; APPLICANT: MORI, HIDEYO
; APPLICANT: NISHIKAWA, NAOTYUKI
; APPLICANT: SATOH, HIDEAKI
; APPLICANT: ORIKASA, ATSUSHI
; APPLICANT: ONO, MITSUNORI
; APPLICANT: AZUMA, ICHIRO
; APPLICANT: SAIKI, IKUO
; TITLE OF INVENTION: PEPTIDE DERIVATIVES AND APPLICATION
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak, & Seas
; STREET: 2100 Pennsylvania Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/834,848  
; FILING DATE: 19920213  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Biggart, Waddell A.  
; REGISTRATION NUMBER: 24,861  
; REFERENCE/DOCKET NUMBER: Q28480  
; TELEPHONE: (202)293-7060  
; TELEFAX: (202)293-7860  
; TELEX: 6491103  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-07-834-848-7

Query Match 16.7%; Score 4; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RFDS 5  
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Db 2 RFDS 5

## RESULT 15

US-07-834-848-10  
; Sequence 10, Application US/07834848  
; Patent No. 5436221  
; GENERAL INFORMATION:  
; APPLICANT: KITAGUCHI, HIROSHI  
; APPLICANT: KOMAZAWA, HIROYUKI  
; APPLICANT: KOJIMA, MASAYOSHI  
; APPLICANT: MORI, HIDEYO  
; APPLICANT: NISHIKAWA, NAOTYUKI  
; APPLICANT: SATOH, HIDEAKI  
; APPLICANT: ORIKASA, ATSUSHI  
; APPLICANT: ONO, MITSUNORI  
; APPLICANT: AZUMA, ICHIRO  
; APPLICANT: SAIKI, IKUO  
; TITLE OF INVENTION: PEPTIDE DERIVATIVES AND APPLICATION  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak, & Seas  
; STREET: 2100 Pennsylvania Ave., NW  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20037-3202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/834,848  
; FILING DATE: 19920213  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Biggart, Waddell A.  
; REGISTRATION NUMBER: 24,861  
; REFERENCE/DOCKET NUMBER: Q28480  
; TELEPHONE: (202)293-7060

;  
; TELEFAX: (202)293-7860  
; TELEX: 6491103  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-07-834-848-10

Query Match 16.7%; Score 4; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RFDS 5  
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Db 2 RFDS 5

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Job time : 29 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2006, 17:53:00 ; Search time 58 Seconds  
(without alignments)  
172.895 Million cell updates/sec

Title: US-10-619-323-1\_COPY\_35\_58

Perfect score: 24

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Gapop 60.0 , Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

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Total number of hits satisfying chosen parameters: 412413

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Listing first 1000 summaries

Database : Published Applications AA\_Main:  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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8	5	20.8	9	3	US-09-935-384-616
9	5	20.8	9	5	US-10-808-187-1154
10	5	20.8	9	5	US-10-705-459-307
11	5	20.8	9	5	US-10-807-807-1154
12	5	20.8	10	3	US-09-935-384-368
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24	5	20.8	23	3	US-09-967-869A-1
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38	4	16.7	4	4	US-10-807-807-1154
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103	4	16.7	9	4	US-10-354-090-44	Sequence 44, Appl	176	4	16.7	13	4	US-10-469-304-67	Sequence 67, Appl
104	4	16.7	9	5	US-10-808-187-2369	Sequence 2369, Ap	177	4	16.7	13	4	US-10-469-304-68	Sequence 68, Appl
105	4	16.7	9	5	US-10-680-557-1	Sequence 1, Appl	178	4	16.7	13	4	US-10-469-304-69	Sequence 69, Appl
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107	4	16.7	9	5	US-10-498-468A-1	Sequence 1, Appl	180	4	16.7	13	4	US-10-469-304-71	Sequence 71, Appl
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112	4	16.7	9	5	US-10-498-468A-13	Sequence 13, Appl	185	4	16.7	13	4	US-10-468-496-1191	Sequence 1191, Ap
113	4	16.7	9	5	US-10-860-050-167	Sequence 167, App	186	4	16.7	13	4	US-10-468-496-1192	Sequence 1192, Ap
114	4	16.7	10	3	US-09-572-404B-1176	Sequence 1176, Ap	187	4	16.7	13	5	US-10-822-173-56	Sequence 56, Appl
115	4	16.7	10	3	US-09-935-384-163	Sequence 163, App	188	4	16.7	13	5	US-10-903-213-55	Sequence 56, Appl
116	4	16.7	10	3	US-09-935-384-289	Sequence 289, App	189	4	16.7	13	5	US-10-498-468A-15	Sequence 15, Appl
117	4	16.7	10	3	US-09-935-384-366	Sequence 366, App	190	4	16.7	13	5	US-10-948-707-1232	Sequence 1232, Ap
118	4	16.7	10	3	US-09-935-384-587	Sequence 587, App	191	4	16.7	13	5	US-09-972-484-33	Sequence 33, Appl
119	4	16.7	10	4	US-10-101-812-1	Sequence 1, Appl	192	4	16.7	14	3	US-09-988-493-264	Sequence 264, App
120	4	16.7	10	4	US-10-101-662A-1	Sequence 1, Appl	193	4	16.7	14	3	US-09-991-225-24	Sequence 24, Appl
121	4	16.7	10	4	US-10-133-210-259	Sequence 259, App	194	4	16.7	14	3	US-09-991-225-25	Sequence 25, Appl
122	4	16.7	10	4	US-10-287-670-1	Sequence 1, Appl	195	4	16.7	14	3	US-09-991-225-42	Sequence 42, Appl
123	4	16.7	10	4	US-10-200-708-322	Sequence 322, App	196	4	16.7	14	3	US-09-991-225-43	Sequence 43, Appl
124	4	16.7	10	4	US-10-200-708-597	Sequence 597, App	197	4	16.7	14	3	US-09-991-225-44	Sequence 44, Appl
125	4	16.7	10	4	US-10-462-452-399	Sequence 399, App	198	4	16.7	14	4	US-10-097-065-553	Sequence 553, App
126	4	16.7	10	4	US-10-462-452-413	Sequence 413, App	199	4	16.7	14	4	US-10-120-604-27	Sequence 27, Appl
127	4	16.7	10	4	US-10-462-452-421	Sequence 421, App	200	4	16.7	14	4	US-10-120-604-28	Sequence 28, Appl
128	4	16.7	10	4	US-10-462-452-434	Sequence 434, App	201	4	16.7	14	4	US-10-120-604-70	Sequence 70, Appl
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136	4	16.7	10	4	US-10-601-953-562	Sequence 562, App	209	4	16.7	14	4	US-10-239-423-24	Sequence 24, Appl
137	4	16.7	10	4	US-10-702-765-129	Sequence 129, App	210	4	16.7	14	4	US-10-372-076-97	Sequence 97, Appl
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142	4	16.7	10	4	US-10-777-053-294	Sequence 294, App	215	4	16.7	14	4	US-10-369-405-43	Sequence 43, Appl
143	4	16.7	10	4	US-10-715-417-51	Sequence 51, Appl	216	4	16.7	14	4	US-10-369-405-44	Sequence 44, Appl
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148	4	16.7	10	4	US-10-354-090-51	Sequence 51, Appl	221	4	16.7	14	5	US-10-677-074-97	Sequence 97, Appl
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150	4	16.7	10	4	US-10-354-090-59	Sequence 59, Appl	223	4	16.7	14	5	US-10-926-386-38	Sequence 38, Appl
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152	4	16.7	10	6	US-11-027-273-1	Sequence 1, Appl	225	4	16.7	14	6	US-11-070-456-27	Sequence 27, Appl
153	4	16.7	11	3	US-09-988-493-67	Sequence 67, Appl	226	4	16.7	14	6	US-11-070-456-28	Sequence 28, Appl
154	4	16.7	11	4	US-10-262-435-109	Sequence 0, Appl	227	4	16.7	14	6	US-11-070-456-70	Sequence 70, Appl
155	4	16.7	11	4	US-10-239-313A-281	Sequence 281, App	228	4	16.7	14	6	US-11-070-456-71	Sequence 71, Appl
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157	4	16.7	11	4	US-10-702-765-128	Sequence 128, App	230	4	16.7	14	6	US-11-070-456-87	Sequence 87, Appl
158	4	16.7	11	5	US-10-808-187-1532	Sequence 1532, Ap	231	4	16.7	14	6	US-11-036-867-10	Sequence 10, Appl
159	4	16.7	11	5	US-10-808-187-1625	Sequence 1625, Ap	232	4	16.7	15	3	US-09-947-925A-17	Sequence 17, Appl
160	4	16.7	11	5	US-10-705-459-332	Sequence 332, App	233	4	16.7	15	3	US-09-768-779A-18	Sequence 18, Appl
161	4	16.7	11	5	US-10-479-933-12	Sequence 12, Appl	234	4	16.7	15	3	US-09-953-510-50	Sequence 50, Appl
162	4	16.7	11	5	US-10-807-807-1532	Sequence 1532, Ap	235	4	16.7	15	3	US-09-953-510-51	Sequence 51, Appl
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169	4	16.7	12	5	US-10-275-652-44	Sequence 44, Appl	242	4	16.7	15	3	US-09-993-767-986	Sequence 986, App
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252	4	16.7	15	4	US-10-147-255-52	Sequence 52, App	325	4	16.7	17	5	US-09-879-957-1172	Sequence 172, App
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255	4	16.7	15	4	US-10-369-405-72	Sequence 72, App	328	4	16.7	18	4	US-10-189-437-384	Sequence 384, App
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259	4	16.7	15	4	US-10-441-952A-243	Sequence 243, App	332	4	16.7	18	4	US-10-685-898-84	Sequence 84, App
260	4	16.7	15	5	US-10-695-155-50	Sequence 50, App	333	4	16.7	18	4	US-10-732-862A-120	Sequence 120, App
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275	4	16.7	16	3	US-09-813-333-20	Sequence 20, App	348	4	16.7	19	5	US-10-862-195-2065	Sequence 2065, App
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292	4	16.7	16	4	US-10-262-794A-18	Sequence 18, App	365	4	16.7	20	4	US-10-414-583-64	Sequence 64, App
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316	4	16.7	17	5	US-10-695-155-155	Sequence 155, App	389	4	16.7	21	4	US-10-253-471-650	Sequence 650, App
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402	4	16.7	21	4	US-10-702-765-153	Sequence 153, App	475	3	12.5	4	4	US-10-084-825-8	Sequence 8, Appli
403	4	16.7	21	4	US-10-702-765-154	Sequence 154, App	476	3	12.5	4	4	US-10-132-920B-54	Sequence 54, Appli
404	4	16.7	21	4	US-10-702-765-155	Sequence 155, App	477	3	12.5	4	4	US-10-285-045-15	Sequence 15, Appli
405	4	16.7	21	4	US-10-702-765-156	Sequence 156, App	478	3	12.5	4	4	US-10-284-660-15	Sequence 15, Appli
406	4	16.7	21	4	US-10-702-765-157	Sequence 157, App	479	3	12.5	4	4	US-10-283-423-43	Sequence 43, Appli
407	4	16.7	21	4	US-10-702-765-158	Sequence 158, App	480	3	12.5	4	4	US-10-283-423-44	Sequence 44, Appli
408	4	16.7	21	4	US-10-702-765-159	Sequence 159, App	481	3	12.5	4	4	US-10-283-423-44	Sequence 44, Appli
409	4	16.7	21	4	US-10-702-765-160	Sequence 160, App	482	3	12.5	4	4	US-10-283-423-134	Sequence 134, App
410	4	16.7	21	4	US-10-702-765-161	Sequence 161, App	483	3	12.5	4	4	US-10-283-423-147	Sequence 147, App
411	4	16.7	21	4	US-10-702-765-162	Sequence 162, App	484	3	12.5	4	4	US-10-197-927-22	Sequence 22, Appli
412	4	16.7	21	4	US-10-641-340-3	Sequence 3, Appli	485	3	12.5	4	4	US-10-213-821-43	Sequence 43, Appli
413	4	16.7	21	5	US-10-479-166-18	Sequence 18, Appli	486	3	12.5	4	4	US-10-213-821-44	Sequence 44, Appli
414	4	16.7	21	5	US-10-808-187-1373	Sequence 1373, Ap	487	3	12.5	4	4	US-10-213-821-147	Sequence 134, App
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416	4	16.7	21	5	US-10-748-033-9	Sequence 9, Appli	489	3	12.5	4	4	US-10-237-467-13	Sequence 13, Appli
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419	4	16.7	22	3	US-09-991-548-30	Sequence 30, Appli	492	3	12.5	4	4	US-10-283-722-723	Sequence 723, App
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421	4	16.7	22	4	US-10-044-539-92	Sequence 92, Appli	494	3	12.5	4	4	US-10-325-810-169	Sequence 169, App
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425	4	16.7	22	5	US-10-877-124-92	Sequence 92, Appli	498	3	12.5	4	4	US-10-283-903-721	Sequence 721, App
426	4	16.7	22	5	US-10-877-022-92	Sequence 92, Appli	499	3	12.5	4	4	US-10-283-903-723	Sequence 723, App
427	4	16.7	22	5	US-10-877-146-92	Sequence 92, Appli	500	3	12.5	4	4	US-10-013-312-1291	Sequence 1291, Ap
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429	4	16.7	23	4	US-10-212-628-196	Sequence 196, App	502	3	12.5	4	4	US-10-306-631-55	Sequence 55, Appli
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432	4	16.7	23	5	US-10-990-767-39	Sequence 39, Appli	505	3	12.5	4	4	US-10-363-208-52	Sequence 52, Appli
433	4	16.7	23	5	US-10-860-050-202	Sequence 202, App	506	3	12.5	4	4	US-10-435-751-54	Sequence 54, Appli
434	4	16.7	24	3	US-09-892-877-279	Sequence 279, App	507	3	12.5	4	4	US-10-438-181A-54	Sequence 54, Appli
435	4	16.7	24	3	US-09-948-783-291	Sequence 291, App	508	3	12.5	4	4	US-10-422-571-62	Sequence 62, Appli
436	4	16.7	24	4	US-10-385-415-82	Sequence 82, App	509	3	12.5	4	4	US-10-693-802-1	Sequence 1, Appli
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465	3	12.5	4	3	US-09-924-099-8	Sequence 8, Appli	538	3	12.5	4	5	US-10-892-402-141	Sequence 141, App



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540	3	12.5	4	5	US-10-650-467-126	Sequence 126, App	613	3	12.5	5	5	US-10-874-923-129	Sequence 129, App
541	3	12.5	4	5	US-10-650-467-128	Sequence 128, App	614	3	12.5	5	5	US-10-760-085-23	Sequence 23, Appl
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543	3	12.5	4	5	US-10-807-807-810	Sequence 810, App	616	3	12.5	5	5	US-10-884-355A-31	Sequence 31, Appl
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554	3	12.5	5	3	US-09-939-481-37	Sequence 37, Appl	627	3	12.5	5	5	US-10-715-810-19	Sequence 19, Appl
555	3	12.5	5	3	US-09-939-481-38	Sequence 38, Appl	628	3	12.5	5	5	US-10-715-810-34	Sequence 34, Appl
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557	3	12.5	5	3	US-09-751-100B-26	Sequence 26, Appl	630	3	12.5	5	5	US-10-939-309-89	Sequence 89, Appl
558	3	12.5	5	3	US-09-925-179-63	Sequence 63, Appl	631	3	12.5	5	5	US-10-650-467-153	Sequence 153, App
559	3	12.5	5	3	US-09-387-715-7	Sequence 7, Appl	632	3	12.5	5	5	US-10-650-467-154	Sequence 154, App
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562	3	12.5	5	3	US-09-933-767-858	Sequence 858, App	635	3	12.5	5	5	US-10-841-049-41	Sequence 41, Appl
563	3	12.5	5	4	US-10-014-485A-72	Sequence 72, Appl	636	3	12.5	5	5	US-11-029-331-13	Sequence 13, Appl
564	3	12.5	5	4	US-10-014-485A-84	Sequence 84, Appl	637	3	12.5	5	6	US-11-066-697-1079	Sequence 1079, App
565	3	12.5	5	4	US-10-099-895-19	Sequence 19, Appl	638	3	12.5	5	6	US-11-066-697-1179	Sequence 1179, App
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577	3	12.5	5	4	US-10-327-288-21	Sequence 21, Appl	650	3	12.5	5	6	US-09-234-395-241	Sequence 241, App
578	3	12.5	5	4	US-10-364-843-7	Sequence 7, Appl	651	3	12.5	5	6	US-09-234-395-256	Sequence 256, App
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591	3	12.5	5	4	US-10-181-937-55	Sequence 55, Appl	664	3	12.5	5	6	US-09-727-963A-33	Sequence 33, Appl
592	3	12.5	5	4	US-10-416-090-46	Sequence 46, Appl	665	3	12.5	5	6	US-09-878-603-24	Sequence 24, Appl
593	3	12.5	5	4	US-10-320-730A-2	Sequence 2, Appl	666	3	12.5	5	6	US-09-264-516A-265	Sequence 265, App
594	3	12.5	5	4	US-10-320-730A-3	Sequence 3, Appl	667	3	12.5	5	6	US-09-264-516A-280	Sequence 280, App
595	3	12.5	5	4	US-10-742-344-2	Sequence 2, Appl	668	3	12.5	5	6	US-09-912-414-1	Sequence 1, Appl
596	3	12.5	5	4	US-10-731-921-5	Sequence 5, Appl	669	3	12.5	5	6	US-09-962-863-6	Sequence 6, Appl
597	3	12.5	5	4	US-10-716-204-28	Sequence 28, Appl	670	3	12.5	5	6	US-09-858-852A-66	Sequence 66, Appl
598	3	12.5	5	4	US-10-773-229-7	Sequence 7, Appl	671	3	12.5	5	6	US-09-925-179-61	Sequence 61, Appl
599	3	12.5	5	4	US-10-677-093-53	Sequence 53, Appl	672	3	12.5	5	6	US-09-387-715-49	Sequence 49, Appl
600	3	12.5	5	4	US-10-712-425-69	Sequence 69, Appl	673	3	12.5	5	6	US-09-791-524-101	Sequence 101, App
601	3	12.5	5	4	US-10-712-425-318	Sequence 318, App	674	3	12.5	5	6	US-09-833-245-599	Sequence 599, App
602	3	12.5	5	4	US-10-712-425-311	Sequence 351, App	675	3	12.5	5	6	US-10-024-632-27	Sequence 27, Appl
603	3	12.5	5	4	US-10-712-425-382	Sequence 382, App	676	3	12.5	5	6	US-10-157-240-2	Sequence 2, Appl
604	3	12.5	5	4	US-10-712-425-383	Sequence 383, App	677	3	12.5	5	6	US-10-006-869-855	Sequence 855, App
605	3	12.5	5	4	US-10-712-425-419	Sequence 419, App	678	3	12.5	5	6	US-10-006-869-870	Sequence 870, App
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607	3	12.5	5	5	US-10-841-056-41	Sequence 41, Appl	680	3	12.5	5	6	US-10-141-357-265	Sequence 265, App
608	3	12.5	5	5	US-10-841-121-40	Sequence 40, Appl	681	3	12.5	5	6	US-10-141-357-280	Sequence 280, App
609	3	12.5	5	5	US-10-841-121-41	Sequence 41, Appl	682	3	12.5	5	6	US-10-054-968-14	Sequence 14, Appl
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611	3	12.5	5	5	US-10-823-964A-17	Sequence 17, Appl	684	3	12.5	5	6	US-10-159-006-64	Sequence 64, Appl

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686	3	12.5	6	4	US-10-283-423-66	Sequence 66, Appl	759	3	12.5	6	5	US-10-691-330-13	Sequence 13, Appl
687	3	12.5	6	4	US-10-364-842-49	Sequence 49, Appl	760	3	12.5	6	5	US-10-699-114-205	Sequence 205, App
688	3	12.5	6	4	US-10-188-608-31	Sequence 31, Appl	761	3	12.5	6	5	US-10-699-114-218	Sequence 218, App
689	3	12.5	6	4	US-10-188-608-32	Sequence 32, Appl	762	3	12.5	6	5	US-10-699-114-219	Sequence 219, App
690	3	12.5	6	4	US-10-213-821-65	Sequence 65, Appl	763	3	12.5	6	5	US-10-699-114-278	Sequence 278, App
691	3	12.5	6	4	US-10-213-821-66	Sequence 66, Appl	764	3	12.5	6	5	US-10-699-114-279	Sequence 279, App
692	3	12.5	6	4	US-10-348-232-46	Sequence 46, Appl	765	3	12.5	6	5	US-10-699-114-438	Sequence 438, App
693	3	12.5	6	4	US-10-348-232-134	Sequence 134, App	766	3	12.5	6	5	US-10-699-114-439	Sequence 439, App
694	3	12.5	6	4	US-10-441-626-33	Sequence 33, Appl	767	3	12.5	6	5	US-10-699-114-561	Sequence 561, App
695	3	12.5	6	4	US-10-436-826-33	Sequence 33, Appl	768	3	12.5	6	5	US-10-699-114-613	Sequence 613, App
696	3	12.5	6	4	US-10-441-625-33	Sequence 33, Appl	769	3	12.5	6	5	US-10-699-114-1022	Sequence 1022, Ap
697	3	12.5	6	4	US-10-414-524-89	Sequence 89, Appl	770	3	12.5	6	5	US-10-699-114-1045	Sequence 1045, Ap
698	3	12.5	6	4	US-10-407-079-26	Sequence 26, Appl	771	3	12.5	6	5	US-10-699-114-1046	Sequence 1046, Ap
699	3	12.5	6	4	US-10-395-032-885	Sequence 855, App	772	3	12.5	6	5	US-10-486-595-10	Sequence 10, Appl
700	3	12.5	6	4	US-10-395-032-870	Sequence 870, App	773	3	12.5	6	5	US-10-884-355A-9	Sequence 9, Appl
701	3	12.5	6	4	US-10-378-173-211	Sequence 211, App	774	3	12.5	6	5	US-10-884-355A-14	Sequence 14, Appl
702	3	12.5	6	4	US-10-394-980-256	Sequence 256, App	775	3	12.5	6	5	US-10-884-355A-15	Sequence 15, Appl
703	3	12.5	6	4	US-10-363-208-54	Sequence 54, Appl	776	3	12.5	6	5	US-10-884-355A-16	Sequence 16, Appl
704	3	12.5	6	4	US-10-363-208-56	Sequence 56, Appl	777	3	12.5	6	5	US-10-884-355A-17	Sequence 17, Appl
705	3	12.5	6	4	US-10-328-953-34	Sequence 34, Appl	778	3	12.5	6	5	US-10-884-355A-18	Sequence 18, Appl
706	3	12.5	6	4	US-10-367-580-304	Sequence 304, App	779	3	12.5	6	5	US-10-884-355A-19	Sequence 19, Appl
707	3	12.5	6	4	US-10-367-593-304	Sequence 304, App	780	3	12.5	6	5	US-10-884-355A-20	Sequence 20, Appl
708	3	12.5	6	4	US-10-367-594-304	Sequence 304, App	781	3	12.5	6	5	US-10-884-355A-21	Sequence 21, Appl
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710	3	12.5	6	4	US-10-367-658-304	Sequence 304, App	783	3	12.5	6	5	US-10-884-355A-23	Sequence 23, Appl
711	3	12.5	6	4	US-10-367-668-304	Sequence 304, App	784	3	12.5	6	5	US-10-884-355A-24	Sequence 24, Appl
712	3	12.5	6	4	US-10-702-765-203	Sequence 203, App	785	3	12.5	6	5	US-10-884-355A-32	Sequence 32, Appl
713	3	12.5	6	4	US-10-736-048-65	Sequence 65, Appl	786	3	12.5	6	5	US-10-884-355A-33	Sequence 33, Appl
714	3	12.5	6	4	US-10-736-048-66	Sequence 66, Appl	787	3	12.5	6	5	US-10-884-355A-34	Sequence 34, Appl
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716	3	12.5	6	4	US-10-801-994-66	Sequence 66, Appl	789	3	12.5	6	5	US-10-884-355A-36	Sequence 36, Appl
717	3	12.5	6	4	US-10-398-932-2	Sequence 2, Appl	790	3	12.5	6	5	US-10-884-355A-37	Sequence 37, Appl
718	3	12.5	6	4	US-10-699-088-205	Sequence 205, App	791	3	12.5	6	5	US-10-884-355A-38	Sequence 38, Appl
719	3	12.5	6	4	US-10-699-088-218	Sequence 218, App	792	3	12.5	6	5	US-10-884-355A-42	Sequence 42, Appl
720	3	12.5	6	4	US-10-699-088-219	Sequence 219, App	793	3	12.5	6	5	US-10-884-355A-43	Sequence 43, Appl
721	3	12.5	6	4	US-10-699-088-278	Sequence 278, App	794	3	12.5	6	5	US-10-884-355A-44	Sequence 44, Appl
722	3	12.5	6	4	US-10-699-088-279	Sequence 279, App	795	3	12.5	6	5	US-10-884-355A-45	Sequence 45, Appl
723	3	12.5	6	4	US-10-699-088-438	Sequence 438, App	796	3	12.5	6	5	US-10-884-355A-46	Sequence 46, Appl
724	3	12.5	6	4	US-10-699-088-439	Sequence 439, App	797	3	12.5	6	5	US-10-884-355A-47	Sequence 47, Appl
725	3	12.5	6	4	US-10-699-088-561	Sequence 561, App	798	3	12.5	6	5	US-10-968-237-61	Sequence 61, Appl
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730	3	12.5	6	4	US-10-786-850-43	Sequence 43, Appl	803	3	12.5	6	5	US-10-806-924-74	Sequence 74, Appl
731	3	12.5	6	4	US-10-786-850-48	Sequence 48, Appl	804	3	12.5	6	5	US-10-806-924-97	Sequence 97, Appl
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733	3	12.5	6	5	US-10-486-605-11	Sequence 11, Appl	806	3	12.5	6	5	US-10-806-924-168	Sequence 168, App
734	3	12.5	6	5	US-10-699-113-111	Sequence 111, App	807	3	12.5	6	5	US-10-806-924-181	Sequence 181, App
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737	3	12.5	6	5	US-10-699-113-205	Sequence 205, App	810	3	12.5	6	5	US-10-806-924-242	Sequence 242, App
738	3	12.5	6	5	US-10-699-113-218	Sequence 218, App	811	3	12.5	6	5	US-10-806-924-401	Sequence 401, App
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740	3	12.5	6	5	US-10-699-113-278	Sequence 278, App	813	3	12.5	6	5	US-10-806-924-524	Sequence 524, App
741	3	12.5	6	5	US-10-699-113-279	Sequence 279, App	814	3	12.5	6	5	US-10-806-924-576	Sequence 576, App
742	3	12.5	6	5	US-10-699-113-438	Sequence 438, App	815	3	12.5	6	5	US-10-931-260-272	Sequence 272, App
743	3	12.5	6	5	US-10-699-113-439	Sequence 439, App	816	3	12.5	6	5	US-10-496-869-10	Sequence 10, Appl
744	3	12.5	6	5	US-10-699-113-561	Sequence 561, App	817	3	12.5	6	5	US-10-650-467-155	Sequence 155, App
745	3	12.5	6	5	US-10-699-113-613	Sequence 613, App	818	3	12.5	6	5	US-10-650-467-163	Sequence 163, App
746	3	12.5	6	5	US-10-486-582-7	Sequence 7, Appl	819	3	12.5	6	5	US-10-650-467-164	Sequence 164, App
747	3	12.5	6	5	US-10-759-379-241	Sequence 241, App	820	3	12.5	6	5	US-10-807-807-564	Sequence 564, App
748	3	12.5	6	5	US-10-759-379-256	Sequence 256, App	821	3	12.5	6	5	US-10-807-807-1041	Sequence 1041, Ap
749	3	12.5	6	5	US-10-759-507-241	Sequence 241, App	822	3	12.5	6	5	US-10-807-807-2165	Sequence 2165, Ap
750	3	12.5	6	5	US-10-759-507-256	Sequence 256, App	823	3	12.5	6	5	US-10-952-557-256	Sequence 256, App
751	3	12.5	6	5	US-10-691-157-13	Sequence 13, Appl	824	3	12.5	6	6	US-10-820-057A-286	Sequence 286, App
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757	3	12.5	6	5	US-10-637-317-31	Sequence 31, Appl	830	3	12.5	6	6	US-11-131-054-36	Sequence 36, Appl
												US-11-003-150-243	Sequence 243, App

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832	3	12.5	6	US-11-131-042-36	Sequence 36, Appl	905	3	12.5	7	3	US-09-990-586-5	Sequence 5, Appl
833	3	12.5	7	US-08-765-837-7	Sequence 7, Appl	906	3	12.5	7	3	US-09-968-744A-15	Sequence 15, Appl
834	3	12.5	7	US-09-785-474-16	Sequence 16, Appl	907	3	12.5	7	3	US-09-968-744A-39	Sequence 39, Appl
835	3	12.5	7	US-09-865-483-10	Sequence 10, Appl	908	3	12.5	7	3	US-09-968-744A-57	Sequence 57, Appl
836	3	12.5	7	US-09-845-667-9	Sequence 9, Appl	909	3	12.5	7	3	US-09-968-744A-60	Sequence 60, Appl
837	3	12.5	7	US-09-845-667-14	Sequence 14, Appl	910	3	12.5	7	3	US-09-968-744A-75	Sequence 75, Appl
838	3	12.5	7	US-09-845-667-40	Sequence 40, Appl	911	3	12.5	7	3	US-09-968-744A-135	Sequence 135, App
839	3	12.5	7	US-09-845-667-41	Sequence 41, Appl	912	3	12.5	7	3	US-09-968-744A-171	Sequence 171, App
840	3	12.5	7	US-09-845-667-48	Sequence 48, Appl	913	3	12.5	7	3	US-09-968-744A-189	Sequence 189, App
841	3	12.5	7	US-09-845-667-49	Sequence 49, Appl	914	3	12.5	7	3	US-09-968-744A-261	Sequence 261, App
842	3	12.5	7	US-09-845-667-50	Sequence 50, Appl	915	3	12.5	7	3	US-09-968-744A-273	Sequence 273, App
843	3	12.5	7	US-09-192-854-11	Sequence 11, Appl	916	3	12.5	7	3	US-09-968-744A-303	Sequence 303, App
844	3	12.5	7	US-09-192-854-27	Sequence 27, Appl	917	3	12.5	7	3	US-09-962-756-2014	Sequence 2014, Ap
845	3	12.5	7	US-09-192-854-38	Sequence 38, Appl	918	3	12.5	7	3	US-09-261-894-68	Sequence 68, Appl
846	3	12.5	7	US-09-192-854-40	Sequence 40, Appl	919	3	12.5	7	3	US-09-968-561A-15	Sequence 15, Appl
847	3	12.5	7	US-09-192-854-50	Sequence 50, Appl	920	3	12.5	7	3	US-09-968-561A-39	Sequence 39, Appl
848	3	12.5	7	US-09-192-854-80	Sequence 80, Appl	921	3	12.5	7	3	US-09-968-561A-57	Sequence 57, Appl
849	3	12.5	7	US-09-192-854-97	Sequence 97, Appl	922	3	12.5	7	3	US-09-968-561A-60	Sequence 60, Appl
850	3	12.5	7	US-09-192-854-109	Sequence 109, App	923	3	12.5	7	3	US-09-968-561A-75	Sequence 75, Appl
851	3	12.5	7	US-09-192-854-148	Sequence 148, App	924	3	12.5	7	3	US-09-968-561A-135	Sequence 135, App
852	3	12.5	7	US-09-192-854-155	Sequence 155, App	925	3	12.5	7	3	US-09-968-561A-171	Sequence 171, App
853	3	12.5	7	US-09-192-854-172	Sequence 172, App	926	3	12.5	7	3	US-09-968-561A-189	Sequence 189, App
854	3	12.5	7	US-09-853-080-7	Sequence 7, Appl	927	3	12.5	7	3	US-09-968-561A-261	Sequence 261, App
855	3	12.5	7	US-09-822-270-4	Sequence 4, Appl	928	3	12.5	7	3	US-09-968-561A-273	Sequence 273, App
856	3	12.5	7	US-09-234-395-243	Sequence 243, App	929	3	12.5	7	3	US-09-968-561A-303	Sequence 303, App
857	3	12.5	7	US-09-234-395-258	Sequence 258, App	930	3	12.5	7	3	US-09-973-278-521	Sequence 521, App
858	3	12.5	7	US-09-848-585-22	Sequence 22, Appl	931	3	12.5	7	4	US-10-104-019-47	Sequence 47, Appl
859	3	12.5	7	US-09-305-928-243	Sequence 243, App	932	3	12.5	7	4	US-10-104-019-48	Sequence 48, Appl
860	3	12.5	7	US-09-305-928-258	Sequence 258, App	933	3	12.5	7	4	US-10-104-019-49	Sequence 49, Appl
861	3	12.5	7	US-09-823-829-80	Sequence 80, Appl	934	3	12.5	7	4	US-10-104-019-50	Sequence 50, Appl
862	3	12.5	7	US-09-956-086-18	Sequence 18, Appl	935	3	12.5	7	4	US-10-032-482-16	Sequence 16, Appl
863	3	12.5	7	US-09-956-087-18	Sequence 18, Appl	936	3	12.5	7	4	US-10-127-691-8	Sequence 8, Appl
864	3	12.5	7	US-09-968-561A-15	Sequence 15, Appl	937	3	12.5	7	4	US-10-024-123-2	Sequence 2, Appl
865	3	12.5	7	US-09-968-561A-39	Sequence 39, Appl	938	3	12.5	7	4	US-10-113-417-7	Sequence 7, Appl
866	3	12.5	7	US-09-968-561A-57	Sequence 57, Appl	939	3	12.5	7	4	US-10-015-979-98	Sequence 98, Appl
867	3	12.5	7	US-09-968-561A-60	Sequence 60, Appl	940	3	12.5	7	4	US-10-062-710-232	Sequence 232, App
868	3	12.5	7	US-09-968-561A-75	Sequence 75, Appl	941	3	12.5	7	4	US-10-014-340-424	Sequence 424, App
869	3	12.5	7	US-09-968-561A-135	Sequence 135, App	942	3	12.5	7	4	US-10-014-340-648	Sequence 648, App
870	3	12.5	7	US-09-968-561A-171	Sequence 171, App	943	3	12.5	7	4	US-10-273-541-39	Sequence 39, Appl
871	3	12.5	7	US-09-968-561A-189	Sequence 189, App	944	3	12.5	7	4	US-10-273-541-43	Sequence 43, Appl
872	3	12.5	7	US-09-968-561A-261	Sequence 261, App	945	3	12.5	7	4	US-10-273-541-44	Sequence 44, Appl
873	3	12.5	7	US-09-968-561A-273	Sequence 273, App	946	3	12.5	7	4	US-10-273-541-46	Sequence 46, Appl
874	3	12.5	7	US-09-968-561A-303	Sequence 303, App	947	3	12.5	7	4	US-10-273-541-50	Sequence 50, Appl
875	3	12.5	7	US-09-486-734A-25	Sequence 25, Appl	948	3	12.5	7	4	US-10-273-541-64	Sequence 64, Appl
876	3	12.5	7	US-09-293-854-5	Sequence 5, Appl	949	3	12.5	7	4	US-10-006-869-857	Sequence 857, App
877	3	12.5	7	US-09-264-516A-267	Sequence 267, App	950	3	12.5	7	4	US-10-006-869-872	Sequence 872, App
878	3	12.5	7	US-09-264-516A-282	Sequence 282, App	951	3	12.5	7	4	US-10-006-869-1833	Sequence 1833, Ap
879	3	12.5	7	US-09-884-767A-85	Sequence 85, Appl	952	3	12.5	7	4	US-10-006-869-1863	Sequence 1863, Ap
880	3	12.5	7	US-09-861-687-8	Sequence 8, Appl	953	3	12.5	7	4	US-10-006-869-2121	Sequence 2121, Ap
881	3	12.5	7	US-09-983-803-366	Sequence 366, App	954	3	12.5	7	4	US-10-006-869-2141	Sequence 2141, Ap
882	3	12.5	7	US-09-995-973-20	Sequence 20, Appl	955	3	12.5	7	4	US-10-006-869-2189	Sequence 2189, Ap
883	3	12.5	7	US-09-995-973-24	Sequence 24, Appl	956	3	12.5	7	4	US-10-006-869-2219	Sequence 2219, Ap
884	3	12.5	7	US-09-995-973-27	Sequence 27, Appl	957	3	12.5	7	4	US-10-006-869-2863	Sequence 2863, Ap
885	3	12.5	7	US-09-229-751A-78	Sequence 78, Appl	958	3	12.5	7	4	US-10-006-869-2926	Sequence 2926, Ap
886	3	12.5	7	US-09-281-495-5	Sequence 5, Appl	959	3	12.5	7	4	US-10-006-869-3805	Sequence 3805, Ap
887	3	12.5	7	US-09-997-961-29	Sequence 29, Appl	960	3	12.5	7	4	US-10-293-417-5	Sequence 5, Appl
888	3	12.5	7	US-09-984-490-366	Sequence 366, App	961	3	12.5	7	4	US-10-155-922-128	Sequence 128, App
889	3	12.5	7	US-09-990-186-733	Sequence 733, App	962	3	12.5	7	4	US-10-155-922-129	Sequence 129, App
890	3	12.5	7	US-09-990-186-836	Sequence 836, App	963	3	12.5	7	4	US-10-155-922-130	Sequence 130, App
891	3	12.5	7	US-09-990-186-941	Sequence 941, App	964	3	12.5	7	4	US-10-141-357-267	Sequence 267, App
892	3	12.5	7	US-09-940-727B-32	Sequence 32, Appl	965	3	12.5	7	4	US-10-141-357-282	Sequence 282, App
893	3	12.5	7	US-09-940-727B-35	Sequence 35, Appl	966	3	12.5	7	4	US-10-272-411-49	Sequence 49, Appl
894	3	12.5	7	US-09-563-222-53	Sequence 53, Appl	967	3	12.5	7	4	US-10-062-623A-19	Sequence 19, Appl
895	3	12.5	7	US-09-596-484-20	Sequence 20, Appl	968	3	12.5	7	4	US-10-062-623A-20	Sequence 20, Appl
896	3	12.5	7	US-09-596-484-24	Sequence 24, Appl	969	3	12.5	7	4	US-10-091-300-11	Sequence 11, Appl
897	3	12.5	7	US-09-596-484-27	Sequence 27, Appl	970	3	12.5	7	4	US-10-272-328A-49	Sequence 49, Appl
898	3	12.5	7	US-09-954-385-214	Sequence 214, App	971	3	12.5	7	4	US-10-209-323-30	Sequence 30, Appl
899	3	12.5	7	US-09-954-385-229	Sequence 229, App	972	3	12.5	7	4	US-10-052-578-156	Sequence 156, App
900	3	12.5	7	US-09-954-385-238	Sequence 238, App	973	3	12.5	7	4	US-10-052-578-158	Sequence 158, App
901	3	12.5	7	US-09-954-385-260	Sequence 260, App	974	3	12.5	7	4	US-10-052-578-171	Sequence 171, App
902	3	12.5	7	US-09-989-994-903	Sequence 733, App	975	3	12.5	7	4	US-10-052-578-263	Sequence 263, App
903	3	12.5	7	US-09-989-994-836	Sequence 836, App	976	3	12.5	7	4	US-10-052-578-269	Sequence 269, App

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980 3 12.5 7 4 US-10-104-019-49 Sequence 49, Appl  
981 3 12.5 7 4 US-10-104-019-50 Sequence 50, Appl  
982 3 12.5 7 4 US-10-190-082-23 Sequence 23, Appl  
983 3 12.5 7 4 US-10-190-082-34 Sequence 34, Appl  
984 3 12.5 7 4 US-10-190-082-85 Sequence 85, Appl  
985 3 12.5 7 4 US-10-190-082-232 Sequence 232, App  
986 3 12.5 7 4 US-10-190-082-297 Sequence 297, App  
987 3 12.5 7 4 US-10-169-351-21 Sequence 21, Appl  
988 3 12.5 7 4 US-10-203-754A-14 Sequence 14, Appl  
989 3 12.5 7 4 US-10-253-904-7 Sequence 7, Appl  
990 3 12.5 7 4 US-10-271-708-12 Sequence 12, Appl  
991 3 12.5 7 4 US-10-271-708-28 Sequence 28, Appl  
992 3 12.5 7 4 US-10-283-423-42 Sequence 42, Appl  
993 3 12.5 7 4 US-10-283-423-99 Sequence 99, Appl  
994 3 12.5 7 4 US-10-283-423-136 Sequence 136, App  
995 3 12.5 7 4 US-10-283-423-137 Sequence 137, App  
996 3 12.5 7 4 US-10-283-423-168 Sequence 168, App  
997 3 12.5 7 4 US-10-062-109A-727 Sequence 727, App  
998 3 12.5 7 4 US-10-053-520-156 Sequence 156, App  
999 3 12.5 7 4 US-10-053-520-158 Sequence 158, App  
1000 3 12.5 7 5 US-10-471-934-5 Sequence 5, Appl

ALIGNMENTS

RESULT 1  
US-09-978-343-4  
; Sequence 4, Application US/09978343  
; Publication No. US20030082680A1  
; GENERAL INFORMATION:  
; APPLICANT: HOSTETTER, MARGARET K.  
; GALE, CHERYL A.  
; BENDEL, CATHERINE M.  
; TAO, NIAN-JUN  
; KENDRICK, KATHLEEN  
; TITLE OF INVENTION: CANDIDA ALBICANS GENE, INTEGRIN-LIKE  
; PROTEIN, ANTIBODIES, AND METHODS OF USE  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MUEITING, RAASCH, GERHARDT & SCHWAPPACH, P.A.  
; STREET: 119 NORTH FOURTH STREET, SUITE 203  
; CITY: MINNEAPOLIS  
; STATE: MINNESOTA  
; COUNTRY: USA  
; ZIP: 55401  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/09/978,343  
; FILING DATE: 15-Oct-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/642,846  
; FILING DATE: 03-MAY-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MUEITING, ANN M.  
; REGISTRATION NUMBER: 33,977  
; REFERENCE/DOCKET NUMBER: 110.00280101  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612-305-1217  
; TELEFAX: 612-305-1228  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 23 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single

; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-978-343-4  
Query Match 25.0%; Score 6; DB 3; Length 23;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 15 TNNNS 20  
Db 5 TNNNS 10  
RESULT 2  
US-09-935-384-41  
; Sequence 41, Application US/09935384  
; Publication No. US20030166526A1  
; GENERAL INFORMATION:  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: FARIS, MARY  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1H4  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; TITLE OF INVENTION: OTHER CANCERS  
; FILE REFERENCE: 51158-20033.00  
; CURRENT APPLICATION NUMBER: US/09/935,384  
; CURRENT FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 783  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 41  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-935-384-41  
Query Match 20.8%; Score 5; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 DSQTK 8  
Db 4 DSQTK 8  
RESULT 3  
US-09-935-384-131  
; Sequence 131, Application US/09935384  
; Publication No. US20030166526A1  
; GENERAL INFORMATION:  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: FARIS, MARY  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1H4  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; TITLE OF INVENTION: OTHER CANCERS  
; FILE REFERENCE: 51158-20033.00  
; CURRENT APPLICATION NUMBER: US/09/935,384  
; CURRENT FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22

; NUMBER OF SEQ ID NOS: 783  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 131  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-935-384-131

Query Match 20.8%; Score 5; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DSQTK 8  
Db 3 DSQTK 7

RESULT 4  
US-09-935-384-229  
; Sequence 229, Application US/09935384  
; Publication No. US20030166526A1  
; GENERAL INFORMATION:  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: PARIS, MARY  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOWITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PIH4  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; FILE REFERENCE: 51158-20033.00  
; CURRENT APPLICATION NUMBER: US/09/935,384  
; CURRENT FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 783  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 229  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-935-384-229

Query Match 20.8%; Score 5; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DSQTK 8  
Db 5 DSQTK 9

RESULT 5  
US-09-935-384-310  
; Sequence 310, Application US/09935384  
; Publication No. US20030166526A1  
; GENERAL INFORMATION:  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: PARIS, MARY  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOWITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PIH4  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; FILE REFERENCE: 51158-20033.00  
; CURRENT APPLICATION NUMBER: US/09/935,384

; CURRENT FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; NUMBER OF SEQ ID NOS: 783  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 310  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-935-384-310

Query Match 20.8%; Score 5; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DSQTK 8  
Db 5 DSQTK 9

RESULT 6  
US-09-935-384-419  
; Sequence 419, Application US/09935384  
; Publication No. US20030166526A1  
; GENERAL INFORMATION:  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: PARIS, MARY  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOWITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PIH4  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; FILE REFERENCE: 51158-20033.00  
; CURRENT APPLICATION NUMBER: US/09/935,384  
; CURRENT FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 783  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 419  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-935-384-419

Query Match 20.8%; Score 5; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DSQTK 8  
Db 1 DSQTK 5

RESULT 7  
US-09-935-384-529  
; Sequence 529, Application US/09935384  
; Publication No. US20030166526A1  
; GENERAL INFORMATION:  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: PARIS, MARY  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOWITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PIH4  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND

```
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20033.00
; CURRENT APPLICATION NUMBER: US/09/935,384
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 529
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-384-529

Query Match      20.8%; Score 5; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 DSQTK 8
Db      1 DSQTK 5

RESULT 8
US-09-935-384-616
; Sequence 616, Application US/09935384
; Publication No. US20030166526A1
; GENERAL INFORMATION:
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: APAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: FARIAS, MARY
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PIH4
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20033.00
; CURRENT APPLICATION NUMBER: US/09/935,384
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 616
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-384-616

Query Match      20.8%; Score 5; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 DSQTK 8
Db      1 DSQTK 5

RESULT 9
US-10-808-187-1154
; Sequence 1154, Application US/10808187
; Publication No. US2005009009A1
; GENERAL INFORMATION:
; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN
; TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE
```

```
; TITLE OF INVENTION: RESPIRATORY SYNDROME (SARS)
; FILE REFERENCE: V9661.0078
; CURRENT APPLICATION NUMBER: US/10/808,187
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,031
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: 60/457,730
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/459,931
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/460,357
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/461,265
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/462,805
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/468,139
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: 60/464,886
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 60/471,200
; PRIOR FILING DATE: 2003-05-16
; NUMBER OF SEQ ID NOS: 2476
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 1154
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human severe acute respiratory system virus
US-10-808-187-1154

Query Match      20.8%; Score 5; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 NNNNS 20
Db      5 NNNNS 9

RESULT 10
US-10-705-459-307
; Sequence 307, Application US/10705459
; Publication No. US2005005918A1
; GENERAL INFORMATION:
; APPLICANT: Barnea, Eilon
; APPLICANT: Beer, Ilan
; APPLICANT: Ziv, Tamar
; APPLICANT: Admon, Arie
; APPLICANT: Daseau, Lior
; APPLICANT: Buchsbaum, Samuel
; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECULE
; FILE REFERENCE: 26884
; CURRENT APPLICATION NUMBER: US/10/705,459
; CURRENT FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 372
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 307
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-705-459-307

Query Match      20.8%; Score 5; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 KSIPE 12
Db      4 KSIPE 8
```

```
RESULT 11
US-10-807-807-1154
; Sequence 1154, Application US/10807807
; Publication No. US20050181357A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, FREDERICK C.
; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN M.
; TITLE OF INVENTION: A HIGH-THROUGHPUT DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS
; TITLE OF INVENTION: CAUSING SEVERE ACUTE RESPIRATORY SYNDROME (SARS)
; FILE REFERENCE: V9661.0077
; CURRENT APPLICATION NUMBER: US/10/807,807
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,031
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: 60/457,730
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/459,931
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/460,357
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/461,265
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/462,805
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/464,886
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 60/465,738
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: 60/470,935
; PRIOR FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 2487
; SOFTWARE: Patent in ver. 3.2
; SEQ ID NO 1154
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human severe acute respiratory system virus
US-10-807-807-1154

Query Match          20.8%; Score 5; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 NNNNS 20
        |||||
Db       5 NNNNS 9

RESULT 12
US-09-935-384-368
; Sequence 368, Application US/09935384
; Publication No. US20030166526A1
; GENERAL INFORMATION:
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: FARIS, MARY
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1H4
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20033.00
; CURRENT APPLICATION NUMBER: US/09/935,384
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 2001-08-22
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 2487
; SOFTWARE: Patent in ver. 3.2
; SEQ ID NO 1154
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-384-368

Query Match          20.8%; Score 5; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 NNNNS 20
        |||||
Db       5 NNNNS 9

RESULT 13
US-09-935-384-661
; Sequence 661, Application US/09935384
; Publication No. US20030166526A1
; GENERAL INFORMATION:
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: FARIS, MARY
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1H4
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20033.00
; CURRENT APPLICATION NUMBER: US/09/935,384
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 661
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-384-661

Query Match          20.8%; Score 5; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 DSQTK 8
        |||||
Db       6 DSQTK 10

RESULT 14
US-09-982-172-186
; Sequence 186, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODI
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERA
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 186
; LENGTH: 12
; TYPE: PRT
US-09-982-172-186

Query Match          20.8%; Score 5; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 DSQTK 8
        |||||
Db       5 DSQTK 9
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; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-186

Query Match      20.8%; Score 5; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      19 NSSFY 23
Db      7 NSSFY 11

RESULT 15
US-09-982-172-245
; Sequence 245, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22263
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 245
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-245

Query Match      20.8%; Score 5; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      19 NSSFY 23
Db      7 NSSFY 11

Search completed: January 20, 2006, 17:57:56
Job time : 67 secs
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OM protein - protein search, using sw model

Run on: January 20, 2006, 17:54:55 ; Search time 8 Seconds  
(without alignments)  
30.402 Million cell updates/sec

Title: US-10-619-323-1\_COPY\_35\_58

Perfect score: 24  
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263	3	12.5	10	7	US-11-097-864-79	Sequence 79, Appl	336	3	12.5	10	7	US-11-045-024-8182	Sequence 8182, Ap
264	3	12.5	10	7	US-11-097-864-180	Sequence 180, App	337	3	12.5	10	7	US-11-045-024-8205	Sequence 8205, Ap
265	3	12.5	10	7	US-11-097-864-420	Sequence 420, App	338	3	12.5	10	7	US-11-045-024-8211	Sequence 8211, Ap
266	3	12.5	10	7	US-11-097-864-535	Sequence 535, App	339	3	12.5	10	7	US-11-045-024-8263	Sequence 8263, Ap
267	3	12.5	10	7	US-11-097-864-617	Sequence 617, App	340	3	12.5	10	7	US-11-045-024-8299	Sequence 8299, Ap
268	3	12.5	10	7	US-11-097-864-639	Sequence 639, App	341	3	12.5	10	7	US-11-045-024-8301	Sequence 8301, Ap
269	3	12.5	10	7	US-11-097-864-646	Sequence 646, App	342	3	12.5	10	7	US-11-045-024-8330	Sequence 8330, Ap
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271	3	12.5	10	7	US-11-097-912-79	Sequence 79, Appl	344	3	12.5	10	7	US-11-045-024-8629	Sequence 8629, Ap
272	3	12.5	10	7	US-11-097-912-180	Sequence 180, App	345	3	12.5	10	7	US-11-045-024-9551	Sequence 9551, Ap
273	3	12.5	10	7	US-11-097-912-420	Sequence 420, App	346	3	12.5	10	7	US-11-045-024-9557	Sequence 9557, Ap
274	3	12.5	10	7	US-11-097-912-535	Sequence 535, App	347	3	12.5	10	7	US-11-045-024-9674	Sequence 9674, Ap
275	3	12.5	10	7	US-11-097-912-617	Sequence 617, App	348	3	12.5	10	7	US-11-045-024-9989	Sequence 9989, Ap
276	3	12.5	10	7	US-11-097-912-639	Sequence 639, App	349	3	12.5	10	7	US-11-045-024-9999	Sequence 9999, Ap
277	3	12.5	10	7	US-11-097-912-646	Sequence 646, App	350	3	12.5	10	7	US-11-045-024-10274	Sequence 10274, A
278	3	12.5	10	7	US-11-166-288-10	Sequence 10, Appl	351	3	12.5	10	7	US-11-045-024-10291	Sequence 10291, A
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282	3	12.5	10	7	US-11-045-024-767	Sequence 767, App	355	3	12.5	10	7	US-11-045-024-10974	Sequence 10974, A
283	3	12.5	10	7	US-11-045-024-789	Sequence 789, App	356	3	12.5	10	7	US-11-045-024-11168	Sequence 11168, A
284	3	12.5	10	7	US-11-045-024-853	Sequence 853, App	357	3	12.5	10	7	US-11-045-024-11571	Sequence 11571, A
285	3	12.5	10	7	US-11-045-024-855	Sequence 855, App	358	3	12.5	10	7	US-11-045-024-11587	Sequence 11587, A
286	3	12.5	10	7	US-11-045-024-1271	Sequence 1271, Ap	359	3	12.5	10	7	US-11-045-024-11593	Sequence 11593, A
287	3	12.5	10	7	US-11-045-024-1319	Sequence 1319, Ap	360	3	12.5	10	7	US-11-045-024-11678	Sequence 11678, A
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292	3	12.5	10	7	US-11-045-024-2154	Sequence 2154, Ap	365	3	12.5	10	7	US-11-045-024-14295	Sequence 14295, A
293	3	12.5	10	7	US-11-045-024-2186	Sequence 2186, Ap	366	3	12.5	10	7	US-11-045-024-14334	Sequence 14334, A
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296	3	12.5	10	7	US-11-045-024-2217	Sequence 2217, Ap	369	3	12.5	10	7	US-11-129-104-82	Sequence 82, Appl
297	3	12.5	10	7	US-11-045-024-2218	Sequence 2218, Ap	370	3	12.5	10	7	US-11-107-096-35	Sequence 35, Appl
298	3	12.5	10	7	US-11-045-024-2219	Sequence 2219, Ap	371	3	12.5	10	6	US-10-665-658-16	Sequence 16, Appl
299	3	12.5	10	7	US-11-045-024-2220	Sequence 2220, Ap	372	3	12.5	11	6	US-10-841-956A-22	Sequence 22, Appl
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301	3	12.5	10	7	US-11-045-024-2847	Sequence 2847, Ap	374	3	12.5	11	6	US-10-877-961B-143	Sequence 143, App
302	3	12.5	10	7	US-11-045-024-3299	Sequence 3299, Ap	375	3	12.5	11	6	US-10-877-961B-165	Sequence 165, App
303	3	12.5	10	7	US-11-045-024-3346	Sequence 3346, Ap	376	3	12.5	11	6	US-10-877-961B-183	Sequence 183, App
304	3	12.5	10	7	US-11-045-024-3347	Sequence 3347, Ap	377	3	12.5	11	6	US-10-877-961B-209	Sequence 209, App
305	3	12.5	10	7	US-11-045-024-3846	Sequence 3846, Ap	378	3	12.5	11	6	US-10-877-961B-210	Sequence 210, App
306	3	12.5	10	7	US-11-045-024-3874	Sequence 3874, Ap	379	3	12.5	11	6	US-10-877-961B-211	Sequence 211, App
307	3	12.5	10	7	US-11-045-024-4656	Sequence 4656, Ap	380	3	12.5	11	6	US-10-877-961B-212	Sequence 212, App
308	3	12.5	10	7	US-11-045-024-4657	Sequence 4657, Ap	381	3	12.5	11	6	US-10-877-961B-213	Sequence 213, App
309	3	12.5	10	7	US-11-045-024-4668	Sequence 4668, Ap	382	3	12.5	11	6	US-10-877-961B-214	Sequence 214, App
310	3	12.5	10	7	US-11-045-024-4685	Sequence 4685, Ap	383	3	12.5	11	6	US-10-877-961B-215	Sequence 215, App
311	3	12.5	10	7	US-11-045-024-4686	Sequence 4686, Ap	384	3	12.5	11	6	US-10-877-961B-216	Sequence 216, App
312	3	12.5	10	7	US-11-045-024-4702	Sequence 4702, Ap	385	3	12.5	11	6	US-10-877-961B-217	Sequence 217, App
313	3	12.5	10	7	US-11-045-024-5139	Sequence 5139, Ap	386	3	12.5	11	6	US-10-877-961B-218	Sequence 218, App
314	3	12.5	10	7	US-11-045-024-5375	Sequence 5375, Ap	387	3	12.5	11	6	US-10-877-961B-219	Sequence 219, App
315	3	12.5	10	7	US-11-045-024-5375	Sequence 5375, Ap	388	3	12.5	11	6	US-10-877-961B-220	Sequence 220, App
316	3	12.5	10	7	US-11-045-024-5367	Sequence 5367, Ap	389	3	12.5	11	6	US-10-877-961B-227	Sequence 227, App
317	3	12.5	10	7	US-11-045-024-6087	Sequence 6087, Ap	390	3	12.5	11	6	US-10-877-961B-239	Sequence 239, App
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391	3	12.5	11	7	US-11-025-712-8	Sequence 8, Appli	464	3	12.5	11	7	US-11-045-024-9532	Sequence 9532, Ap
392	3	12.5	11	7	US-11-054-515-3164	Sequence 3164, Ap	465	3	12.5	11	7	US-11-045-024-9561	Sequence 9561, Ap
393	3	12.5	11	7	US-11-029-003-26	Sequence 26, Appl	466	3	12.5	11	7	US-11-045-024-9562	Sequence 9562, Ap
394	3	12.5	11	7	US-11-058-735-33	Sequence 33, Appl	467	3	12.5	11	7	US-11-045-024-9570	Sequence 9570, Ap
395	3	12.5	11	7	US-11-045-024-87	Sequence 87, Appl	468	3	12.5	11	7	US-11-045-024-9571	Sequence 9571, Ap
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397	3	12.5	11	7	US-11-045-024-323	Sequence 323, App	470	3	12.5	11	7	US-11-045-024-9841	Sequence 9841, Ap
398	3	12.5	11	7	US-11-045-024-337	Sequence 337, App	471	3	12.5	11	7	US-11-045-024-9891	Sequence 9891, Ap
399	3	12.5	11	7	US-11-045-024-929	Sequence 929, App	472	3	12.5	11	7	US-11-045-024-9968	Sequence 9968, Ap
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401	3	12.5	11	7	US-11-045-024-983	Sequence 983, App	474	3	12.5	11	7	US-11-045-024-10001	Sequence 10001, Ap
402	3	12.5	11	7	US-11-045-024-1416	Sequence 1416, Ap	475	3	12.5	11	7	US-11-045-024-10239	Sequence 10239, A
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404	3	12.5	11	7	US-11-045-024-2383	Sequence 2383, Ap	477	3	12.5	11	7	US-11-045-024-10281	Sequence 10281, A
405	3	12.5	11	7	US-11-045-024-2384	Sequence 2384, Ap	478	3	12.5	11	7	US-11-045-024-10295	Sequence 10295, A
406	3	12.5	11	7	US-11-045-024-2385	Sequence 2385, Ap	479	3	12.5	11	7	US-11-045-024-10774	Sequence 10774, A
407	3	12.5	11	7	US-11-045-024-2422	Sequence 2422, Ap	480	3	12.5	11	7	US-11-045-024-10802	Sequence 10802, A
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409	3	12.5	11	7	US-11-045-024-2424	Sequence 2424, Ap	482	3	12.5	11	7	US-11-045-024-10881	Sequence 10881, A
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412	3	12.5	11	7	US-11-045-024-2427	Sequence 2427, Ap	485	3	12.5	11	7	US-11-045-024-11146	Sequence 11146, A
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422	3	12.5	11	7	US-11-045-024-3438	Sequence 3438, Ap	495	3	12.5	11	7	US-11-045-024-11835	Sequence 11835, A
423	3	12.5	11	7	US-11-045-024-3439	Sequence 3439, Ap	496	3	12.5	11	7	US-11-045-024-11889	Sequence 11889, A
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425	3	12.5	11	7	US-11-045-024-3933	Sequence 3933, Ap	498	3	12.5	11	7	US-11-045-024-11910	Sequence 11910, A
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428	3	12.5	11	7	US-11-045-024-4761	Sequence 4761, Ap	501	3	12.5	11	7	US-11-127-677-84	Sequence 84, Appl
429	3	12.5	11	7	US-11-045-024-4819	Sequence 4819, Ap	502	3	12.5	11	7	US-11-127-677-88	Sequence 88, Appl
430	3	12.5	11	7	US-11-045-024-4820	Sequence 4820, Ap	503	3	12.5	11	7	US-11-192-219-43	Sequence 43, Appl
431	3	12.5	11	7	US-11-045-024-4840	Sequence 4840, Ap	504	3	12.5	11	7	US-11-157-360-32	Sequence 32, Appl
432	3	12.5	11	7	US-11-045-024-4841	Sequence 4841, Ap	505	3	12.5	11	7	US-11-038-980-72	Sequence 72, Appl
433	3	12.5	11	7	US-11-045-024-4860	Sequence 4860, Ap	506	3	12.5	11	7	US-11-038-980-100	Sequence 100, App
434	3	12.5	11	7	US-11-045-024-4861	Sequence 4861, Ap	507	3	12.5	11	6	US-10-997-066-44	Sequence 44, Appl
435	3	12.5	11	7	US-11-045-024-4862	Sequence 4862, Ap	508	3	12.5	12	6	US-10-507-662-12	Sequence 12, Appl
436	3	12.5	11	7	US-11-045-024-5390	Sequence 5390, Ap	509	3	12.5	12	6	US-10-467-657-9168	Sequence 9168, Ap
437	3	12.5	11	7	US-11-045-024-5407	Sequence 5407, Ap	510	3	12.5	12	6	US-10-467-657-9168	Sequence 9168, Ap
438	3	12.5	11	7	US-11-045-024-5586	Sequence 5586, Ap	511	3	12.5	12	6	US-10-929-988-172	Sequence 172, App
439	3	12.5	11	7	US-11-045-024-6088	Sequence 6088, Ap	512	3	12.5	12	6	US-10-834-397-268	Sequence 268, App
440	3	12.5	11	7	US-11-045-024-6089	Sequence 6089, Ap	513	3	12.5	12	7	US-11-045-173-3	Sequence 3, Appl
441	3	12.5	11	7	US-11-045-024-6118	Sequence 6118, Ap	514	3	12.5	12	7	US-11-054-515-3197	Sequence 3197, Ap
442	3	12.5	11	7	US-11-045-024-6338	Sequence 6338, Ap	515	3	12.5	12	7	US-11-069-834-22	Sequence 22, Appl
443	3	12.5	11	7	US-11-045-024-6523	Sequence 6523, Ap	516	3	12.5	12	7	US-11-069-834-30	Sequence 30, Appl
444	3	12.5	11	7	US-11-045-024-6547	Sequence 6547, Ap	517	3	12.5	12	7	US-11-069-834-32	Sequence 32, Appl
445	3	12.5	11	7	US-11-045-024-6669	Sequence 6669, Ap	518	3	12.5	12	7	US-11-098-763-21	Sequence 21, Appl
446	3	12.5	11	7	US-11-045-024-6707	Sequence 6707, Ap	519	3	12.5	12	7	US-11-129-104-24	Sequence 24, Appl
447	3	12.5	11	7	US-11-045-024-6785	Sequence 6785, Ap	520	3	12.5	12	7	US-11-129-104-36	Sequence 36, Appl
448	3	12.5	11	7	US-11-045-024-6800	Sequence 6800, Ap	521	3	12.5	12	7	US-11-047-383-25	Sequence 25, Appl
449	3	12.5	11	7	US-11-045-024-7222	Sequence 7222, Ap	522	3	12.5	13	6	US-10-986-501-290	Sequence 290, App
450	3	12.5	11	7	US-11-045-024-7287	Sequence 7287, Ap	523	3	12.5	13	6	US-10-511-559-193	Sequence 193, App
451	3	12.5	11	7	US-11-045-024-7494	Sequence 7494, Ap	524	3	12.5	13	6	US-10-511-559-194	Sequence 194, App
452	3	12.5	11	7	US-11-045-024-7509	Sequence 7509, Ap	525	3	12.5	13	6	US-10-511-559-195	Sequence 195, App
453	3	12.5	11	7	US-11-045-024-7840	Sequence 7840, Ap	526	3	12.5	13	6	US-10-511-559-196	Sequence 196, App
454	3	12.5	11	7	US-11-045-024-7937	Sequence 7937, Ap	527	3	12.5	13	6	US-10-511-559-197	Sequence 197, App
455	3	12.5	11	7	US-11-045-024-7938	Sequence 7938, Ap	528	3	12.5	13	6	US-10-511-559-234	Sequence 234, App
456	3	12.5	11	7	US-11-045-024-8180	Sequence 8180, Ap	529	3	12.5	13	6	US-10-511-559-235	Sequence 235, App
457	3	12.5	11	7	US-11-045-024-8236	Sequence 8236, Ap	530	3	12.5	13	6	US-10-511-559-236	Sequence 236, App
458	3	12.5	11	7	US-11-045-024-8264	Sequence 8264, Ap	531	3	12.5	13	6	US-10-511-559-237	Sequence 237, App
459	3	12.5	11	7	US-11-045-024-8304	Sequence 8304, Ap	532	3	12.5	13	6	US-10-511-559-238	Sequence 238, App
460	3	12.5	11	7	US-11-045-024-8333	Sequence 8333, Ap	533	3	12.5	13	6	US-10-511-559-304	Sequence 304, App
461	3	12.5	11	7	US-11-045-024-8387	Sequence 8387, Ap	534	3	12.5	13	6	US-10-511-559-305	Sequence 305, App
462	3	12.5	11	7	US-11-045-024-8574	Sequence 8574, Ap	535	3	12.5	13	6	US-10-511-559-306	Sequence 306, App
463	3	12.5	11	7	US-11-045-024-8878	Sequence 8878, Ap	536	3	12.5	13	6	US-10-511-559-307	Sequence 307, App

537	3	12.5	13	6	US-10-511-559-308	Sequence 308, App	610	3	12.5	14	6	US-10-726-554-9	Sequence 9, Appl
538	3	12.5	13	6	US-10-511-559-309	Sequence 309, App	611	3	12.5	14	6	US-10-467-657-9003	Sequence 9003, Ap
539	3	12.5	13	6	US-10-511-559-310	Sequence 310, App	612	3	12.5	14	7	US-11-012-353-41	Sequence 41, Appl
540	3	12.5	13	6	US-10-511-559-311	Sequence 311, App	613	3	12.5	14	7	US-11-054-515-2360	Sequence 2360, Ap
541	3	12.5	13	6	US-10-511-559-348	Sequence 348, App	614	3	12.5	14	7	US-11-054-515-2375	Sequence 2375, Ap
542	3	12.5	13	6	US-10-511-559-349	Sequence 349, App	615	3	12.5	14	7	US-11-054-515-2393	Sequence 2393, Ap
543	3	12.5	13	6	US-10-511-559-350	Sequence 350, App	616	3	12.5	14	7	US-11-054-515-2410	Sequence 2410, Ap
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842	3	12.5	20	7	US-11-022-562-304	Sequence 304, App	915	2	8.3	3	6	US-10-431-638-11	Sequence 11, Appl
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844	3	12.5	20	7	US-11-187-989-4	Sequence 4, Appli	917	2	8.3	3	6	US-10-506-223-10	Sequence 10, Appl
845	3	12.5	20	7	US-11-058-735-45	Sequence 45, Appl	918	2	8.3	3	6	US-10-506-223-13	Sequence 13, Appl
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887	3	12.5	21	7	US-11-033-039-1423	Sequence 1423, Ap	960	2	8.3	4	6	US-10-485-788A-529	Sequence 529, App
888	3	12.5	21	7	US-11-041-893-205	Sequence 205, App	961	2	8.3	4	6	US-10-956-755A-99	Sequence 99, Appl
889	3	12.5	21	7	US-11-147-111-15	Sequence 15, Appl	962	2	8.3	4	6	US-10-500-878-17	Sequence 17, Appl
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891	3	12.5	22	6	US-10-353-783-76	Sequence 76, Appl	964	2	8.3	4	6	US-10-793-388-7	Sequence 7, Appli
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## ALIGNMENTS

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; Sequence 616, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epiimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 616
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS

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Sequence 58, Appl
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Sequence 702, App
Sequence 706, App
Sequence 710, App
Sequence 716, App
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Sequence 23, Appl
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Sequence 4, Appli
Sequence 11, Appli
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US-11-045-024-616
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; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epiimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
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; PRIOR APPLICATION NUMBER: US 08/159,184
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; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
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US-11-045-024-770
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Best Local Similarity 100.0%; Pred. No. 6.4;
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Db      4 NNNNS 8
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; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
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; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; PRIOR FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
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; SEQ ID NO 8871  
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; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-8871

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; Publication No. US20050276819A1  
; GENERAL INFORMATION:  
; APPLICANT: Covacci, Antonello  
; APPLICANT: Bugnoli, Massimo  
; APPLICANT: Telford, John  
; APPLICANT: Macchia, Giovanni  
; APPLICANT: Rappuoli, Rino  
; TITLE OF INVENTION: Helicobacter Pylori CAI Antigen Polynucleotides  
; FILE REFERENCE: CHIR0337  
; CURRENT APPLICATION NUMBER: US/10/615,668  
; CURRENT FILING DATE: 2003-07-08  
; PRIOR FILING DATE: 08/471,491  
; PRIOR FILING DATE: 1995-06-06  
; PRIOR APPLICATION NUMBER: 08/256,848  
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; PRIOR APPLICATION NUMBER: 09/410,835  
; PRIOR FILING DATE: 1999-10-01  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.2  
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; TYPE: PRT  
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US-10-615-668-23

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RESULT 5  
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; Sequence 96, Application US/11096706  
; Publication No. US20050245476A1  
; GENERAL INFORMATION:  
; APPLICANT: Sangamo Biosciences, Inc.  
; APPLICANT: Collingwood, Trevor  
; TITLE OF INVENTION: Treatment of Neuropathic Pain with Zinc Finger Proteins  
; FILE REFERENCE: 019496-008220US  
; CURRENT APPLICATION NUMBER: US/11/096,706  
; CURRENT FILING DATE: 2005-04-01  
; PRIOR APPLICATION NUMBER: US 60/560,535

; PRIOR FILING DATE: 2004-04-08  
; PRIOR APPLICATION NUMBER: US 60/576,757  
; PRIOR FILING DATE: 2004-06-02  
; NUMBER OF SEQ ID NOS: 227  
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US-11-096-706-96

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Qy 17 NNNN 20  
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RESULT 6  
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; Publication No. US20060002941A1  
; GENERAL INFORMATION:  
; APPLICANT: Mahairas, Gregory G.  
; TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE  
; FILE REFERENCE: 100123.401  
; CURRENT APPLICATION NUMBER: US/11/041,893  
; CURRENT FILING DATE: 2005-01-24  
; PRIOR APPLICATION NUMBER: US 60/616,855  
; PRIOR FILING DATE: 2004-10-06  
; PRIOR APPLICATION NUMBER: US 60/538,713  
; PRIOR FILING DATE: 2004-01-23  
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; ORGANISM: Mycobacterium tuberculosis  
US-11-041-893-31

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Qy 20 SSFY 23  
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Db 7 SSFY 10

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; Publication No. US20050260730A1  
; GENERAL INFORMATION:  
; APPLICANT: FISCHER, PETER MARTIN  
; TITLE OF INVENTION: CDK2/CYCLIN A CRYSTALS AND USES THEREOF  
; FILE REFERENCE: CCI-032  
; CURRENT APPLICATION NUMBER: US/10/914,842A  
; CURRENT FILING DATE: 2004-08-10  
; PRIOR APPLICATION NUMBER: UK 0324465.4  
; PRIOR FILING DATE: 2003-10-20  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 3.2  
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; TYPE: PRT  
; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-10-914-842A-12

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Best Local Similarity 100.0%; Pred. No. 73;  
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; Publication No. US20050276811A1  
; GENERAL INFORMATION:  
; APPLICANT: CARROLL, MICHAEL C.  
; APPLICANT: MOORE JR., FRANCIS B.  
; APPLICANT: HECHTMAN, HERBERT B.  
; TITLE OF INVENTION: NATURAL IGM ANTIBODIES AND INHIBITORS THEREOF  
; FILE REFERENCE: CRA-002.01  
; CURRENT APPLICATION NUMBER: US/11/069,834  
; CURRENT FILING DATE: 2005-03-01  
; PRIOR APPLICATION NUMBER: 60/588,648  
; PRIOR FILING DATE: 2004-07-16  
; PRIOR APPLICATION NUMBER: 60/549,123  
; PRIOR FILING DATE: 2004-03-01  
; NUMBER OF SEQ ID NOS: 65  
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; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (8)  
; OTHER INFORMATION: Variable amino acid  
US-11-069-834-14

Query Match 16.7%; Score 4; DB 7; Length 12;  
Best Local Similarity 100.0%; Pred. No. 79;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 NNNN 19  
|||  
Db 9 NNNN 12

## RESULT 9

US-11-069-834-16  
; Sequence 16, Application US/11069834  
; Publication No. US20050276811A1  
; GENERAL INFORMATION:  
; APPLICANT: CARROLL, MICHAEL C.  
; APPLICANT: MOORE JR., FRANCIS B.  
; APPLICANT: HECHTMAN, HERBERT B.  
; TITLE OF INVENTION: NATURAL IGM ANTIBODIES AND INHIBITORS THEREOF  
; FILE REFERENCE: CRA-002.01  
; CURRENT APPLICATION NUMBER: US/11/069,834

; CURRENT FILING DATE: 2005-03-01  
; PRIOR APPLICATION NUMBER: 60/588,648  
; PRIOR FILING DATE: 2004-07-16  
; PRIOR APPLICATION NUMBER: 60/549,123  
; PRIOR FILING DATE: 2004-03-01  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 16  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-11-069-834-16

Query Match 16.7%; Score 4; DB 7; Length 12;  
Best Local Similarity 100.0%; Pred. No. 79;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 NNNN 19  
|||  
Db 2 NNNN 5

## RESULT 10

US-11-069-834-18  
; Sequence 18, Application US/11069834  
; Publication No. US20050276811A1  
; GENERAL INFORMATION:  
; APPLICANT: CARROLL, MICHAEL C.  
; APPLICANT: MOORE JR., FRANCIS B.  
; APPLICANT: HECHTMAN, HERBERT B.  
; TITLE OF INVENTION: NATURAL IGM ANTIBODIES AND INHIBITORS THEREOF  
; FILE REFERENCE: CRA-002.01  
; CURRENT APPLICATION NUMBER: US/11/069,834  
; CURRENT FILING DATE: 2005-03-01  
; PRIOR APPLICATION NUMBER: 60/588,648  
; PRIOR FILING DATE: 2004-07-16  
; PRIOR APPLICATION NUMBER: 60/549,123  
; PRIOR FILING DATE: 2004-03-01  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 18  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-11-069-834-18

Query Match 16.7%; Score 4; DB 7; Length 12;  
Best Local Similarity 100.0%; Pred. No. 79;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TNNN 18  
|||  
Db 8 TNNN 11

## RESULT 11

US-11-069-834-34  
; Sequence 34, Application US/11069834  
; Publication No. US20050276811A1  
; GENERAL INFORMATION:  
; APPLICANT: CARROLL, MICHAEL C.  
; APPLICANT: MOORE JR., FRANCIS B.  
; APPLICANT: HECHTMAN, HERBERT B.  
; TITLE OF INVENTION: NATURAL IGM ANTIBODIES AND INHIBITORS THEREOF  
; FILE REFERENCE: CRA-002.01  
; CURRENT APPLICATION NUMBER: US/11/069,834  
; CURRENT FILING DATE: 2005-03-01

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; PRIOR APPLICATION NUMBER: 60/588,648
; PRIOR FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: 60/549,123
; PRIOR FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 34
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-11-069-834-34

Query Match      16.7%; Score 4; DB 7; Length 12;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      16 NNNN 19
Db      3 NNNN 6

RESULT 12
US-10-467-657-8838
; Sequence 8838, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 8838
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8838

Query Match      16.7%; Score 4; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      10 IPEQ 13
Db      1 IPEQ 4

RESULT 13
US-11-045-024-13116
; Sequence 13116, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Bateban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
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; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13116
; LENGTH: 15
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-13116

Query Match      16.7%; Score 4; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 RFDS 5
Db      3 RFDS 6

RESULT 14
US-11-033-039-1242
; Sequence 1242, Application US/11033039
; Publication No. US20060002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1242
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: hybrid peptide
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: Ava
US-11-033-039-1242

Query Match      16.7%; Score 4; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 20 SSFY 23  
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Db 8 SSFY 11

RESULT 15  
US-11-033-039-1308  
; Sequence 1308, Application US/11033039  
; Publication No. US2006002947A1  
; GENERAL INFORMATION:  
; APPLICANT: HUMPHREYS, ROBERT  
; APPLICANT: XU, MINZHEN  
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES  
; FILE REFERENCE: REH-2017US01  
; CURRENT APPLICATION NUMBER: US/11/033,039  
; PRIOR FILING DATE: 2005-01-11  
; PRIOR APPLICATION NUMBER: 10/245,871  
; PRIOR FILING DATE: 2002-09-17  
; PRIOR APPLICATION NUMBER: 10/197,000  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: 09/396,813  
; PRIOR FILING DATE: 1999-09-14  
; NUMBER OF SEQ ID NOS: 1452  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1308  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: hybrid peptide  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (5)..(5)  
; OTHER INFORMATION: Ava  
US-11-033-039-1308

Query Match 16.7%; Score 4; DB 7; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 SSFY 23  
|||  
Db 8 SSFY 11

Search completed: January 20, 2006, 17:58:10  
Job time : 11 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2006, 17:51:34 ; Search time 16 Seconds  
(without alignments)  
144.325 Million cell updates/sec

Title: US-10-619-323-1\_COPY\_35\_58

Perfect score: 24

Sequence: 1 LRFDSQTKSIFQETNNNSPYT 24

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4989

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Listing first 1000 summaries

Database :

PIR 80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	20.8	20	I59073	MHC class II histo
2	4	16.7	12	A44874	proboscipedia - fr
3	4	16.7	17	I76673	hypothetical COII/
4	4	16.7	18	A40256	interleukin-7 rece
5	4	16.7	19	PC1323	endopeptidase Clp
6	4	16.7	20	I79432	MHC class II histo
7	4	16.7	20	S67990	neurotoxin-associ
8	4	16.7	22	B40256	interleukin-7 rece
9	3	12.5	4	D41654	hypothetical prote
10	3	12.5	5	PT0644	T-cell receptor be
11	3	12.5	7	B39127	phosphotransferase
12	3	12.5	7	A59489	protein kinase C i
13	3	12.5	8	PH1407	Ig heavy chain v r
14	3	12.5	8	S55622	metallothionein is
15	3	12.5	8	JS0316	leucokinin VI - Ma
16	3	12.5	8	B27867	homeotic protein U
17	3	12.5	8	A59028	MHC class I histoc
18	3	12.5	8	S43972	tumor-associated a
19	3	12.5	8	S43971	tumor-associated a
20	3	12.5	9	A60427	macrophage cytotox
21	3	12.5	9	A61386	macrophage inhibit
22	3	12.5	9	PD0443	3-oxoacid CoA-tran
23	3	12.5	10	PU0037	alpha-peptide/alg
24	3	12.5	10	S70721	heat shock protein
25	3	12.5	10	PH0916	T-cell receptor be
26	3	12.5	10	PH0923	T-cell receptor be
27	3	12.5	10	A43977	FMramide-like pro
28	3	12.5	10	A56633	neomycin suppressin
29	3	12.5	10	B61033	ranatachikin B -

30	3	12.5	10	A32543	cardioexcitatory n
31	3	12.5	11	B60769	Ig H2 chain - Paci
32	3	12.5	11	I60434	68kDa neurofilamen
33	3	12.5	11	PH0904	T-cell receptor be
34	3	12.5	12	PH1675	Ig heavy chain v r
35	3	12.5	12	S26554	T-cell receptor be
36	3	12.5	12	S26559	T-cell receptor be
37	3	12.5	12	A40763	sucrose-6-phosphat
38	3	12.5	12	S68402	NAD(+)-glycohydrol
39	3	12.5	12	PH0771	T-cell receptor be
40	3	12.5	12	PH1467	T-cell receptor be
41	3	12.5	12	PH1462	T-cell receptor be
42	3	12.5	12	PH1469	T-cell receptor be
43	3	12.5	12	PH1457	T-cell receptor be
44	3	12.5	12	PH1468	T-cell receptor be
45	3	12.5	12	S29479	hypothetical prote
46	3	12.5	12	PA0030	protein QM300025 -
47	3	12.5	12	A56878	light yellow cell
48	3	12.5	13	A4818	extracellular lipa
49	3	12.5	13	PH1676	Ig heavy chain v r
50	3	12.5	13	S09395	pancreatic elastas
51	3	12.5	13	S70441	hypothetical prote
52	3	12.5	13	PH0138	T-cell receptor be
53	3	12.5	13	I54984	aeg-46.5 protein -
54	3	12.5	13	S60046	early nodulin 40 -
55	3	12.5	13	C61576	ribosomal protein
56	3	12.5	14	PH1677	Ig heavy chain v r
57	3	12.5	14	PH1705	Ig heavy chain v r
58	3	12.5	14	PT0077	proteochondroitin c
59	3	12.5	14	PH0753	T-cell receptor be
60	3	12.5	14	I54945	gene C protein - E
61	3	12.5	14	S14336	mastoparan B - hor
62	3	12.5	14	B56884	Pax-QNR, long form
63	3	12.5	14	PC7079	unidentified 27.2K
64	3	12.5	14	B83836	hypothetical prote
65	3	12.5	14	A42473	ermk leader peptid
66	3	12.5	15	JF0101	fibrinogen alpha c
67	3	12.5	15	PS0452	32K protein 3306 -
68	3	12.5	15	PA0052	protein QF200015 -
69	3	12.5	15	D28587	T-cell receptor be
70	3	12.5	15	PH0764	T-cell receptor be
71	3	12.5	15	PH0629	integration host f
72	3	12.5	15	PA0008	lectin B2 - Paopho
73	3	12.5	15	PA0062	fumarate hydratase
74	3	12.5	15	PA0054	protein QF200017 -
75	3	12.5	15	A32921	beaded-chain filam
76	3	12.5	15	A61522	7.5K surfactant-as
77	3	12.5	16	F44908	chitinase (EC 3.2.
78	3	12.5	16	B35491	retinol-binding pr
79	3	12.5	16	PH0749	T-cell receptor be
80	3	12.5	16	S33589	beta-crystallin A4
81	3	12.5	16	PH1476	T-cell receptor be
82	3	12.5	16	PH1474	T-cell receptor be
83	3	12.5	16	T09741	photosystem I chai
84	3	12.5	16	S22040	cob protein - comm
85	3	12.5	16	S54271	GATA-2 protein - A
86	3	12.5	16	S65430	pyrogallol hydroxy
87	3	12.5	17	S15778	insulin chain B -
88	3	12.5	17	S32587	L-ascorbate peroxi
89	3	12.5	17	C37396	pollen allergen Fe
90	3	12.5	17	PH1822	T cell receptor al
91	3	12.5	17	PH0769	T-cell receptor be
92	3	12.5	17	I78870	gene R81 protein -
93	3	12.5	17	A34704	protein-tyrosine k
94	3	12.5	17	A29834	trp leader peptide
95	3	12.5	18	C40433	Nada protein - Cya
96	3	12.5	18	A56871	retinol-binding pr
97	3	12.5	18	S09731	photosystem I prot
98	3	12.5	18	S10452	hypothetical prote
99	3	12.5	18	S33125	cysteine-rich secr
100	3	12.5	18	A32917	protein phosphatas
101	3	12.5	18	S71592	serine proteinase
102	3	12.5	18	PL0025	T-cell surface gly

103	3	12.5	18	2	S48862	murine cyclin H -	176	3	12.5	23	2	PH1695	Ig heavy chain V r
104	3	12.5	18	2	T13132	protein gp45.1 - p	177	3	12.5	23	2	PH1726	Ig heavy chain V r
105	3	12.5	18	2	S48863	cyclin C - mouse (	178	3	12.5	23	2	PH1708	Ig heavy chain V r
106	3	12.5	19	1	LFSAP9	ermC leader peptid	179	3	12.5	23	2	PH1724	Ig heavy chain V r
107	3	12.5	19	2	A92058	pepsin-like protei	180	3	12.5	23	2	PH1693	Ig heavy chain V r
108	3	12.5	19	2	C32735	thyroglobulin - pi	181	3	12.5	23	2	PH1728	Ig heavy chain V r
109	3	12.5	19	2	B32735	thyroglobulin - sh	182	3	12.5	23	2	PH1723	Ig heavy chain V r
110	3	12.5	19	2	B38837	T-cell receptor be	183	3	12.5	23	2	PH1681	Ig heavy chain V r
111	3	12.5	19	2	S01203	patatin (clone lfo	184	3	12.5	23	2	PH1727	Ig heavy chain V r
112	3	12.5	19	2	B26930	ermG leader peptid	185	3	12.5	23	2	PH1722	Ig heavy chain V r
113	3	12.5	19	2	T50329	wd-repeat protein	186	3	12.5	23	2	PH1682	Ig heavy chain V r
114	3	12.5	19	2	PC1315	large granule L2 c	187	3	12.5	23	2	PH1725	Ig heavy chain V r
115	3	12.5	19	2	S57515	T cell receptor be	188	3	12.5	23	2	PH1729	Ig heavy chain V r
116	3	12.5	19	2	S57516	T cell receptor be	189	3	12.5	23	2	PH1707	Ig heavy chain V r
117	3	12.5	19	2	A60459	aminopeptidase, 30	190	3	12.5	23	2	PH1691	Ig heavy chain V r
118	3	12.5	19	2	S68393	H+-transporting tw	191	3	12.5	23	2	I56028	MHC class II prote
119	3	12.5	19	2	PQ0548	capsid protein vp2	192	3	12.5	23	2	I77910	beta 3-adrenergic
120	3	12.5	19	2	S63476	dihydrolipoamide d	193	3	12.5	23	2	I54773	neural cell adhesi
121	3	12.5	19	2	I33327	pre-T/NK cell-asso	194	3	12.5	23	2	S00921	patatin (clone lfo
122	3	12.5	20	2	FN0115	insulin-like growt	195	3	12.5	23	2	S74178	4-hydroxyphenylpyr
123	3	12.5	20	2	A54083	p190/210, fatty ac	196	3	12.5	23	2	S13298	benzaldehyde dehyd
124	3	12.5	20	2	PQ0751	self-incompatibili	197	3	12.5	23	2	A56357	tyrosine kinase su
125	3	12.5	20	2	A33160	H+-transporting tw	198	3	12.5	23	2	D64707	hypothetical prote
126	3	12.5	20	2	E49164	chromogranin-B - r	199	3	12.5	23	2	B37843	vrg 18 protein - B
127	3	12.5	20	2	E39419	collagen alpha 5(I	200	3	12.5	23	2	G59812	hypothetical prote
128	3	12.5	20	2	H49034	nuclear antigen BB	201	3	12.5	24	2	S77982	cytochrome-c oxida
129	3	12.5	20	2	D37396	pollen allergen Fe	202	3	12.5	24	2	PH1698	Ig heavy chain V r
130	3	12.5	20	2	A38600	trypsin inhibitor	203	3	12.5	24	2	PH1713	Ig heavy chain V r
131	3	12.5	20	2	PH1326	Ig heavy chain DJ	204	3	12.5	24	2	PH1684	Ig heavy chain V r
132	3	12.5	20	2	A41437	alpha-1-antiprotei	205	3	12.5	24	2	PH1685	Ig heavy chain V r
133	3	12.5	20	2	C44920	2-halobenzoate 1,2	206	3	12.5	24	2	PH1711	Ig heavy chain V r
134	3	12.5	20	2	FL0039	outer membrane pro	207	3	12.5	24	2	PH1710	Ig heavy chain V r
135	3	12.5	20	2	T48881	leader peptide lim	208	3	12.5	24	2	PH1732	Ig heavy chain V r
136	3	12.5	20	2	S29636	jacalin beta-I cha	209	3	12.5	24	2	PH1712	Ig heavy chain V r
137	3	12.5	20	2	S50743	proteinase inhibit	210	3	12.5	24	2	PH1697	Ig heavy chain V r
138	3	12.5	20	2	S65605	dimeric protein (B	211	3	12.5	24	2	PH1683	Ig heavy chain V r
139	3	12.5	20	2	S77992	cytochrome-c oxida	212	3	12.5	24	2	E39690	neural cell adhesi
140	3	12.5	20	2	JC5589	ribonuclease RCL2	213	3	12.5	24	2	S70329	omega 1-40 secalin
141	3	12.5	20	2	S71593	serine proteinase	214	3	12.5	24	2	S65714	lectin GNL alpha c
142	3	12.5	20	2	D56046	urinary tract ston	215	3	12.5	24	2	D53288	major pollen aller
143	3	12.5	20	2	A61506	alpha-1-antitrypsi	216	3	12.5	24	2	PC2001	major allergen - B
144	3	12.5	20	2	A60897	class I histocompa	217	3	12.5	24	2	S47281	hypothetical prote
145	3	12.5	20	2	I58192	glial fibrillary a	218	3	12.5	24	2	T46628	hypothetical prote
146	3	12.5	20	2	B46174	RNA-binding protei	219	3	12.5	24	2	C47689	flagellar core pro
147	3	12.5	21	2	I40066	shikimate 5-dehydr	220	3	12.5	24	2	G4615	hypothetical prote
148	3	12.5	21	2	PC2214	fibrinogenolytic p	221	3	12.5	24	2	D81853	probable transposa
149	3	12.5	21	2	I49414	gene CTLA-1 protei	222	3	12.5	24	2	PN0653	alkaline trypsin-1
150	3	12.5	21	2	D38837	T-cell receptor be	223	3	12.5	24	2	S10618	superoxide dismuta
151	3	12.5	21	2	A38837	T-cell receptor be	224	3	12.5	24	2	I73619	endothelial growth
152	3	12.5	21	2	C38837	T-cell receptor be	225	3	12.5	24	2	C85846	unknown protein en
153	3	12.5	21	2	PH1731	Ig heavy chain V r	226	3	12.5	24	2	G85602	hypothetical prote
154	3	12.5	21	2	PH1730	Ig heavy chain V r	227	3	12.5	25	1	ZJBPQ4	gene J protein - p
155	3	12.5	21	2	PH1688	Ig heavy chain V r	228	3	12.5	25	2	I51565	protein-tyrosine k
156	3	12.5	21	2	S49040	Ig heavy chain V r	229	3	12.5	25	2	S21204	H+-transporting tw
157	3	12.5	21	2	S39455	dps-protein 19K -	230	3	12.5	25	2	D41575	bovinin-like pept
158	3	12.5	21	2	B33676	34K ribonucleoprot	231	3	12.5	25	2	PH1734	Ig heavy chain V r
159	3	12.5	21	2	B33600	glutamate-ammonia	232	3	12.5	25	2	PH1716	Ig heavy chain V r
160	3	12.5	22	2	PH1680	Ig heavy chain V r	233	3	12.5	25	2	PH1733	Ig heavy chain V r
161	3	12.5	22	2	PH1706	Ig heavy chain V r	234	3	12.5	25	2	F49533	T-cell receptor be
162	3	12.5	22	2	PH1679	Ig heavy chain V r	235	3	12.5	25	2	PH1700	Ig heavy chain V r
163	3	12.5	22	2	PH1678	Ig heavy chain V r	236	3	12.5	25	2	PH1717	Ig heavy chain V r
164	3	12.5	22	2	PH1714	Ig heavy chain V r	237	3	12.5	25	2	PH1701	Ig heavy chain V r
165	3	12.5	22	2	PH1721	Ig heavy chain V r	238	3	12.5	25	2	PH1686	Ig heavy chain V r
166	3	12.5	22	2	B41833	40K iron-repressed	239	3	12.5	25	2	PH1715	Ig heavy chain V r
167	3	12.5	22	2	A41833	40K iron-repressed	240	3	12.5	25	2	A40534	ryanodine receptor
168	3	12.5	22	2	S17303	tegumental Glycopr	241	3	12.5	25	2	A60412	xenopsin-related p
169	3	12.5	22	2	B60701	31K antigen - Camp	242	3	12.5	25	2	S28993	antifungal protein
170	3	12.5	22	2	S65370	tRNA-guanine trans	243	3	12.5	25	2	I38002	calcium channel be
171	3	12.5	22	2	H49410	t-complex polypept	244	3	12.5	25	2	D47689	flagellar core pro
172	3	12.5	22	2	I40064	shikimate 5-dehydr	245	3	12.5	25	2	B47689	flagellar core pro
173	3	12.5	22	2	G83924	hypothetical prote	246	3	12.5	25	2	S78343	hypothetical prote
174	3	12.5	23	2	PH1689	Ig heavy chain V r	247	3	12.5	25	2	S30361	1,2-alpha-D-mannos
175	3	12.5	23	2	PH1694	Ig heavy chain V r	248	3	12.5	25	2	A61457	alpha-glucosidase

249	3	12.5	25	2	2	E41606	homeotic protein M	322	2	8.3	6	2	PT0510	T-cell receptor be
250	2	8.3	3	3	3	PT0622	T-cell receptor be	323	2	8.3	6	2	PT0531	T-cell receptor be
251	2	8.3	3	3	3	S68328	blood cell protein	324	2	8.3	6	2	PT0532	T-cell receptor be
252	2	8.3	3	3	3	A33802	thyrotropin-releas	325	2	8.3	6	2	PT0519	T-cell receptor be
253	2	8.3	4	1	1	ECXAA	antho-RFamide neur	326	2	8.3	6	2	PT0599	T-cell receptor be
254	2	8.3	4	2	2	A02147	phagocytosis9-stimu	327	2	8.3	6	2	PT0637	T-cell receptor be
255	2	8.3	4	2	2	A25844	antho-RF amide neu	328	2	8.3	6	2	PT0621	T-cell receptor be
256	2	8.3	4	2	2	S47552	branched-chain-ami	329	2	8.3	6	2	PT0616	T-cell receptor be
257	2	8.3	4	2	2	ubiquitin - rat	D-mannosate hydrol	330	2	8.3	6	2	PT0618	T-cell receptor be
258	2	8.3	4	2	2	I57745	neuropeptide Antho	331	2	8.3	6	2	PT0619	T-cell receptor be
259	2	8.3	4	2	2	A35779	FMRFamide - polych	332	2	8.3	6	2	PT0641	T-cell receptor be
260	2	8.3	4	2	2	A60418	T-cell receptor be	333	2	8.3	6	2	PT0657	T-cell receptor be
261	2	8.3	4	2	2	PT0696	T-cell receptor be	334	2	8.3	6	2	PT0668	T-cell receptor be
262	2	8.3	4	2	2	PT0645	T-cell receptor be	335	2	8.3	6	2	PT0650	T-cell receptor be
263	2	8.3	4	2	2	PT0712	T-cell receptor be	336	2	8.3	6	2	PT0648	T-cell receptor be
264	2	8.3	4	2	2	PT0698	T-cell receptor be	337	2	8.3	6	2	PT0533	T-cell receptor be
265	2	8.3	4	2	2	PT0551	T-cell receptor be	338	2	8.3	6	2	PT0720	T-cell receptor be
266	2	8.3	4	2	2	PT0897	T-cell receptor be	339	2	8.3	6	2	PT0550	T-cell receptor be
267	2	8.3	4	2	2	ECNK	cardioexcitatory n	340	2	8.3	6	2	PT0718	T-cell receptor be
268	2	8.3	5	2	2	B31836	20K protein - Rick	341	2	8.3	6	2	PT0589	T-cell receptor be
269	2	8.3	5	2	2	I39964	ribosomal protein	342	2	8.3	6	2	PT0693	T-cell receptor be
270	2	8.3	5	2	2	I39966	ribosomal protein	343	2	8.3	6	2	PT0593	T-cell receptor be
271	2	8.3	5	2	2	I39965	ribosomal protein	344	2	8.3	6	2	PT0715	T-cell receptor be
272	2	8.3	5	2	2	D60274	major protein anti	345	2	8.3	6	2	PT0730	T-cell receptor be
273	2	8.3	5	2	2	S70615	endo-1,4-beta-xyla	346	2	8.3	6	2	A61068	locustakinin - mig
274	2	8.3	5	2	2	A60803	neuropeptide - sea	347	2	8.3	6	2	A43129	neuropeptide GNFRP
275	2	8.3	5	2	2	A37114	hypoxanthine phosph	348	2	8.3	6	2	A60224	Met-enkephalin-Arg
276	2	8.3	5	2	2	PT0308	Ig heavy chain CRD	349	2	8.3	7	2	PHI408	Ig heavy chain V r
277	2	8.3	5	2	2	B44823	synaptosomal-assoc	350	2	8.3	7	2	A44428	platelet aggregati
278	2	8.3	5	2	2	PT0596	T-cell receptor be	351	2	8.3	7	2	S42407	gramicidin S synth
279	2	8.3	5	2	2	PT0610	T-cell receptor be	352	2	8.3	7	2	PT0087	ribulose-bisphosph
280	2	8.3	5	2	2	PT0597	T-cell receptor be	353	2	8.3	7	2	A34818	vicilin 72K chain
281	2	8.3	5	2	2	PT0729	T-cell receptor be	354	2	8.3	7	2	S70335	endosperm protein,
282	2	8.3	5	2	2	PT0624	T-cell receptor be	355	2	8.3	7	2	PC1316	large granule L3 c
283	2	8.3	5	2	2	PT0825	T-cell receptor be	356	2	8.3	7	2	S09027	carboxylesterase (
284	2	8.3	5	2	2	PT0672	T-cell receptor be	357	2	8.3	7	2	S68004	hucolin, 75K chain
285	2	8.3	5	2	2	PT0660	T-cell receptor be	358	2	8.3	7	2	PT0283	Ig heavy chain CRD
286	2	8.3	5	2	2	PT0656	T-cell receptor be	359	2	8.3	7	2	PH1602	Ig H chain V-D-J r
287	2	8.3	5	2	2	PT0659	T-cell receptor be	360	2	8.3	7	2	PH3932	Ig mu chain D regi
288	2	8.3	5	2	2	PT0535	T-cell receptor be	361	2	8.3	7	2	PT0611	T-cell receptor be
289	2	8.3	5	2	2	PT0699	T-cell receptor be	362	2	8.3	7	2	PT0524	T-cell receptor be
290	2	8.3	5	2	2	PT0561	T-cell receptor be	363	2	8.3	7	2	PT0520	T-cell receptor be
291	2	8.3	5	2	2	PT0684	T-cell receptor be	364	2	8.3	7	2	PT0521	T-cell receptor be
292	2	8.3	5	2	2	PT0577	T-cell receptor be	365	2	8.3	7	2	PT0523	T-cell receptor be
293	2	8.3	5	2	2	PT0580	T-cell receptor be	366	2	8.3	7	2	PT0623	T-cell receptor be
294	2	8.3	5	2	2	PT0700	T-cell receptor be	367	2	8.3	7	2	PT0628	T-cell receptor be
295	2	8.3	5	2	2	PT0713	T-cell receptor be	368	2	8.3	7	2	PT0642	T-cell receptor be
296	2	8.3	5	2	2	H44817	34.5K structural p	369	2	8.3	7	2	PT0620	T-cell receptor be
297	2	8.3	5	2	2	F44817	34.5K structural p	370	2	8.3	7	2	PT0667	T-cell receptor be
298	2	8.3	5	2	2	B44817	34.5K structural p	371	2	8.3	7	2	PT0663	T-cell receptor be
299	2	8.3	5	2	2	D44817	35K structural pro	372	2	8.3	7	2	PT0683	T-cell receptor be
300	2	8.3	5	2	2	I40698	biotin B - Citroba	373	2	8.3	7	2	PT0719	T-cell receptor be
301	2	8.3	5	2	2	PT0600	T-cell receptor be	374	2	8.3	7	2	PT0586	T-cell receptor be
302	2	8.3	5	2	2	PT0686	T-cell receptor be	375	2	8.3	7	2	PT0576	T-cell receptor be
303	2	8.3	5	2	2	PT0601	T-cell receptor be	376	2	8.3	7	2	PT0579	T-cell receptor be
304	2	8.3	5	2	2	PT0565	T-cell receptor be	377	2	8.3	7	2	PT0581	T-cell receptor be
305	2	8.3	5	2	2	PT0714	T-cell receptor be	378	2	8.3	7	2	PT0702	T-cell receptor be
306	2	8.3	5	2	2	PT0701	T-cell receptor be	379	2	8.3	7	2	PT0008	glucuronosyltransf
307	2	8.3	5	2	2	PT0717	T-cell receptor be	380	2	8.3	7	2	PT0029	pev-kinin 1 - pena
308	2	8.3	5	2	2	A26830	mitosis inhibiting	381	2	8.3	7	2	S09066	globulin IV alpha
309	2	8.3	5	3	3	PT0870	phytosulfokine alp	382	2	8.3	7	2	B35890	RNA-directed DNA p
310	2	8.3	6	2	2	A61419	sarcosine dehydrog	383	2	8.3	7	2	A25269	sex pheromone cM3
311	2	8.3	6	2	2	T11779	phosphoglycerate t	384	2	8.3	7	2	S17976	glucose isomerase
312	2	8.3	6	2	2	S14159	paraspinal crystal	385	2	8.3	7	2	PC2132	FMRFamide-related
313	2	8.3	6	2	2	JU0355	lipopeptide WS1279	386	2	8.3	7	2	A28340	myomodulin - Calif
314	2	8.3	6	2	2	C22565	R-phycocerythrin be	387	2	8.3	7	2	B44787	calliFMRFamide 11
315	2	8.3	6	2	2	S29637	jacalin beta-II ch	388	2	8.3	7	2	PT0529	T-cell receptor be
316	2	8.3	6	2	2	A31263	dihydrofolate redu	389	2	8.3	7	2	ECWUCR	catch-relaxing pep
317	2	8.3	6	2	2	B31263	dihydrofolate redu	390	2	8.3	7	4	I56695	hypothetical L2 pr
318	2	8.3	6	2	2	JH0784	neuropeptide RE-6	391	2	8.3	8	2	A32523	peptidyl-di-peptida
319	2	8.3	6	2	2	A60494	antineoplastic gly	392	2	8.3	8	2	PT0184	capsid protein VP-
320	2	8.3	6	2	2	A11490	pyruvate kinase (E	393	2	8.3	8	2	S70727	ipgf protein - Sh1
321	2	8.3	6	2	2	B33932	Ig mu chain D regi	394	2	8.3	8	2	PA0035	protein QA300039 -

395	2	8.3	8	2	S78036	ribosomal protein	468	2	8.3	9	2	D44787
396	2	8.3	8	2	B33099	158K exoantigen -	469	2	8.3	9	2	B41978
397	2	8.3	8	2	A42057	fibroblast growth	470	2	8.3	9	2	C41978
398	2	8.3	8	2	PN0043	phosphatidylethano	471	2	8.3	9	2	D41978
399	2	8.3	8	2	PT0595	T-cell receptor be	472	2	8.3	9	2	E41978
400	2	8.3	8	2	PT0627	T-cell receptor be	473	2	8.3	9	2	F41978
401	2	8.3	8	2	PT0530	T-cell receptor be	474	2	8.3	9	2	G41978
402	2	8.3	8	2	PT0522	T-cell receptor be	475	2	8.3	9	2	JN0027
403	2	8.3	8	2	PT0509	T-cell receptor be	476	2	8.3	9	2	B20569
404	2	8.3	8	2	PT0639	T-cell receptor be	477	2	8.3	9	2	A45199
405	2	8.3	8	2	PT0613	T-cell receptor be	478	2	8.3	9	2	S77984
406	2	8.3	8	2	PT0547	T-cell receptor be	479	2	8.3	9	2	JQ0914
407	2	8.3	8	2	PT0716	T-cell receptor be	480	2	8.3	9	2	I46016
408	2	8.3	8	2	A38887	T-cell receptor ga	481	2	8.3	9	2	A28924
409	2	8.3	8	2	PH0934	T-cell receptor be	482	2	8.3	9	2	PC7076
410	2	8.3	8	2	PC1002	leucine-tRNA ligas	483	2	8.3	9	2	PC7078
411	2	8.3	8	2	S53008	citrate synthase -	484	2	8.3	9	2	G85802
412	2	8.3	8	2	S37141	tpsa protein - Erw	485	2	8.3	9	2	S30494
413	2	8.3	8	2	S21273	cellulase (EC 3.2.	486	2	8.3	9	2	B60246
414	2	8.3	8	2	A37521	R-phycocerythrin ga	487	2	8.3	9	2	JN0026
415	2	8.3	8	2	S11078	glucose-6-phosphat	488	2	8.3	9	2	B24362
416	2	8.3	8	2	C61512	variant surface gl	489	2	8.3	9	4	S15595
417	2	8.3	8	2	D61512	variant surface gl	490	2	8.3	9	4	I73804
418	2	8.3	8	2	JS0315	leucokinin V - Mad	491	2	8.3	10	1	RHPGS
419	2	8.3	8	2	JS0317	leucokinin VII - M	492	2	8.3	10	1	RHSHG
420	2	8.3	8	2	JS0318	leucokinin VIII -	493	2	8.3	10	1	ECLQ1M
421	2	8.3	8	2	A23967	leucopyrokinin - M	494	2	8.3	10	1	ECLQ3M
422	2	8.3	8	2	H41978	calliFMRPamide 8 -	495	2	8.3	10	1	GMROL2
423	2	8.3	8	2	D47393	neuropeptide calla	496	2	8.3	10	2	S28055
424	2	8.3	8	2	S71919	alcohol dehydrogen	497	2	8.3	10	2	S63478
425	2	8.3	8	2	A14683	aspartate transami	498	2	8.3	10	2	S24190
426	2	8.3	8	2	A61467	penalbumin - Adeli	499	2	8.3	10	2	JC1367
427	2	8.3	8	2	I48934	apolipoprotein A-I	500	2	8.3	10	2	A60410
428	2	8.3	8	2	I57018	gene Cfr protein	501	2	8.3	10	2	A31571
429	2	8.3	8	2	S20162	leghemoglobin III	502	2	8.3	10	2	JN0024
430	2	8.3	8	2	B24749	neuropeptide B - p	503	2	8.3	10	2	A61337
431	2	8.3	9	1	YFPG	thymic factor - pi	504	2	8.3	10	2	A47593
432	2	8.3	9	2	S13889	phosphoenolpyruvat	505	2	8.3	10	2	S66458
433	2	8.3	9	2	A60957	thymocyte growth p	506	2	8.3	10	2	S74176
434	2	8.3	9	2	A24244	adipokinetic hormo	507	2	8.3	10	2	C39191
435	2	8.3	9	2	S07205	litorin 2-Glu - Au	508	2	8.3	10	2	S42282
436	2	8.3	9	2	A61357	phyllocaerulein -	509	2	8.3	10	2	C39745
437	2	8.3	9	2	A60108	exotoxin A - Strep	510	2	8.3	10	2	S62208
438	2	8.3	9	2	A44873	caldesmon - rabbit	511	2	8.3	10	2	PA0050
439	2	8.3	9	2	E28854	fibrinopeptide B -	512	2	8.3	10	2	C38925
440	2	8.3	9	2	F28854	fibrinopeptide B -	513	2	8.3	10	2	B49033
441	2	8.3	9	2	D28854	fibrinopeptide B -	514	2	8.3	10	2	B24736
442	2	8.3	9	2	D58503	translation elonga	515	2	8.3	10	2	PT0230
443	2	8.3	9	2	C36730	hutu protein - Kle	516	2	8.3	10	2	PT0243
444	2	8.3	9	2	S70334	endosperm protein -	517	2	8.3	10	2	PT0251
445	2	8.3	9	2	B33098	231K exoantigen -	518	2	8.3	10	2	PT0291
446	2	8.3	9	2	PT0231	Ig heavy chain CDR	519	2	8.3	10	2	PT0309
447	2	8.3	9	2	PT0247	Ig heavy chain CDR	520	2	8.3	10	2	PT0322
448	2	8.3	9	2	PT0270	Ig heavy chain CDR	521	2	8.3	10	2	S23370
449	2	8.3	9	2	PT0288	Ig heavy chain CDR	522	2	8.3	10	2	S23371
450	2	8.3	9	2	PT0315	Ig heavy chain CDR	523	2	8.3	10	2	B49033
451	2	8.3	9	2	S65865	collagen alpha 2(V	524	2	8.3	10	2	B24736
452	2	8.3	9	2	S65913	pyrimidine synthes	525	2	8.3	10	2	S10785
453	2	8.3	9	2	PT0670	T-cell receptor be	526	2	8.3	10	2	A37268
454	2	8.3	9	2	PT0562	T-cell receptor be	527	2	8.3	10	2	PH0807
455	2	8.3	9	2	G41946	T-cell receptor ga	528	2	8.3	10	2	PT0215
456	2	8.3	9	2	PH0942	T-cell receptor be	529	2	8.3	10	2	C41946
457	2	8.3	9	2	PH0935	T-cell receptor be	530	2	8.3	10	2	B38887
458	2	8.3	9	2	PH0902	T-cell receptor be	531	2	8.3	10	2	S65385
459	2	8.3	9	2	PH0917	T-cell receptor be	532	2	8.3	10	2	PX0060
460	2	8.3	9	2	PH0918	T-cell receptor be	533	2	8.3	10	2	PH0900
461	2	8.3	9	2	PH0921	T-cell receptor be	534	2	8.3	10	2	PH0927
462	2	8.3	9	2	JP0073	ribosomal protein	535	2	8.3	10	2	PH0944
463	2	8.3	9	2	A39841	sucrose 3-glucosyl	536	2	8.3	10	2	PH0933
464	2	8.3	9	2	D57444	neuropeptide grb-A	537	2	8.3	10	2	PH0894
465	2	8.3	9	2	A29477	diuretic neuropept	538	2	8.3	10	2	PH0946
466	2	8.3	9	2	A41978	calliFMRPamide 1 -	539	2	8.3	10	2	PH0925
467	2	8.3	9	2	A44787	calliFMRPamide 10	540	2	8.3	10	2	PH0926





687	2	8.3	12	2	S17869	glutathione transf	760	2	8.3	12	2	PH1463	T-cell receptor be
688	2	8.3	12	2	A23169	phospholipase A2 (	761	2	8.3	12	2	PH1470	T-cell receptor be
689	2	8.3	12	2	I64829	gene HEXA protein	762	2	8.3	12	2	PH1481	T-cell receptor be
690	2	8.3	12	2	A28856	fructose-bisphosph	763	2	8.3	12	2	PH1464	T-cell receptor be
691	2	8.3	12	2	S25485	transcription fact	764	2	8.3	12	2	PH1466	T-cell receptor be
692	2	8.3	12	2	S26552	T-cell receptor be	765	2	8.3	12	2	PH1461	T-cell receptor be
693	2	8.3	12	2	S26548	T-cell receptor be	766	2	8.3	12	2	PH1459	T-cell receptor be
694	2	8.3	12	2	S26549	T-cell receptor be	767	2	8.3	12	2	PH1459	T-cell receptor be
695	2	8.3	12	2	S26544	T-cell receptor be	768	2	8.3	12	2	B58502	43.2K bile stone p
696	2	8.3	12	2	S26556	ig heavy chain - m	769	2	8.3	12	2	S43013	outer membrane por
697	2	8.3	12	2	S26553	T-cell receptor be	770	2	8.3	12	2	T44420	hypothetical prote
698	2	8.3	12	2	S26557	T-cell receptor be	771	2	8.3	12	2	T46794	hypothetical prote
699	2	8.3	12	2	S26556	T-cell receptor be	772	2	8.3	12	2	PA0047	hypothetical prote
700	2	8.3	12	2	S26547	T-cell receptor be	773	2	8.3	12	2	B61497	protein QAI00045 -
701	2	8.3	12	2	S26558	T-cell receptor be	774	2	8.3	12	2	JU0356	seed protein ws-17
702	2	8.3	12	2	S26555	T-cell receptor be	775	2	8.3	12	2	S28215	cycloleonorinin -
703	2	8.3	12	2	S26546	T-cell receptor be	776	2	8.3	12	2	P00730	glucan endo-1,3-be
704	2	8.3	12	2	S26541	T-cell receptor be	777	2	8.3	12	2	PN0170	unidentified 5.4/3
705	2	8.3	12	2	A54315	entactin/nidogen -	778	2	8.3	12	2	PN0170	alcohol dehydrogen
706	2	8.3	12	2	S36902	Em protein - wheat	779	2	8.3	12	2	PA0098	ribosomal protein
707	2	8.3	12	2	S01222	translation elonga	780	2	8.3	12	2	T46656	hypothetical prote
708	2	8.3	12	2	S15815	translation elonga	781	2	8.3	12	2	B44787	callimRFamide 1 -
709	2	8.3	12	2	B44818	extracellular lipa	782	2	8.3	12	2	A49261	coagulation factor
710	2	8.3	12	2	S56122	type I DNA methylt	783	2	8.3	12	2	A61503	sterol carrier pro
711	2	8.3	12	2	C64030	hypothetical prote	784	2	8.3	12	2	A49637	MHC class II histo
712	2	8.3	12	2	S49547	hypothetical prote	785	2	8.3	12	2	I77529	estrogen receptor
713	2	8.3	12	2	A30083	protein QA600022 -	786	2	8.3	12	2	S43170	genes light chai
714	2	8.3	12	2	A38925	seed storage prote	787	2	8.3	12	2	I46922	gene Bota protein
715	2	8.3	12	2	S18722	matK protein - bee	788	2	8.3	12	2	P84132	hypothetical prote
716	2	8.3	12	2	A33099	163K exoantigen -	789	2	8.3	12	2	S07436	tachykinin - Afric
717	2	8.3	12	2	A03985	gamma-crystallin -	790	2	8.3	12	2	S07206	kassinin - Senegal
718	2	8.3	12	2	S10626	lipovitellin - Afr	791	2	8.3	12	2	S65409	histone H2B - huma
719	2	8.3	12	2	B47171	chondroitin sulfat	792	2	8.3	12	4	PC2121	amino-transferase c
720	2	8.3	12	2	PT0228	ig heavy chain CDR	793	2	8.3	13	1	NTKNAS	alpha-conotoxin SI
721	2	8.3	12	2	PT0257	ig heavy chain CDR	794	2	8.3	13	2	P00491	self-incompatibili
722	2	8.3	12	2	PT0274	ig heavy chain CDR	795	2	8.3	13	2	A53608	neurotensin - guin
723	2	8.3	12	2	PH1324	ig heavy chain CDR	796	2	8.3	13	2	A35245	histone H1a - mous
724	2	8.3	12	2	PH1308	ig heavy chain bu	797	2	8.3	13	2	B35245	histone H1.c - mou
725	2	8.3	12	2	S43957	ig mu chain V regi	798	2	8.3	13	2	S78519	ribosomal protein
726	2	8.3	12	2	S57570	T cell receptor V-	799	2	8.3	13	2	S48210	collagen alpha 1(V
727	2	8.3	12	2	S47360	T-cell antigen rec	800	2	8.3	13	2	S39413	tubulin beta chain
728	2	8.3	12	2	S47363	T-cell antigen rec	801	2	8.3	13	2	A33208	calreticulin, hepa
729	2	8.3	12	2	S47391	T-cell antigen rec	802	2	8.3	13	2	PU0038	alpha-peptide/algi
730	2	8.3	12	2	S47393	T-cell antigen rec	803	2	8.3	13	2	PC2371	probable endopepti
731	2	8.3	12	2	S47394	T-cell antigen rec	804	2	8.3	13	2	S36887	ribosomal protein
732	2	8.3	12	2	S47395	T-cell antigen rec	805	2	8.3	13	2	S36736	lipid transfer pro
733	2	8.3	12	2	PH1187	T-cell receptor al	806	2	8.3	13	2	PA0023	protein QA300052 -
734	2	8.3	12	2	S51737	T-cell receptor be	807	2	8.3	13	2	H44957	protein P18 - comm
735	2	8.3	12	2	B49033	T-cell receptor de	808	2	8.3	13	2	E60396	antigen JH8/2 - ma
736	2	8.3	12	2	S74144	aggreccan - bovine	809	2	8.3	13	2	PC1149	equinatoxin IA - s
737	2	8.3	12	2	PN0663	dyatrophin-associ	810	2	8.3	13	2	PS0443	potassium channel
738	2	8.3	12	2	A20907	ig kappa chain J1	811	2	8.3	13	2	S29488	GRP-binding protei
739	2	8.3	12	2	C20907	ig kappa-1 chain J	812	2	8.3	13	2	A33660	osteoclast functio
740	2	8.3	12	2	F20907	ig kappa-2 chain J	813	2	8.3	13	2	A54326	glandular kallikre
741	2	8.3	12	2	B60228	PC mu (IgM) recept	814	2	8.3	13	2	S23356	hypothetical prote
742	2	8.3	12	2	PH1606	ig H chain V-D-J r	815	2	8.3	13	2	PT0305	ig heavy chain CDR
743	2	8.3	12	2	PH1581	ig H chain V-D-J r	816	2	8.3	13	2	PH1309	ig heavy chain CDR
744	2	8.3	12	2	S68271	major urinary prot	817	2	8.3	13	2	S23640	ig kappa chain J s
745	2	8.3	12	2	PH0802	T-cell receptor al	818	2	8.3	13	2	E61458	ig kappa chain V-I
746	2	8.3	12	2	PH0790	T-cell receptor al	819	2	8.3	13	2	S57567	T cell receptor V-
747	2	8.3	12	2	PH0746	T-cell receptor be	820	2	8.3	13	2	S47356	T-cell antigen rec
748	2	8.3	12	2	PT0216	T-cell receptor be	821	2	8.3	13	2	S47357	T-cell antigen rec
749	2	8.3	12	2	H41946	T-cell receptor ga	822	2	8.3	13	2	S47358	T-cell antigen rec
750	2	8.3	12	2	A42324	cytochrome P450c27	823	2	8.3	13	2	S47359	T-cell antigen rec
751	2	8.3	12	2	PH0931	T-cell receptor be	824	2	8.3	13	2	S47361	T-cell antigen rec
752	2	8.3	12	2	PH0936	T-cell receptor be	825	2	8.3	13	2	S47362	T-cell antigen rec
753	2	8.3	12	2	PH0920	T-cell receptor be	826	2	8.3	13	2	S47365	T-cell antigen rec
754	2	8.3	12	2	I57678	gene rPLP-A protei	827	2	8.3	13	2	S47368	T-cell antigen rec
755	2	8.3	12	2	B56049	urinary tract ston	828	2	8.3	13	2	S47371	T-cell antigen rec
756	2	8.3	12	2	A61332	Na+/K+-exchanging	829	2	8.3	13	2	S47372	T-cell antigen rec
757	2	8.3	12	2	I41235	glutamine-tRNA lig	830	2	8.3	13	2	S47373	T-cell antigen rec
758	2	8.3	12	2	PH1454	T-cell receptor al	831	2	8.3	13	2	S47376	T-cell antigen rec
759	2	8.3	12	2	PH1458	T-cell receptor be	832	2	8.3	13	2	S47377	T-cell antigen rec

833	2	8.3	13	2	S47378	T-cell antigen rec	906	2	8.3	14	1	LFECW	trp operon leader
834	2	8.3	13	2	S47380	T-cell antigen rec	907	2	8.3	14	1	LFECFS	phesT operon leade
835	2	8.3	13	2	S47381	T-cell antigen rec	908	2	8.3	14	2	A47421	leukotriene B-4 12
836	2	8.3	13	2	S47382	T-cell antigen rec	909	2	8.3	14	2	PC3373	proable IMP denyd
837	2	8.3	13	2	S47383	T-cell antigen rec	910	2	8.3	14	2	C40944	S-allele-associate
838	2	8.3	13	2	S47384	T-cell antigen rec	911	2	8.3	14	2	S39932	hypothetical prote
839	2	8.3	13	2	S47385	T-cell antigen rec	912	2	8.3	14	2	S21247	H+-transporting tw
840	2	8.3	13	2	S47388	T-cell antigen rec	913	2	8.3	14	2	S23747	alpha-1-antichymot
841	2	8.3	13	2	S47389	T-cell antigen rec	914	2	8.3	14	2	A60622	somatostatin - spo
842	2	8.3	13	2	S47390	T-cell antigen rec	915	2	8.3	14	2	B61309	lutropin beta chal
843	2	8.3	13	2	S47392	T-cell antigen rec	916	2	8.3	14	2	S19803	ubiquitin - potato
844	2	8.3	13	2	S47400	T-cell antigen rec	917	2	8.3	14	2	A49018	myosin heavy chain
845	2	8.3	13	2	S47374	T-cell antigen rec	918	2	8.3	14	2	B29743	translation initia
846	2	8.3	13	2	S23372	T-cell receptor al	919	2	8.3	14	2	S29209	avenin alpha-2 - o
847	2	8.3	13	2	B61233	conceptus protein	920	2	8.3	14	2	T46634	acyl carrier prote
848	2	8.3	13	2	S10562	zona pellucida-bin	921	2	8.3	14	2	PA0109	porin por 1B - Ara
849	2	8.3	13	2	B56864	dipeptidyl-peptida	922	2	8.3	14	2	S50900	chlorophyll a/b-bi
850	2	8.3	13	2	C53275	Ig kappa-1 chain J	923	2	8.3	14	2	E90858	trp operon leader
851	2	8.3	13	2	B53275	Ig kappa-1 chain J	924	2	8.3	14	2	B85761	trp operon leader
852	2	8.3	13	2	B25448	Ig kappa-1 chain,	925	2	8.3	14	2	F90931	phesT operon leade
853	2	8.3	13	2	PH1593	Ig H chain V-D-J r	926	2	8.3	14	2	B85780	phesT operon leade
854	2	8.3	13	2	G37266	Ig heavy chain C r	927	2	8.3	14	2	S60353	amylopolysacchar
855	2	8.3	13	2	D37267	Ig heavy chain C r	928	2	8.3	14	2	B58502	36K kidney stone p
856	2	8.3	13	2	B26406	Ig kappa chain J r	929	2	8.3	14	2	PL0142	carbon-monoxide de
857	2	8.3	13	2	PH0788	T-cell receptor al	930	2	8.3	14	2	B38222	excinnuclease ABC c
858	2	8.3	13	2	PH0796	T-cell receptor al	931	2	8.3	14	2	PA0015	seed storage prote
859	2	8.3	13	2	PH0787	T-cell receptor al	932	2	8.3	14	2	S17766	beta-glucosidase (
860	2	8.3	13	2	PH0799	T-cell receptor al	933	2	8.3	14	2	F61497	seed protein ws-21
861	2	8.3	13	2	PH0786	T-cell receptor al	934	2	8.3	14	2	A61002	photosystem II oxy
862	2	8.3	13	2	PH0928	unidentified QM002	935	2	8.3	14	2	A60737	pollen allergen Lo
863	2	8.3	13	2	PH0928	T-cell receptor be	936	2	8.3	14	2	PS0278	ribulose-bisphosph
864	2	8.3	13	2	A47630	Ig kappa chain J r	937	2	8.3	14	2	PA0101	protein QP20020 -
865	2	8.3	13	2	C47630	Ig kappa chain J r	938	2	8.3	14	2	PA0096	pyruvate decarboxy
866	2	8.3	13	2	B47630	Ig kappa chain J r	939	2	8.3	14	2	A35105	hypothetical prote
867	2	8.3	13	2	D47630	Ig kappa chain J r	940	2	8.3	14	2	B34135	DNA-binding protei
868	2	8.3	13	2	E47630	Ig kappa chain J r	941	2	8.3	14	2	C33098	223K exoantigen -
869	2	8.3	13	2	S03063	Ig lambda chain J	942	2	8.3	14	2	PL0152	metal-binding prot
870	2	8.3	13	2	E42762	proteasome endopep	943	2	8.3	14	2	S38307	DEB-A protein - fr
871	2	8.3	13	2	PH1479	T-cell receptor be	944	2	8.3	14	2	S29486	GTP-binding protei
872	2	8.3	13	2	S08575	botulinum neurotox	945	2	8.3	14	2	I54284	Cl-inhibitor - hum
873	2	8.3	13	2	A01825	botulinum toxins -	946	2	8.3	14	2	A60770	cell surface alloa
874	2	8.3	13	2	G22565	R-phycoerythrin ga	947	2	8.3	14	2	PT0223	Ig heavy chain CDR
875	2	8.3	13	2	S20578	ribosomal protein	948	2	8.3	14	2	PT0232	Ig heavy chain CRD
876	2	8.3	13	2	S14316	photosystem I 9K c	949	2	8.3	14	2	PT0252	Ig heavy chain CRD
877	2	8.3	13	2	D56661	S-locus specific g	950	2	8.3	14	2	PT0254	Ig heavy chain CRD
878	2	8.3	13	2	S04013	lignin peroxidase	951	2	8.3	14	2	PH1321	Ig heavy chain DJ
879	2	8.3	13	2	S04014	lignin peroxidase	952	2	8.3	14	2	PH1305	Ig heavy chain DJ
880	2	8.3	13	2	S32471	lynnadFamide 1 - g	953	2	8.3	14	2	PH1306	Ig kappa chain J s
881	2	8.3	13	2	S32472	lynnadFamide 2 - g	954	2	8.3	14	2	S23639	interferon alpha r
882	2	8.3	13	2	S32474	lynnadFamide 4 - g	955	2	8.3	14	2	S41601	MUC1 enhancer bind
883	2	8.3	13	2	S32475	lynnadFamide 5 - g	956	2	8.3	14	2	A59018	T cell receptor al
884	2	8.3	13	2	B58533	CD61 homolog - cha	957	2	8.3	14	2	PH1763	T cell receptor al
885	2	8.3	13	2	B28955	polyisialoglycoprot	958	2	8.3	14	2	PH1757	T cell receptor al
886	2	8.3	13	2	S09018	hemolytic protein	959	2	8.3	14	2	PH1758	T cell receptor al
887	2	8.3	13	2	A57789	gallbladder stone	960	2	8.3	14	2	PH1759	T cell receptor al
888	2	8.3	13	2	S23638	Ig kappa chain J s	961	2	8.3	14	2	PH1766	T cell receptor al
889	2	8.3	13	2	H56046	urinary tract ston	962	2	8.3	14	2	PH1767	T cell receptor al
890	2	8.3	13	2	G56046	urinary tract ston	963	2	8.3	14	2	PH1768	T cell receptor al
891	2	8.3	13	2	S78766	ribosomal protein	964	2	8.3	14	2	PH1769	T cell receptor al
892	2	8.3	13	2	I49637	deoxynucleotidylr	965	2	8.3	14	2	PH1806	T cell receptor al
893	2	8.3	13	2	H33932	Ig kappa chain J r	966	2	8.3	14	2	S57569	T cell receptor V-
894	2	8.3	13	2	A33933	Ig kappa chain J r	967	2	8.3	14	2	S57574	T cell receptor V-
895	2	8.3	13	2	PC4391	cysteine proteinas	968	2	8.3	14	2	S57638	T cell receptor V-
896	2	8.3	13	2	G83988	hypothetical prote	969	2	8.3	14	2	S47366	T-cell antigen rec
897	2	8.3	13	2	S66558	serine proteinase	970	2	8.3	14	2	S23369	T-cell receptor al
898	2	8.3	13	2	S01904	H+-transporting tw	971	2	8.3	14	2	A28018	very late antigen-
899	2	8.3	13	2	JZVHP1	crabrolin - Europe	972	2	8.3	14	2	S58426	spermadhesin AWN h
900	2	8.3	13	2	S21152	tryptophyllin-rela	973	2	8.3	14	2	S66234	sperm motility inh
901	2	8.3	13	2	A05174	tryptophyllin-13 -	974	2	8.3	14	2	PN0666	dysotrophin-associ
902	2	8.3	13	2	A23695	myosin heavy chain	975	2	8.3	14	2	C43847	Ig mu chain V regi
903	2	8.3	13	2	A60336	outer membrane pro	976	2	8.3	14	2	C44823	synaptosomal-assoc
904	2	8.3	13	2	I70075	glycophorin B (mis	977	2	8.3	14	2	PH1625	Ig H chain V-D-J r
905	2	8.3	14	1	NYRQ14	hypothalamic tetra	978	2	8.3	14	2	PH1627	Ig H chain V-D-J r

979 2 8.3 14 2 PH1601  
980 2 8.3 14 2 PH1608  
981 2 8.3 14 2 PH0792  
982 2 8.3 14 2 PH0800  
983 2 8.3 14 2 PH0801  
984 2 8.3 14 2 PH0804  
985 2 8.3 14 2 PH0776  
986 2 8.3 14 2 PH0210  
987 2 8.3 14 2 PH0765  
988 2 8.3 14 2 PH0747  
989 2 8.3 14 2 PH0755  
990 2 8.3 14 2 PH0774  
991 2 8.3 14 2 S65392  
992 2 8.3 14 2 PH0945  
993 2 8.3 14 2 PH0915  
994 2 8.3 14 2 PD0020  
995 2 8.3 14 2 C39170  
996 2 8.3 14 2 PA0044  
997 2 8.3 14 2 S72217  
998 2 8.3 14 2 AG0705  
999 2 8.3 14 2 PH1471  
1000 2 8.3 14 2 I39753

## ALIGNMENTS

RESULT 1  
I59073  
MHC class II histocompatibility antigen HLA-DR\*6a-beta-6111 - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 31-May-1996 #sequence\_revision 31-May-1996 #text\_change 09-Jul-2004  
C:Accession: I59073  
R:Angelini, G.; de Preval, C.; Gorski, J.; Mach, B.  
Proc. Natl. Acad. Sci. U.S.A. 83, 4489-4493, 1986  
A:Title: High-resolution analysis of the human HLA-DR polymorphism by hybridization with  
A:Reference number: I59073; MUID:86233452; PMID:3012569  
A:Accession: I59073  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-20 <ANG>  
A:CROSS-references: UNIPROT:Q30135; UNIPARC:UPI00000894DE; GB:M13561; NID:G188310; PIDN:  
C:Genetics:  
A:Gene: HLA-DRB3  
A:Map position: 6p21.3  
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology  
C:Keywords: glycoprotein

Query Match 20.8%; Score 5; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 55;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDS 5  
Db 13 LRFDS 17

RESULT 2  
A44874  
proboscipedia - fruit fly (Drosophila pseudoobscura) (fragment)  
C:Species: Drosophila pseudoobscura  
C>Date: 31-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 31-Dec-2004  
C:Accession: A44874  
R:Randazzo, F.M.; Cribbs, D.L.; Kaufman, T.C.  
Development 113, 257-271, 1991  
A:Title: Rescue and regulation of proboscipedia: a homeotic gene of the Antennapedia Com  
A:Reference number: A44874; MUID:92111389; PMID:1684932  
A:Accession: A44874  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-12 <RAN>  
A:CROSS-references: UNIPROT:Q26429; UNIPARC:UPI0000080847; GB:S77929; NID:G242124; PIDN:  
A:Note: sequence extracted from NCBI backbone (NCBIN:77929, NCBI:77931)

C:Genetics:  
A:Gene: FlyBase:Dpse/pb  
A:CROSS-references: FlyBase:FBgn0012734  
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 16.7%; Score 4; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 NNNN 19  
Db 8 NNNN 11

## RESULT 3

I76673  
hypothetical COII/ND5 mutant fusion protein - mouse mitochondrion (fragment)  
N:Alternate names: COII/ND5 protein  
C:Species: mitochondrion Mus musculus (house mouse)  
C>Date: 12-Aug-1996 #sequence\_revision 16-Jul-1998 #text\_change 20-Apr-2000  
C:Accession: I76673; I76674  
R:Nelson, I.; Gerasimov, S.; Marsac, C.; Lestienne, P.; Boursot, P.  
Mamm. Genome 4, 680-683, 1993  
A:Title: Sequence analysis of a deleted mitochondrial DNA molecule in heteroplasmic mice  
A:Reference number: I57011; MUID:94108239; PMID:8281018  
A:Accession: I76673  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-17 <NEL1>  
A:CROSS-references: UNIPARC:UPI0000017CED5; GB:S68119; NID:G544777  
A:Accession: I76674  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 8-17 <NEL2>  
A:CROSS-references: UNIPARC:UPI0000017CED6; GB:S68119; NID:G544777  
C:Comment: This is the hypothetical translation of a sequence believed to result from a

C:Genetics:  
A:Gene: COII/ND5  
A:Genome: mitochondrion  
A:Genetic code: SGC1  
C:Keywords: fusion protein; mitochondrion  
F:1-7/Region: cytochrome-c oxidase chain II  
F:8-17/Region: NADH dehydrogenase (ubiquinone) chain 5

Query Match 16.7%; Score 4; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TNNN 18  
Db 10 TNNN 13

## RESULT 4

A40256  
interleukin-7 receptor, membrane form - human (fragments)  
C:Species: Homo sapiens (man)  
C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 29-Aug-1997  
C:Accession: A40256  
R:Plaيمان, C.M.; Gimpel, S.D.; Park, L.S.; Harada, H.; Taniguchi, T.; Ziegler, S.F.  
Mol. Cell. Biol. 11, 3052-3059, 1991  
A:Title: Organization of the murine and human interleukin-7 receptor genes: two mRNAs ge  
A:Reference number: A40256; MUID:91246172; PMID:2038316  
A:Accession: A40256  
A:Molecule type: DNA  
A:Residues: 1-18 <PLE>  
A:CROSS-references: UNIPARC:UPI0000017C285

C:Genetics:  
A:Gene: GDB:IL7R  
A:CROSS-references: GDB:127886; OMIM:146661  
A:Map position: 5p13-5p13  
C:Keywords: cytokine receptor; transmembrane protein

Query Match 16.7%; Score 4; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 NNSS 21  
|||||  
DB 2 NNSS 5

## RESULT 5

PC1323

Endopeptidase Clp (EC 3.4.21.92) chain P [similarity] - curled-leaved tobacco chloroplast

C;Species: Chloroplast Nicotiana glauca (curled-leaved tobacco)

C;Date: 03-May-1994 #sequence\_revision 07-Oct-1994 #text\_change 09-Jul-2004

C;Accession: PC1323

R;Pejters, E.; Engler, D.; Maliga, P.

Theor. Appl. Genet. 79, 28-32, 1990

A;Title: Extensive homologous chloroplast DNA recombination in the pt14 Nicotiana somati-

A;Reference number: PC1321

A;Accession: PC1323

A;Molecule type: DNA

A;Residues: 1-19 <FEJ>

A;Cross-references: UNIPROT:Q7M2F6; UNIPARC:UPI0000175C9D

C;Genetics:

A;Genome: chloroplast

C;Function:

A;Description: ATP-driven cleavage of proteins to small peptides

A;Note: magnesium required

C;Superfamily: endopeptidase Clp chain P

C;Keywords: ATP; chloroplast; hydrolase; serine proteinase

F;3/Active site: His #status predicted

Query Match 16.7%; Score 4; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 SSFY 23  
|||||  
DB 7 SSFY 10

## RESULT 6

I79432

MHC class II histocompatibility antigen HLA-DR\*6b-beta-6III - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 31-May-1996 #sequence\_revision 31-May-1996 #text\_change 09-Jul-2004

C;Accession: I79432

R;Angelini, G.; de Preval, C.; Gorski, J.; Mach, B.

Proc. Natl. Acad. Sci. U.S.A. 83, 4489-4493, 1986

A;Title: High-resolution analysis of the human HLA-DR polymorphism by hybridization with

A;Reference number: I59073; MUID:86233452; PMID:3012569

A;Accession: I79432

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-20 <ANG>

A;Cross-references: UNIPROT:O19726; UNIPARC:UPI000008AB92; GB:M13562; NID:G188312; PIDN-

C;Genetics:

A;Gene: HLA-DRB3

A;Map position: 6p21.3

C;Superfamily: class II histocompatibility antigen; immunoglobulin homology

C;Keywords: glycoprotein

Query Match 16.7%; Score 4; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RFDS 5  
|||||  
DB 14 RFDS 17

## RESULT 7

S67990

neurotoxin-associated protein type A Hn+ 17K chain - Clostridium botulinum (fragment)  
N;Alternate names: HA-15 protein  
C;Species: Clostridium botulinum  
C;Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004

C;Accession: S67990; C44644

R;Fujita, R.; Fujinaga, Y.; Inoue, K.; Nakajima, H.; Kumon, H.; Oguma, K.

FEBS Lett. 376, 41-44, 1995

A;Title: Molecular characterization of two forms of nontoxic-nonhemagglutinin component

A;Reference number: S67988; MUID:96096783; PMID:8521962

A;Accession: S67990

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-20 <FUJ>

A;Cross-references: UNIPROT:Q9RSN8; UNIPARC:UPI0000017ACES

R;Somers, E.; DasGupta, B.R.

J. Protein Chem. 10, 415-425, 1991

A;Title: Clostridium botulinum types A, B, C1, and E produce proteins with or without h

A;Reference number: A44644; MUID:92143938; PMID:1781887

A;Contents: type A

A;Accession: C44644

A;Molecule type: protein

A;Residues: 1-19 <SOM>

A;Cross-references: UNIPARC:UPI00000A8A14

A;Note: sequence extracted from NCBI backbone (NCBI:83795)

C;Keywords: hemagglutinin

Query Match 16.7%; Score 4; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KSIF 11  
|||||  
DB 15 KSIF 18

## RESULT 8

B40256

interleukin-7 receptor, soluble form - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 23-May-1997

C;Accession: B40256

R;Pleiman, C.M.; Gimpel, S.D.; Park, L.S.; Harada, H.; Taniguchi, T.; Ziegler, S.F.

Mol. Cell. Biol. 11, 3052-3059, 1991

A;Title: Organization of the murine and human interleukin-7 receptor genes: two mRNAs g

A;Reference number: A40256; MUID:91246172; PMID:2038316

A;Accession: B40256

A;Molecule type: DNA

A;Residues: 1-22 <PLE>

A;Cross-references: UNIPARC:UPI0000176755

A;Note: the authors translated the codon GAA for residue 20 as Gln

C;Superfamily: interleukin-7 receptor; fibronectin type III repeat homology

C;Keywords: cytokine receptor

Query Match 16.7%; Score 4; DB 2; Length 22;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 NNSS 21  
|||||  
DB 2 NNSS 5

## RESULT 9

D41654

hypothetical protein (sodC 5' region) - Haemophilus parainfluenzae (fragment)

C;Species: Haemophilus parainfluenzae

C;Date: 12-Jun-1992 #sequence\_revision 12-Jun-1992 #text\_change 24-Feb-1995

C;Accession: D41654

R;Kroll, J.S.; Langford, P.R.; Loynds, B.M.

J. Bacteriol. 173, 7449-7457, 1991

A;Title: Copper-zinc superoxide dismutase of Haemophilus influenzae and Haemophilus par

A;Reference number: A41654; MUID:92041655; PMID:1938942

A:Accession: D41654  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-4 <KRO>  
A:Cross-references: UNIPARC:UPI000017AB26

Query Match 12.5%; Score 3; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RFD 4  
|||  
Db 2 RFD 4

RESULT 10  
PT0644  
T-cell receptor beta chain V-D-J region (111-1G) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 09-Jul-2004  
C:Accession: PT0644  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601; PMID:1711558  
A:Accession: PT0644  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-5 <FEE>  
A:Cross-references: UNIPROT:Q5Z2T6; UNIPARC:UPI000017C7D2  
A:Experimental source: newborn thymus, strain BALB/c  
C:Keywords: T-cell receptor

Query Match 12.5%; Score 3; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 SSF 22  
|||  
Db 2 SSF 4

RESULT 11  
B39127  
phosphotransferase system enzyme II (EC 2.7.1.69) - Escherichia coli (fragment)  
C:Species: Escherichia coli  
C:Date: 27-Nov-1991 #sequence\_revision 27-Nov-1991 #text\_change 08-Oct-1999  
C:Accession: B39127  
R:Hardesty, C.; Ferran, C.; DiRienzo, J.M.  
J. Bacteriol. 173, 449-456, 1991  
A:Title: Plasmid-mediated sucrose metabolism in Escherichia coli: characterization of sc  
rin.  
A:Reference number: A39127; MUID:91100329; PMID:1846143  
A:Accession: B39127  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-7 <HAR>  
A:Cross-references: UNIPARC:UPI0000170D6E; GB:M38416; NID:g155142; PIDN:AAA98418.1; PID:  
C:Keywords: phosphotransferase

Query Match 12.5%; Score 3; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 FEQ 13  
|||  
Db 3 FEQ 5

RESULT 12  
A59489  
protein kinase C inhibitor - rat (fragment)  
C:Species: Rattus norvegicus

C:Date: 25-Aug-2003 #sequence\_revision 25-Aug-2003 #text\_change 25-Aug-2003  
C:Accession: A59489  
R:Negoro, M.  
A:Description: Purification of PKCI from rat liver.  
submitted to the Protein Sequence Database, June 2003  
A:Reference number: A59489  
A:Accession: A59489  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-7 <NEG>  
A:Experimental source: strain Wistar, liver  
A:Note: p-Hydroxyacetophenone-Sepharose binding protein

Query Match 12.5%; Score 3; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 IFE 12  
|||  
Db 2 IFE 4

RESULT 13  
PH1407  
Ig heavy chain V region (clone micro m+ 46-6 PCR) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 17-Mar-1999  
C:Accession: PH1407  
R:Shirasawa, T.; Miyazoe, I.; Hagiwara, S.; Kimoto, H.; Shigemoto, K.; Taniguchi, M.; Ta  
J. Exp. Med. 176, 1209-1214, 1992  
A:Title: Heavy chain variable (VH) region diversity generated by VH gene replacement in  
ia virus.  
A:Reference number: PH1403; MUID:93018837; PMID:1402663  
A:Accession: PH1407  
A:Molecule type: DNA  
A:Residues: 1-8 <SHI>  
A:Cross-references: UNIPARC:UPI0000176A1C  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

Query Match 12.5%; Score 3; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRF 3  
|||  
Db 5 LRF 7

RESULT 14  
S59622  
metallothionein isoform a, cadmium-binding - Ariantha arbustorum (terrestrial snail) (fra  
C:Species: Ariantha arbustorum  
C:Date: 19-Mar-1997 #sequence\_revision 24-Oct-1997 #text\_change 09-Jul-2004  
C:Accession: S59622  
R:Berger, B.; Hunziker, P.E.; Hauer, C.R.; Birchler, N.; Dallinger, R.  
Biochem. J. 311, 951-957, 1995  
A:Title: Mass spectrometry and amino acid sequencing of two cadmium-binding metallothion  
A:Reference number: S59621; MUID:96067616; PMID:7487956  
A:Accession: S59622  
A:Molecule type: protein  
A:Residues: 1-8 <BER>  
A:Cross-references: UNIPROT:P55946; UNIPARC:UPI0000177CA4  
C:Superfamily: metallothionein  
C:Keywords: chelation; metal binding; metal-thiolate cluster

Query Match 12.5%; Score 3; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 NSS 21  
|||  
Db 2 NSS 4

## RESULT 15

JS0316  
leucokinin VI - Madeira cockroach  
C;Species: Leucophaea maderae (Madeira cockroach)  
C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
C;Accession: JS0316  
R;Holman, G.M.; Cook, B.J.; Nachman, R.J.  
Comp. Biochem. Physiol. C 88, 27-30, 1987  
A;Title: Isolation, primary structure, and synthesis of leucokinins V and VI: myotropic  
A;Reference number: JS0315  
A;Accession: JS0316  
A;Molecule type: protein  
A;Residues: 1-8 <HOL>  
A;Cross-references: UNIPROT:P19988; UNIPARC:UPI000012E29E  
C;Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile act  
C;Keywords: amidated carboxyl end; cephalomyotropic peptide; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 12.5%; Score 3; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 SSF 22  
|||  
Db 2 SSF 4

Search completed: January 20, 2006, 17:56:07  
Job time : 20 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2006, 17:51:04 ; Search time 65 seconds  
(without alignments)  
260.503 Million cell updates/sec

Title: US-10-619-323-1\_COPY\_35\_58

Perfect score: 24

Sequence: 1 LRFDSQTSIFQETNNNSFYT 24

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 0

Total number of hits satisfying chosen parameters: 21620

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Listing first 1000 summaries

Database : UniProt\_05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	20.8	20	Q30135_HUMAN	Q30135 homo sapien
2	5	20.8	23	Q4YXD8_PLABE	Q4YXD8 plasmodium
3	5	20.8	25	Q7REJ5_PLAYO	Q7REJ5 plasmodium
4	4	16.7	12	Q26429_DROPS	Q26429 drosophila
5	4	16.7	16	Q36731_HUMAN	Q36731 homo sapien
6	4	16.7	17	Q4YCW9_PLABE	Q4YCW9 plasmodium
7	4	16.7	19	Q7M2F6_NICPL	Q7M2F6 nicotiana p
8	4	16.7	19	Q9R5N8_CLOBO	Q9R5N8 clostridium
9	4	16.7	20	Q19726_HUMAN	Q19726 homo sapien
10	4	16.7	20	Q4X1L0_PLACH	Q4X1L0 plasmodium
11	4	16.7	21	Q8N337_HUMAN	Q8N337 homo sapien
12	4	16.7	21	Q4YK89_PLABE	Q4YK89 plasmodium
13	4	16.7	21	Q4Z0T6_PLABE	Q4Z0T6 plasmodium
14	4	16.7	22	Q7S122_NEUCR	Q7S122 neurospora
15	4	16.7	22	Q8WSY1_ANOGA	Q8WSY1 anopheles g
16	4	16.7	22	Q4XN91_PLACH	Q4XN91 plasmodium
17	4	16.7	22	Q4XSS7_PLACH	Q4XSS7 plasmodium
18	4	16.7	22	Q4YH58_PLABE	Q4YH58 plasmodium
19	4	16.7	22	Q4Z2L9_PLABE	Q4Z2L9 plasmodium
20	4	16.7	23	Q9UCL8_HUMAN	Q9UCL8 homo sapien
21	4	16.7	23	Q19621_HUMAN	Q19621 homo sapien
22	4	16.7	23	Q4YQV7_PLABE	Q4YQV7 plasmodium
23	4	16.7	24	Q658N7_HUMAN	Q658N7 homo sapien
24	4	16.7	24	Q7RAM4_PLAYO	Q7RAM4 plasmodium
25	4	16.7	24	Q4XG55_PLACH	Q4XG55 plasmodium
26	4	16.7	24	Q4XSL3_PLACH	Q4XSL3 plasmodium
27	4	16.7	24	Q4LSM0_STAHJ	Q4LSM0 staphylococ
28	4	16.7	24	Q68W11_RICTY	Q68W11 rickettsia
29	4	16.7	25	1 SODC_PAROL	P83129 paralichthy
30	4	16.7	25	Q7RLH1_PLAYO	Q7RLH1 plasmodium
31	4	16.7	25	Q9BM38_CABEL	Q9BM38 caenorhabdi

Q9BM39	caenorhabdi	25	16.7	4	Q9BM39_CABEL
Q4XAN1	plasmodium	25	16.7	4	Q4XAN1_PLACH
Q570P0	arabidopsis	25	16.7	4	Q570P0_ARATH
P42562	hirudo medi	4	12.5	3	FAR3_HIRME
P69138	helisoma tr	4	12.5	3	FLRP_HELTI
P69137	hirudo medi	4	12.5	3	FLRP_HIRME
P67308	gallus gall	4	12.5	3	FARP_CHICK
P67979	ascaris suu	7	12.5	3	FAP2_ASCSU
P67980	panagrellus	7	12.5	3	FAP2_PANRE
P41871	helisoma tr	7	12.5	3	FAR1_HELTI
P83274	macrobrachi	7	12.5	3	FAR1_WACRS
P38499	procambarus	7	12.5	3	FAR1_PROCL
P38498	procambarus	7	12.5	3	FAR2_PROCL
P41872	panagrellus	8	12.5	3	FAR1_PANRE
P83316	penaeus mon	8	12.5	3	FAR1_PENMO
P83275	macrobrachi	8	12.5	3	FAR2_WACRS
P41866	hormarus ame	8	12.5	3	FAR3_HOMAM
P41847	hormarus ame	8	12.5	3	FAR4_HOMAM
P19388	leucophaea	8	12.5	3	LCK6_LEUMA
Q61447	homo sapien	8	12.5	3	Q6LD47_HUMAN
Q8MC18	quisqualis	8	12.5	3	Q8MC18_QUIIN
Q8MC20	combretum w	8	12.5	3	Q8MC20_9MIRT
O87471	haemophilus	8	12.5	3	O87471_HABIN
O61DH5	lactococcus	8	12.5	3	O6LDH5_9LACT
Q7M066	mus musculus	8	12.5	3	Q7M066_MOUSE
Q7M067	mus musculus	8	12.5	3	Q7M067_MOUSE
Q99X99	hydrochoeru	8	12.5	3	Q99X99_HYDHY
Q61423	mus musculus	8	12.5	3	Q6LD23_MOUSE
Q91U19	influenza a	8	12.5	3	Q91U19_9INFA
Q91U21	influenza a	8	12.5	3	Q91U21_9INFA
P41873	panagrellus	9	12.5	3	FAR2_PANRE
P83276	macrobrachi	9	12.5	3	FAR3_WACRS
P83318	penaeus mon	9	12.5	3	FAR3_PENMO
P83320	penaeus mon	9	12.5	3	FAR4_PENMO
P83279	macrobrachi	9	12.5	3	FAR5_PENMO
P83281	macrobrachi	9	12.5	3	FAR8_WACRS
P43172	ascaris suu	9	12.5	3	FAR9_ASCSU
P38495	callinectes	9	12.5	3	FARP_CALSI
Q7M4R5	homo sapien	9	12.5	3	Q7M4R5_HUMAN
Q7M4R3	homo sapien	9	12.5	3	Q7M4R3_HUMAN
Q5G6J7	craseonycte	9	12.5	3	Q5G6J7_CRATH
Q5G6J8	eumops auri	9	12.5	3	Q5G6J8_9CHIR
Q5G6J9	natalus str	9	12.5	3	Q5G6J9_NATST
Q5G6K5	rhogeessa t	9	12.5	3	Q5G6K5_9CHIR
Q5G6L3	rhinopoma h	9	12.5	3	Q5G6L3_RHIHA
Q65711	berne virus	9	12.5	3	Q65711_BEV
Q70140	human immun	9	12.5	3	Q70140_9HIV1
P83317	penaeus mon	10	12.5	3	FAR2_PENMO
P83278	macrobrachi	10	12.5	3	FAR5_WACRS
P83280	macrobrachi	10	12.5	3	FAR7_WACRS
P84306	locusta mig	10	12.5	3	FARP_LOCOMI
P18523	manduca sex	10	12.5	3	FARP_MANSE
P84307	schistocerc	10	12.5	3	FARP_SCHGR
P21144	leucophaea	10	12.5	3	LCK6_LEUMA
P61850	sarcophaga	10	12.5	3	NEMS_SARBU
P22589	rana catesb	10	12.5	3	TKNB_RANCA
P56573	rattus norv	10	12.5	3	UH05_RAT
Q6B958	fusarium ox	10	12.5	3	Q6B958_FUSOX
Q78C70	neurospora	10	12.5	3	Q7SC70_NEUCR
Q6E27	homo sapien	10	12.5	3	Q6E27_HUMAN
Q6E29	homo sapien	10	12.5	3	Q96QT9_HUMAN
Q52593	homo sapien	10	12.5	3	Q52RG3_HUMAN
P82217	bombyx mori	10	12.5	3	P82217_BOMMO
Q9TWU1	fusinus fer	10	12.5	3	Q9TWU1_FUSFE
Q4X386	plasmodium	10	12.5	3	Q4X386_PLACH
Q4Z638	plasmodium	10	12.5	3	Q4Z638_PLACH
Q5G6L0	rhynchonyc	10	12.5	3	Q5G6L0_9CHIR
Q58415	prathyrosta	10	12.5	3	Q58415_PSAST
Q58420	crithopsis	10	12.5	3	Q58420_CRIDE
Q58437	eremopyrum	10	12.5	3	Q58437_9POAL
Q58447	australopyr	10	12.5	3	Q58447_9POAL

105	3	12.5	10	2	Q58U54_BROST	Q58U54	bromus ster	178	3	12.5	12	2	Q9BFT8_LEMCA	Q9BFT8	lemur catca
106	3	12.5	10	2	Q915W6_LIBAC	Q915w6	liberibacte	179	3	12.5	12	2	Q9BFT9_TUPMI	Q9BFT9	tupaia mino
107	3	12.5	10	2	Q71V02_PSEAE	Q71v02	pseudomonas	180	3	12.5	12	2	Q9BFU0_CYNVA	Q9BFU0	cynoccephalu
108	3	12.5	10	2	Q47651_ECOLI	Q47651	escherichia	181	3	12.5	12	2	Q9BFU1_OCHHY	Q9BFU1	ochotona hy
109	3	12.5	10	2	Q53VQ7_MOUSE	Q53vq7	mus musculus	182	3	12.5	12	2	Q9BFU2_SYLFL	Q9BFU2	syllilagus
110	3	12.5	10	2	Q84140_9INFA	Q84140	influenza a	183	3	12.5	12	2	Q9BFU3_ORYAF	Q9BFU3	orycteropus
111	3	12.5	10	2	Q85563_MLYMO	Q85563	moloney mur	184	3	12.5	12	2	Q9BFU4_ELERU	Q9BFU4	elephantulu
112	3	12.5	10	2	Q85598_MLYMO	Q85598	moloney mur	185	3	12.5	12	2	Q9BFU5_MACPR	Q9BFU5	macroscecid
113	3	12.5	10	2	Q85619_MLYMO	Q85619	moloney mur	186	3	12.5	12	2	Q9BFU6_LOXAF	Q9BFU6	loxodonta a
114	3	12.5	11	1	FAR6_PENMO	P83321	penaeus mon	187	3	12.5	12	2	Q9BFU7_PROCA	Q9BFU7	procavia ca
115	3	12.5	11	2	Q6LEP5_HUMAN	Q6lep5	homo sapien	188	3	12.5	12	2	Q9BFU8_TRIMA	Q9BFU8	trichechus
116	3	12.5	11	2	Q4YLN6_PLABE	Q4yln6	plasmodium	189	3	12.5	12	2	Q9BFU9_ECHTE	Q9BFU9	echinops te
117	3	12.5	11	2	Q5G6K1_9CHIR	Q5g6k1	thyroptera	190	3	12.5	12	2	Q9BFV0_SORAR	Q9BFV0	sorex arane
118	3	12.5	11	2	Q5G6K2_PTEPA	Q5g6k2	pterototus	191	3	12.5	12	2	Q9BFV1_CONCR	Q9BFV1	condylura c
119	3	12.5	11	2	Q5G6K3_MYZAU	Q5g6k3	myzopoda au	192	3	12.5	12	2	Q9BFV2_TALAL	Q9BFV2	talpa alta
120	3	12.5	11	2	Q5G6K7_ANOGE	Q5g6k7	anoura geof	193	3	12.5	12	2	Q9BFV3_ERICO	Q9BFV3	erinaceus c
121	3	12.5	11	2	Q5G6K8_DESRO	Q5g6k8	desmodus ro	194	3	12.5	12	2	Q9BFV4_MYTRR	Q9BFV4	myrmecophag
122	3	12.5	11	2	Q5G6L1_9CHIR	Q5g6l1	taphozous n	195	3	12.5	12	2	Q9BFV5_TAMTE	Q9BFV5	tamandua te
123	3	12.5	11	2	Q9TRW5_BOVIN	Q9trw5	bos taurus	196	3	12.5	12	2	Q9BFV6_CHAVI	Q9BFV6	chaetophrac
124	3	12.5	11	2	Q06626_BOVLU	Q06626	solanum tub	197	3	12.5	12	2	Q9BFV7_EUPSX	Q9BFV7	euphractus
125	3	12.5	11	2	Q58U09_TAECM	Q58u09	taeniatheru	198	3	12.5	12	2	Q9BFV8_CHODI	Q9BFV8	choloepus d
126	3	12.5	11	2	Q58U22_9POAL	Q58u22	peridictyon	199	3	12.5	12	2	Q9BFV9_CHOHO	Q9BFV9	choloepus h
127	3	12.5	11	2	Q58U24_AEGTA	Q58u24	aegilops ta	200	3	12.5	12	2	Q9BFW0_MACEU	Q9BFW0	macropus eu
128	3	12.5	11	2	Q58U26_LOPEL	Q58u26	lophopyrum	201	3	12.5	12	2	Q9TRU0_BOVIN	Q9TRU0	bos taurus
129	3	12.5	11	2	Q58U43_TRIMO	Q58u43	tritium mo	202	3	12.5	12	2	Q58U39_EREDI	Q58U39	eremopyrum
130	3	12.5	11	2	Q58U51_9POAL	Q58u51	amblyopyrum	203	3	12.5	12	2	Q5FBL6_9ROSI	Q5FBL6	hibiscus ma
131	3	12.5	11	2	Q7X9Y3_CUCSA	Q7x9y3	cucumis sat	204	3	12.5	12	2	Q5FBL8_9ROSI	Q5FBL8	hibiscus ha
132	3	12.5	11	2	Q95E14_DENAA	Q95e14	dendrochili	205	3	12.5	12	2	Q5FBP4_9ROSI	Q5FBP4	hibiscus ti
133	3	12.5	11	2	Q6LBJ0_MOUSE	Q6lbj0	mus musculus	206	3	12.5	12	2	Q5FBR0_9ROSI	Q5FBR0	hibiscus gl
134	3	12.5	12	1	FAR7_PENMO	P83322	penaeus mon	207	3	12.5	12	2	P83196_ORYSA	P83196	oryza sativ
135	3	12.5	12	1	NO40_LOTJA	O22426	lotus japon	208	3	12.5	12	2	Q7M1W6_ARATH	Q7M1W6	arabidopsis
136	3	12.5	12	1	NO40_SESRO	O2x369	sesbania ro	209	3	12.5	12	2	Q8LLC3_TRIRP	Q8LLC3	trifolium r
137	3	12.5	12	1	Q9BYI9_HUMAN	Q9byi9	homo sapient	210	3	12.5	12	2	Q93WB7_LUPLU	Q93WB7	lupinus lut
138	3	12.5	12	2	Q9TWV4_LYMST	Q9twv4	lymnaea sta	211	3	12.5	12	2	Q93WF2_LUPLU	Q93WF2	lupinus lut
139	3	12.5	12	2	Q4X448_PLACH	Q4x448	plasmodium	212	3	12.5	12	2	Q95E12_9ASPA	Q95E12	dendrochili
140	3	12.5	12	2	Q4YQK1_PLABE	Q4yqk1	plasmodium	213	3	12.5	12	2	Q95E16_DENGL	Q95E16	dendrochili
141	3	12.5	12	2	Q5G6K0_MYSTU	Q5g6k0	myotina daub	214	3	12.5	12	2	Q95E18_9ASPA	Q95E18	dendrochili
142	3	12.5	12	2	Q5G6K4_MYODA	Q5g6k4	myotis daub	215	3	12.5	12	2	Q95EJ1_9ASPA	Q95EJ1	dendrochili
143	3	12.5	12	2	Q5G6K6_9CHIR	Q5g6k6	antrozous p	216	3	12.5	12	2	Q95EJ3_9ASPA	Q95EJ3	dendrochili
144	3	12.5	12	2	Q5G6K9_9CHIR	Q5g6k9	tonatia ep	217	3	12.5	12	2	Q95EJ5_9ASPA	Q95EJ5	dendrochili
145	3	12.5	12	2	Q5G6L2_EMBAT	Q5g6l2	emballonura	218	3	12.5	12	2	Q95EJ8_9ASPA	Q95EJ8	dendrochili
146	3	12.5	12	2	Q5G6L4_HIPCO	Q5g6l4	hipposidero	219	3	12.5	12	2	Q95EK0_9ASPA	Q95EK0	dendrochili
147	3	12.5	12	2	Q5G6L5_9CHIR	Q5g6l5	rhinolophus	220	3	12.5	12	2	Q95EK2_9ASPA	Q95EK2	dendrochili
148	3	12.5	12	2	Q5G6L6_NYCAL	Q5g6l6	nyctimene a	221	3	12.5	12	2	Q95EK4_9ASPA	Q95EK4	dendrochili
149	3	12.5	12	2	Q5G6L7_CYNBR	Q5g6l7	cynopterus	222	3	12.5	12	2	Q95EK6_9ASPA	Q95EK6	dendrochili
150	3	12.5	12	2	Q6JC79_9EUTH	Q6jc79	solenodon p	223	3	12.5	12	2	Q95EK8_9ASPA	Q95EK8	dendrochili
151	3	12.5	12	2	Q71BP8_TARSY	Q71bp8	tarsius syr	224	3	12.5	12	2	Q95EL0_9ASPA	Q95EL0	dendrochili
152	3	12.5	12	2	Q71BQ0_CYNVO	Q71bq0	cynoccephalu	225	3	12.5	12	2	Q95EL2_9ASPA	Q95EL2	dendrochili
153	3	12.5	12	2	Q71BQ1_9EUTH	Q71bq1	urogale eve	226	3	12.5	12	2	Q95EL4_9ASPA	Q95EL4	dendrochili
154	3	12.5	12	2	Q9BFR4_9EUTH	Q9bfr4	manis penta	227	3	12.5	12	2	Q95EL6_9ASPA	Q95EL6	dendrochili
155	3	12.5	12	2	Q9BFR5_URSAR	Q9bfr5	ursus arcto	228	3	12.5	12	2	Q95EL8_9ASPA	Q95EL8	dendrochili
156	3	12.5	12	2	Q9BFR6_CANFA	Q9bfr6	canis fami	229	3	12.5	12	2	Q95EM0_9ASPA	Q95EM0	dendrochili
157	3	12.5	12	2	Q9BFR7_PANON	Q9bfr7	panthera on	230	3	12.5	12	2	Q95EM2_9ASPA	Q95EM2	dendrochili
158	3	12.5	12	2	Q9BFR8_LEOPA	Q9bfr8	leopardus p	231	3	12.5	12	2	Q546R2_LOTJA	Q546R2	lotus japon
159	3	12.5	12	2	Q9BER9_FELCA	Q9ber9	felis silve	232	3	12.5	12	2	Q58U56_BROAV	Q58U56	bromus arve
160	3	12.5	12	2	Q9BFS0_TAPIN	Q9bfs0	tapirus ind	233	3	12.5	12	2	Q8SEB7_9FIOR	Q8SEB7	grateloupia
161	3	12.5	12	2	Q9BFS1_CERSI	Q9bfs1	ceratotheri	234	3	12.5	12	2	Q4KUK6_9FLOI	Q4KUK6	grateloupia
162	3	12.5	12	2	Q9BFS2_ORAJE	Q9bfs2	equus cabal	235	3	12.5	12	2	Q47251_ECOLI	Q47251	escherichia
163	3	12.5	12	2	Q9BFS3_HORSE	Q9bfs3	okapia john	236	3	12.5	12	2	Q02128_DPSVU	Q02128	desulfovib
164	3	12.5	12	2	Q9BFS4_PIG	Q9bfs4	sus scrofa	237	3	12.5	12	2	Q99NX7_AGOTA	Q99NX7	agouti tacz
165	3	12.5	12	2	Q9BFS5_TRAEU	Q9bfs5	tragelaphus	238	3	12.5	12	2	Q99NX8_9HYST	Q99NX8	dinomya bra
166	3	12.5	12	2	Q9BFS6_LAMGL	Q9bfs6	lama glama	239	3	12.5	12	2	Q99NY0_9HYST	Q99NY0	cavia tschu
167	3	12.5	12	2	Q9BFS7_HIPAM	Q9bfs7	hippopotamu	240	3	12.5	12	2	Q99NY1_HETGA	Q99NY1	heterocepha
168	3	12.5	12	2	Q9BFS8_TURTR	Q9bfs8	tursiops tr	241	3	12.5	12	2	Q99NY2_DIPHE	Q99NY2	dipodomys h
169	3	12.5	12	2	Q9BFS9_MEGNO	Q9bfs9	megaptera n	242	3	12.5	12	2	Q99NY3_BREDO	Q99NY3	erethizon d
170	3	12.5	12	2	Q9BFT0_NYCTH	Q9bft0	nycteris th	243	3	12.5	12	2	Q99NY4_HYSBR	Q99NY4	hystrix bra
171	3	12.5	12	2	Q9BFT1_ROULA	Q9bft1	rousettus l	244	3	12.5	12	2	Q99NY5_CRIGR	Q99NY5	cricetulus
172	3	12.5	12	2	Q9BFT2_PTEGI	Q9bft2	pteropus gi	245	3	12.5	12	2	Q99NY6_RAT	Q99NY6	rattus norv
173	3	12.5	12	2	Q9BFT3_ARTJA	Q9bft3	artibeus ja	246	3	12.5	12	2	Q99NY7_MOUSE	Q99NY7	mus musculus
174	3	12.5	12	2	Q9BFT4_CALGO	Q9bft4	callimico g	247	3	12.5	12	2	Q99NY8_PSDCA	Q99NY8	pedetes cap
175	3	12.5	12	2	Q9BFT5_MACMU	Q9bft5	macaca mula	248	3	12.5	12	2	Q99NY9_MUSAD	Q99NY9	muscardinus
176	3	12.5	12	2	Q9BFT6_ATEFU	Q9bft6	ateles fusc	249	3	12.5	12	2	Q99NZ0_CASCN	Q99NZ0	caator cana
177	3	12.5	12	2	Q9BFT7_TARBA	Q9bft7	tarsius ban	250	3	12.5	12	2	Q99NZ1_TAMST	Q99NZ1	tamias stri

251	3	12.5	12	2	Q8AEW7_9HIV1	Q8AEW7 human immun	324	3	12.5	15	2	Q85XF8_9ROSI	Q85xf8 clusia gran
252	3	12.5	13	1	FARB_ASCSU	P43173 ascaris suu	325	3	12.5	15	2	Q85XG0_9ROSI	Q85xg0 clusia flum
253	3	12.5	13	1	NO40_PEA	P55959 pium sattiv	326	3	12.5	15	2	Q85XG2_9ROSI	Q85xg2 clusia flav
254	3	12.5	13	1	NO40_VICSA	P55961 vicia sattiv	327	3	12.5	15	2	Q85XG4_9ROSI	Q85xg4 clusia croa
255	3	12.5	13	2	Q7SCD5_NEUCR	Q78cd5 neurospora	328	3	12.5	15	2	Q85XG6_9ROSI	Q85xg6 clusia arip
256	3	12.5	13	2	Q29823_HUMAN	Q29823 homo sapien	329	3	12.5	15	2	Q9S8D3_CYNCA	Q9s8d3 cynara card
257	3	12.5	13	2	Q6SL59_HUMAN	Q6sl59 homo sapien	330	3	12.5	15	2	Q9SAP4_SOUTU	Q9sap4 solanum tub
258	3	12.5	13	2	Q75MV9_HUMAN	Q75mv9 homo sapien	331	3	12.5	15	2	Q9R4T0_RHOSH	Q9r4t0 rhodobacter
259	3	12.5	13	2	Q53S92_HUMAN	Q53s92 homo sapien	332	3	12.5	15	2	Q9R4U8_ACICA	Q9r4u8 acinetobact
260	3	12.5	13	2	Q65YZ5_HORSE	Q65yz5 equus cabal	333	3	12.5	15	2	Q9R533_PSEAE	Q9r533 pseudomonas
261	3	12.5	13	2	Q7YRD1_BISBO	Q7yrd1 bison bonas	334	3	12.5	15	2	Q88175_MOUSE	Q88175 mus musculu
262	3	12.5	13	2	Q7YRI4_BOVIN	Q7yri4 bos taurus	335	3	12.5	15	2	Q88175_MOUSE	Q88175 mus musculu
263	3	12.5	13	2	Q8WNS4_BOVIN	Q8wns4 bos taurus	336	3	12.5	15	2	Q7LZ20_CHICK	Q7l220 gallus gall
264	3	12.5	13	2	Q9BDQ8_PIG	Q9bdq8 sus scrofa	337	3	12.5	15	2	Q8UP12_9HIV1	Q8up12 human immun
265	3	12.5	13	2	Q42373_SOLTU	Q42373 solanum tub	338	3	12.5	15	2	Q5EEK4_HUMAN	Q5eek4 homo sapien
266	3	12.5	13	2	Q71N39_TRIRP	Q71n39 trifolium r	339	3	12.5	16	2	Q9UC44_HUMAN	Q9uc44 homo sapien
267	3	12.5	13	2	Q7X955_CAPBU	Q7x955 caprella bu	340	3	12.5	16	2	Q9UCJ7_HUMAN	Q9ucj7 homo sapien
268	3	12.5	13	2	Q53300_ECOLI	Q53300 escherichia	341	3	12.5	16	2	Q75MY2_HUMAN	Q75my2 homo sapien
269	3	12.5	13	2	Q6XFQ8_BACCS	Q6xfq8 bacillus cl	342	3	12.5	16	2	Q7RE61_PLAYO	Q7re61 plasmodium
270	3	12.5	13	2	Q7MOJ0_9ACTO	Q7moj0 actinomadr	343	3	12.5	16	2	Q7RPP5_PLAYO	Q7rpp5 plasmodium
271	3	12.5	13	2	Q6RSM3_COXBU	Q6rsm3 coxiella bu	344	3	12.5	16	2	Q4XD98_PLACH	Q4xd98 plasmodium
272	3	12.5	13	2	Q71R59_MOUSE	Q71r59 mus musculu	345	3	12.5	16	2	Q5G554_BALMU	Q5g554 balaeopter
273	3	12.5	13	2	Q80WZ0_RAT	Q80wz0 rattus norv	346	3	12.5	16	2	Q19971_GOSHI	Q19971 gossypium h
274	3	12.5	13	2	Q9CU06_MOUSE	Q9cu06 mus musculu	347	3	12.5	16	2	Q19973_GOSBA	Q19973 gossypium b
275	3	12.5	13	1	BNCE_BENHI	P83961 benincasa h	348	3	12.5	16	2	Q19975_GOSTO	Q19975 gossypium t
276	3	12.5	14	1	GLGS_SPIOL	P55235 spinacia ol	349	3	12.5	16	2	Q19977_GOSMU	Q19977 gossypium m
277	3	12.5	14	1	LPER_BACAN	P62187 bacillus an	350	3	12.5	16	2	Q34699_HELAN	Q34699 helianthus
278	3	12.5	14	1	LPER_BACLI	P62188 bacillus li	351	3	12.5	16	2	Q5G6V0_9ARAE	Q5g6v0 philodendro
279	3	12.5	14	1	MAST_VESBA	P21454 vespa basal	352	3	12.5	16	2	Q9S8Y6_LUPAR	Q9s8y6 lupinus arb
280	3	12.5	14	1	UN46_CLOPA	P81362 clostridium	353	3	12.5	16	2	Q6RSJ3_COXBU	Q6rsj3 coxiella bu
281	3	12.5	14	2	Q6E144_BIOGL	Q6e144 biophalari	354	3	12.5	16	2	Q9KJ10_STAHA	Q9kj10 staphylococ
282	3	12.5	14	2	Q6Q9S8_9CARA	Q6q9s8 zabrus colf	355	3	12.5	16	2	Q9L923_SHIHO	Q9l923 shigella bo
283	3	12.5	14	2	Q4XLP6_PLACH	Q4xlp6 plasmodium	356	3	12.5	16	2	Q9L925_SHIFL	Q9l925 shigella fl
284	3	12.5	14	2	Q4XSI2_PLACH	Q4xsi2 plasmodium	357	3	12.5	16	2	Q9L927_SHISO	Q9l927 shigella so
285	3	12.5	14	2	P82333_PEA	P82333 pium sattiv	358	3	12.5	16	2	Q9L937_SHISO	Q9l937 shigella so
286	3	12.5	14	2	Q7X9Y5_CUCSA	Q7x9y5 cucumis sat	359	3	12.5	16	2	Q9R4H3_PORGI	Q9r4h3 porphyrom
287	3	12.5	14	2	Q9ZRS3_ARATH	Q9zrs3 arabidopsis	360	3	12.5	16	2	Q9R5K7_STROI	Q9r5k7 streptomyce
288	3	12.5	14	2	Q47599_ECOLI	Q47599 escherichia	361	3	12.5	16	2	Q8TSR1_9SPHN	Q8tsr1 erythrobaet
289	3	12.5	14	2	Q9R224_CAMJE	Q9r224 campylobact	362	3	12.5	16	2	Q810X4_CRGR	Q810x4 cricetus
290	3	12.5	14	2	Q9KCS9_BACHD	Q9kcs9 bacillus ha	363	3	12.5	16	2	Q9CTB2_MOUSE	Q9ctb2 mus musculu
291	3	12.5	14	2	Q73591_CHICK	Q73591 gallus gall	364	3	12.5	16	2	Q04246_9PARA	Q04246 sendai viru
292	3	12.5	14	2	Q07378_COTCO	Q07378 coturnix co	365	3	12.5	16	2	Q718K5_9PARA	Q718k5 newcastle d
293	3	12.5	15	1	COXSA_SCYCA	P83012 scyliorhinu	366	3	12.5	16	2	Q99154_9PARA	Q99154 sendai viru
294	3	12.5	15	1	FIBA_ANAPL	P12801 anas platyr	367	3	12.5	16	2	Q7LZS2_XENLA	Q7lzs2 xenopus lae
295	3	12.5	15	1	LECB2_PSOSC	P22585 psophocartu	368	3	12.5	16	2	Q75710_9HIV1	Q75710 human immun
296	3	12.5	15	1	LG29_VIGUS	P83955 vigna ungui	369	3	12.5	17	1	BIOP1_EHYTH	P84521 phyllomedus
297	3	12.5	15	1	LG31_VIGUS	P83956 vigna ungui	370	3	12.5	17	1	CHX1_ASPFL	P83488 aspergillus
298	3	12.5	15	1	TLP_CASCH	P83957 castanopsis	371	3	12.5	17	1	LPW_CORGL	P06556 corynebacte
299	3	12.5	15	2	Q7M4Y4_FUSSP	Q7m4y4 fusarium sp	372	3	12.5	17	1	RACYE_RANES	P83663 rana escul
300	3	12.5	15	2	Q7M4Z3_FUSSP	Q7m4z3 fusarium sp	373	3	12.5	17	2	Q95795_HUMAN	Q95795 homo sapien
301	3	12.5	15	2	Q7S219_NEUCR	Q7s219 neurospora	374	3	12.5	17	2	Q7KZ00_HUMAN	Q7kz00 homo sapien
302	3	12.5	15	2	Q43378_9LECA	Q4w378 neurospora	375	3	12.5	17	2	Q92727_HUMAN	Q92727 homo sapien
303	3	12.5	15	2	Q13377_HUMAN	Q13377 homo sapien	376	3	12.5	17	2	Q9UCD3_HUMAN	Q9ucd3 homo sapien
304	3	12.5	15	2	Q7M4R1_HUMAN	Q7m4r1 homo sapien	377	3	12.5	17	2	Q9UCP4_HUMAN	Q9ucp4 homo sapien
305	3	12.5	15	2	Q5C1X6_SCHJA	Q5c1x6 schistosoma	378	3	12.5	17	2	Q61238_ONCVO	Q61238 onchocerca
306	3	12.5	15	2	P82206_BOMJO	P82206 bombyx mori	379	3	12.5	17	2	Q5BX20_SCHJA	Q5bx20 schistosoma
307	3	12.5	15	2	Q9TWE9_GALME	Q9twe9 galleria me	380	3	12.5	17	2	Q5K157_DROBP	Q5k157 drosophila
308	3	12.5	15	2	Q7RHM0_PLAYO	Q7rhm0 plasmodium	381	3	12.5	17	2	Q6E154_BIOGL	Q6e154 biophalari
309	3	12.5	15	2	Q4X8J7_PLACH	Q4x8j7 plasmodium	382	3	12.5	17	2	Q8HKG6_9ACAR	Q8hkg6 boophilus k
310	3	12.5	15	2	Q4XH30_PLACH	Q4xh30 plasmodium	383	3	12.5	17	2	Q7R6U3_PLAYO	Q7r6u3 plasmodium
311	3	12.5	15	2	Q6JHD7_CANFA	Q6jhd7 canis famil	384	3	12.5	17	2	Q7RAJ1_PLAYO	Q7raj1 plasmodium
312	3	12.5	15	2	Q85C67_9ROSI	Q85c67 clusia mult	385	3	12.5	17	2	Q7RCI9_PLAYO	Q7rci9 plasmodium
313	3	12.5	15	2	Q85C68_9ROSI	Q85c68 clusia mino	386	3	12.5	17	2	Q7RQU2_PLAYO	Q7rqu2 plasmodium
314	3	12.5	15	2	Q85C69_9ROSI	Q85c69 clusia duc	387	3	12.5	17	2	Q4X3Y9_PLACH	Q4x3y9 plasmodium
315	3	12.5	15	2	Q85XD9_9ROSI	Q85xd9 clusia vale	388	3	12.5	17	2	Q4X4S0_PLACH	Q4x4s0 plasmodium
316	3	12.5	15	2	Q85XBI_9ROSI	Q85xbi clusia-toxr	389	3	12.5	17	2	Q4X8E1_PLACH	Q4x8e1 plasmodium
317	3	12.5	15	2	Q85XE3_9ROSI	Q85xe3 clusia tocu	390	3	12.5	17	2	Q4XB01_PLACH	Q4xb01 plasmodium
318	3	12.5	15	2	Q85XE5_9ROSI	Q85xe5 clusia sten	391	3	12.5	17	2	Q4XB08_PLACH	Q4xb08 plasmodium
319	3	12.5	15	2	Q85XE7_9ROSI	Q85xe7 clusia rose	392	3	12.5	17	2	Q4XT04_PLACH	Q4xt04 plasmodium
320	3	12.5	15	2	Q85XE9_9ROSI	Q85xe9 clusia nemo	393	3	12.5	17	2	Q95JAI_PIG	Q95jai sus scrofa
321	3	12.5	15	2	Q85XF2_9ROSI	Q85xf2 clusia majo	394	3	12.5	17	2	Q714T4_9RHOD	Q714t4 rhodosorus
322	3	12.5	15	2	Q85XFP_9ROSI	Q85xf4 clusia lanc	395	3	12.5	17	2	Q7XY76_9ROSI	Q7xy76 kandelia ca
323	3	12.5	15	2	Q85XF6_9ROSI	Q85xf6 clusia inte	396	3	12.5	17	2	Q7YMZ1_9BRYO	Q7ymz1 porotrichum

397	3	12.5	17	2	Q7YM24_9BRVO	Q7ymz4	porothamni	470	3	12.5	18	2	Q73559_9HIV1	Q73559	human	immun
398	3	12.5	17	2	Q7YN51_HOOLU	Q7yn51	hookeria lu	471	3	12.5	18	2	Q73561_9HIV1	Q73561	human	immun
399	3	12.5	17	2	Q85UP3_9BRIO	Q85up3	acroccladium	472	3	12.5	18	2	Q73563_9HIV1	Q73563	human	immun
400	3	12.5	17	2	Q8HAS3_MAIZE	Q8has3	zea mays (m	473	3	12.5	18	2	Q73565_9HIV1	Q73565	human	immun
401	3	12.5	17	2	Q8HCD7_MAIZE	Q8hcd7	zea mays (m	474	3	12.5	18	2	Q73567_9HIV1	Q73567	human	immun
402	3	12.5	17	2	Q9S7E8_ARATH	Q9s7e8	arabidopsis	475	3	12.5	18	2	Q73569_9HIV1	Q73569	human	immun
403	3	12.5	17	2	Q6UGR4_PETHV	Q6ugr4	petunia hyb	476	3	12.5	18	2	Q73571_9HIV1	Q73571	human	immun
404	3	12.5	17	2	Q7X4Q4_NODSP	Q7x4q4	nodularia s	477	3	12.5	18	2	Q73573_9HIV1	Q73573	human	immun
405	3	12.5	17	2	Q4ZGZ9_5CHRO	Q4zgz9	aphanocapea	478	3	12.5	18	2	Q73575_9HIV1	Q73575	human	immun
406	3	12.5	17	2	Q9QVC2_9MURI	Q9qvc2	rattus sp.	479	3	12.5	18	2	Q73577_9HIV1	Q73577	human	immun
407	3	12.5	17	2	Q9QVH8_9MURI	Q9qv8	mus sp. sup	480	3	12.5	18	2	Q73579_9HIV1	Q73579	human	immun
408	3	12.5	17	2	Q8QVK3_9MURI	Q8gvk3	rattus sp.	481	3	12.5	18	2	Q73581_9HIV1	Q73581	human	immun
409	3	12.5	17	2	Q8QVK3_MOUSE	Q8gvk3	mus musculus	482	3	12.5	18	2	Q73583_9HIV1	Q73583	human	immun
410	3	12.5	17	2	Q6PV10_9HEPC	Q6pv10	hepatitis c	483	3	12.5	18	2	Q73585_9HIV1	Q73585	human	immun
411	3	12.5	17	2	Q6PV18_9HEPC	Q6pv18	hepatitis c	484	3	12.5	18	2	Q73587_9HIV1	Q73587	human	immun
412	3	12.5	17	2	Q6PV21_9HEPC	Q6pv21	hepatitis c	485	3	12.5	18	2	Q73589_9HIV1	Q73589	human	immun
413	3	12.5	17	2	Q9DFB5_BRARE	Q9dfb5	brachydanio	486	3	12.5	18	2	Q73591_9HIV1	Q73591	human	immun
414	3	12.5	17	2	Q73531_9HIV1	Q73531	human immun	487	3	12.5	18	2	Q73593_9HIV1	Q73593	human	immun
415	3	12.5	17	2	Q73533_9HIV1	Q73533	human immun	488	3	12.5	18	2	Q73595_9HIV1	Q73595	human	immun
416	3	12.5	17	2	Q73535_9HIV1	Q73535	human immun	489	3	12.5	18	2	Q73597_9HIV1	Q73597	human	immun
417	3	12.5	17	2	Q73537_9HIV1	Q73537	human immun	490	3	12.5	18	2	Q73599_9HIV1	Q73599	human	immun
418	3	12.5	17	2	Q73539_9HIV1	Q73539	human immun	491	3	12.5	18	2	Q73601_9HIV1	Q73601	human	immun
419	3	12.5	17	2	Q73541_9HIV1	Q73541	human immun	492	3	12.5	18	2	Q73603_9HIV1	Q73603	human	immun
420	3	12.5	17	2	Q73543_9HIV1	Q73543	human immun	493	3	12.5	18	2	Q73605_9HIV1	Q73605	human	immun
421	3	12.5	17	2	Q73545_9HIV1	Q73545	human immun	494	3	12.5	18	2	Q73607_9HIV1	Q73607	human	immun
422	3	12.5	17	2	Q73547_9HIV1	Q73547	human immun	495	3	12.5	18	2	Q73609_9HIV1	Q73609	human	immun
423	3	12.5	17	2	Q73611_9HIV1	Q73611	human immun	496	3	12.5	18	2	Q73613_9HIV1	Q73613	human	immun
424	3	12.5	18	1	AROF_STRMB	P80575	streptomyce	497	3	12.5	18	2	Q73615_9HIV1	Q73615	human	immun
425	3	12.5	18	1	SULT_1CTPU	P82609	ictalurus p	498	3	12.5	18	2	Q73617_9HIV1	Q73617	human	immun
426	3	12.5	18	1	TAMP_STRMB	P83543	streptomyce	499	3	12.5	18	2	Q73619_9HIV1	Q73619	human	immun
427	3	12.5	18	2	Q7S757_NEUCR	Q7s757	neurospora	500	3	12.5	18	2	Q73621_9HIV1	Q73621	human	immun
428	3	12.5	18	2	Q9UC87_HUMAN	Q9uc87	homo sapien	501	3	12.5	18	2	Q73623_9HIV1	Q73623	human	immun
429	3	12.5	18	2	Q6LCK5_HUMAN	Q6lck5	homo sapien	502	3	12.5	18	2	Q73625_9HIV1	Q73625	human	immun
430	3	12.5	18	2	Q5BRP6_SCHJA	Q5brp6	schistosoma	503	3	12.5	18	2	Q73627_9HIV1	Q73627	human	immun
431	3	12.5	18	2	Q5BY25_SCHJA	Q5by25	schistosoma	504	3	12.5	18	2	Q73629_9HIV1	Q73629	human	immun
432	3	12.5	18	2	Q5K168_9DIPT	Q5k168	drosophila	505	3	12.5	18	2	Q73631_9HIV1	Q73631	human	immun
433	3	12.5	18	2	Q6JCM1_9HMYE	Q6jcm1	prenolepis	506	3	12.5	18	2	Q73633_9HIV1	Q73633	human	immun
434	3	12.5	18	2	Q8HK12_9ACAR	Q8hk12	apronoma co	507	3	12.5	18	2	Q73635_9HIV1	Q73635	human	immun
435	3	12.5	18	2	Q9X7V8_9HMYE	Q9x7v8	gryon sp. c	508	3	12.5	18	2	Q73637_9HIV1	Q73637	human	immun
436	3	12.5	18	2	Q4X7V0_PLACH	Q4x7v0	plasmidium	509	3	12.5	18	2	Q73639_9HIV1	Q73639	human	immun
437	3	12.5	18	2	Q4XKC9_PLACH	Q4xkc9	plasmidium	510	3	12.5	18	2	Q73641_9HIV1	Q73641	human	immun
438	3	12.5	18	2	Q4XKA7_PLACH	Q4xka7	plasmidium	511	3	12.5	18	2	Q73643_9HIV1	Q73643	human	immun
439	3	12.5	18	2	Q4Y8A5_PLACH	Q4y8a5	plasmidium	512	3	12.5	18	2	Q73645_9HIV1	Q73645	human	immun
440	3	12.5	18	2	Q4YAB9_PLACH	Q4yab9	plasmidium	513	3	12.5	18	2	Q73647_9HIV1	Q73647	human	immun
441	3	12.5	18	2	Q4YIB9_PLACH	Q4yib9	plasmidium	514	3	12.5	18	2	Q73649_9HIV1	Q73649	human	immun
442	3	12.5	18	2	Q4Z4N4_PLACH	Q4z4n4	plasmidium	515	3	12.5	18	2	Q73651_9HIV1	Q73651	human	immun
443	3	12.5	18	2	Q4Z7I4_PLACH	Q4z7i4	plasmidium	516	3	12.5	18	2	Q73653_9HIV1	Q73653	human	immun
444	3	12.5	18	2	Q7M3F4_RABIT	Q7m3f4	oryctolagus	517	3	12.5	18	2	Q73655_9HIV1	Q73655	human	immun
445	3	12.5	18	2	Q9TQRO_FIG	Q9tqr0	sus scrofa	518	3	12.5	18	2	Q73657_9HIV1	Q73657	human	immun
446	3	12.5	18	2	Q9TRG2_RABIT	Q9trg2	oryctolagus	519	3	12.5	18	2	Q73659_9HIV1	Q73659	human	immun
447	3	12.5	18	2	Q9TS26_FIG	Q9te26	sus scrofa	520	3	12.5	18	2	Q73661_9HIV1	Q73661	human	immun
448	3	12.5	18	2	Q64353_BFN15	O64353	bacterioph	521	3	12.5	19	1	CUCN_CUCNA	P84158	cucurbita m	
449	3	12.5	18	2	O19969_GOSAR	O19969	gossypium a	522	3	12.5	19	1	CX6A2_SHEEP	P61901	ovis aries	
450	3	12.5	18	2	O19979_GOSDA	O19979	gossypium d	523	3	12.5	19	1	LPRM_STAAR	P03063	staphylococ	
451	3	12.5	18	2	O85UNI_9BRVO	O85un1	camptochaet	524	3	12.5	19	1	Q7603_HUMAN	Q07603	homo sapien	
452	3	12.5	18	2	Q9S7E5_ARATH	Q9s7e5	arabidopsis	525	3	12.5	19	2	Q9UDB7_HUMAN	Q9udb7	homo sapien	
453	3	12.5	18	2	Q9ZG65_CHLTR	Q9zge5	chlamydia t	526	3	12.5	19	2	Q9Y3R8_HUMAN	Q9y3r8	homo sapien	
454	3	12.5	18	2	Q9R334_PSEME	Q9r334	pseudomonas	527	3	12.5	19	2	Q7M4R0_HUMAN	Q7m4r0	homo sapien	
455	3	12.5	18	2	Q49250_MYCGE	Q49250	mycoplasma	528	3	12.5	19	2	Q9BVX6_HUMAN	Q9bv6	homo sapien	
456	3	12.5	18	2	Q61840_MOUSE	Q61840	mus musculus	529	3	12.5	19	2	Q4TMD9_HUMAN	Q4tmd9	homo sapien	
457	3	12.5	18	2	Q61CE8_MOUSE	Q61ce8	mus musculus	530	3	12.5	19	2	Q5C5Q4_SCHJA	Q5c5q4	schistosoma	
458	3	12.5	18	2	Q99MDS_MOUSE	Q99md5	mus musculus	531	3	12.5	19	2	Q8T3N1_DROME	Q8t3n1	drosophila	
459	3	12.5	18	2	Q77WL5_ADE04	Q77wl5	human adeno	532	3	12.5	19	2	Q9GNL6_DROR	Q9gnl6	drosophila	
460	3	12.5	18	2	Q9DSS9_ADE04	Q9dss9	human adeno	533	3	12.5	19	2	Q952L3_SCHJA	Q952l3	diadema ant	
461	3	12.5	18	2	Q9W9C1_ADE04	Q9w9c1	human adeno	534	3	12.5	19	2	Q4X4E2_PLACH	Q4x4e2	plasmidium	
462	3	12.5	18	2	Q94PS2_9PERC	Q94ps2	macropodus	535	3	12.5	19	2	Q4XAW0_PLACH	Q4xaw0	plasmidium	
463	3	12.5	18	2	Q9PSD2_CHICK	Q9psd2	gallus gall	536	3	12.5	19	2	Q4XJZ2_PLACH	Q4xjz2	plasmidium	
464	3	12.5	18	2	Q73511_9HIV1	Q73511	human immun	537	3	12.5	19	2	Q4XQC6_PLACH	Q4xqc6	plasmidium	
465	3	12.5	18	2	Q73523_9HIV1	Q73523	human immun	538	3	12.5	19	2	Q4XUR2_PLACH	Q4xur2	plasmidium	
466	3	12.5	18	2	Q73549_9HIV1	Q73549	human immun	539	3	12.5	19	2	Q4Y326_PLACH	Q4y326	plasmidium	
467	3	12.5	18	2	Q73551_9HIV1	Q73551	human immun	540	3	12.5	19	2	Q4Y4A8_PLACH	Q4y4a8	plasmidium	
468	3	12.5	18	2	Q73553_9HIV1	Q73553	human immun	541	3	12.5	19	2	Q4YJU3_PLACH	Q4yju3	plasmidium	
469	3	12.5	18	2	Q73555_9HIV1	Q73555	human immun	542	3	12.5	19	2	Q4YSN2_PLACH	Q4ysn2	plasmidium	

543	3	12.5	19	2	Q7M221_SHEEP	Q7m221 ovis aries	616	3	12.5	20	2	Q426T1_PLABE	Q426t1 plasmodium
544	3	12.5	19	2	Q7M222_PIG	Q7m222 sus scrofa	617	3	12.5	20	2	Q7M357_PIG	Q7m357 sus scrofa
545	3	12.5	19	2	Q82685_GERHY	Q82685 gerbera hyb	618	3	12.5	20	2	Q7M2X3_BOVIN	Q7m2x3 bos taurus
546	3	12.5	19	2	Q39381_BRAOL	Q39381 brassica ol	619	3	12.5	20	2	Q39458_BPPH1	Q39458 bacterioph
547	3	12.5	19	2	Q41466_SOLITU	Q41466 solanum tub	620	3	12.5	20	2	Q41468_SOLITU	Q41468 solanum tub
548	3	12.5	19	2	Q41471_SOLITU	Q41471 solanum tub	621	3	12.5	20	2	Q41469_SOLITU	Q41469 solanum tub
549	3	12.5	19	2	Q41474_SOLITU	Q41474 solanum tub	622	3	12.5	20	2	Q41475_SOLITU	Q41475 solanum tub
550	3	12.5	19	2	Q8LVH6_9STRA	Q8lvh6 aulacoseira	623	3	12.5	20	2	Q5J4U3_9POAL	Q5j4u3 phyllostach
551	3	12.5	19	2	Q8MCJ2_9STRA	Q8mcj2 aulacoseira	624	3	12.5	20	2	Q5J4U4_9ORYZ	Q5j4u4 chikusichlo
552	3	12.5	19	2	Q8MCJ2_9STRA	Q8mcj2 aulacoseira	625	3	12.5	20	2	Q5J4U5_9ORYZ	Q5j4u5 hygryryza a
553	3	12.5	19	2	Q9S8G6_COLES	Q9s8g6 colocasia e	626	3	12.5	20	2	Q5J4U6_9ORYZ	Q5j4u6 luziola lei
554	3	12.5	19	2	Q562K7_ARATH	Q562k7 arabidopsis	627	3	12.5	20	2	Q5J4U7_9ORYZ	Q5j4u7 rhynchoryza
555	3	12.5	19	2	Q05601_PSSSP	Q05601 pseudomonas	628	3	12.5	20	2	Q5J4U8_9ORYZ	Q5j4u8 potamophila
556	3	12.5	19	2	Q07479_STRYP	Q07479 streptococc	629	3	12.5	20	2	Q5J4U9_9ORYZ	Q5j4u9 prophytoch
557	3	12.5	19	2	Q57313_9STAP	Q57313 staphylococ	630	3	12.5	20	2	Q5J4V0_9ORYZ	Q5j4v0 zizaniopsis
558	3	12.5	19	2	Q5DU98_9STAP	Q5du98 staphylococ	631	3	12.5	20	2	Q5J4V1_9ORYZ	Q5j4v1 zizania lat
559	3	12.5	19	2	Q799A5_STAAU	Q799a5 staphylococ	632	3	12.5	20	2	Q5J4V2_9ORYZ	Q5j4v2 leersia hex
560	3	12.5	19	2	Q799E4_STARP	Q799e4 staphylococ	633	3	12.5	20	2	Q5J4V3_9ORYZ	Q5j4v3 leersia tis
561	3	12.5	19	2	Q7AY86_9STAP	Q7ay86 staphylococ	634	3	12.5	20	2	Q5J4V4_9ORYZ	Q5j4v4 oryza granu
562	3	12.5	19	2	Q7WS42_NODSP	Q7ws42 nodularia s	635	3	12.5	20	2	Q5J4V5_9ORYZ	Q5j4v5 oryza austr
563	3	12.5	19	2	Q9EWB6_STAIN	Q9ewb6 staphylococ	636	3	12.5	20	2	Q5J4V6_9ORYZ	Q5j4v6 oryza schle
564	3	12.5	19	2	Q45558_BACSH	Q45558 bacillus sp	637	3	12.5	20	2	Q5J4V7_9ORYZ	Q5j4v7 oryza coarc
565	3	12.5	19	2	Q57012_STAAU	Q57012 staphylococ	638	3	12.5	20	2	Q5J4V8_9ORYZ	Q5j4v8 oryza brach
566	3	12.5	19	2	Q7MQQ1_PSEPU	Q7mqq1 pseudomonas	639	3	12.5	20	2	Q5J4V9_9ORYZ	Q5j4v9 oryza longi
567	3	12.5	19	2	Q799W9_STAHO	Q799w9 staphylococ	640	3	12.5	20	2	Q5J4W0_9ORYZ	Q5j4w0 oryza offic
568	3	12.5	19	2	Q4JH5 STAAU	Q4jhh5 staphylococ	641	3	12.5	20	2	Q5J4W1_ORYPU	Q5j4w1 oryza punct
569	3	12.5	19	2	Q5HNP7_STABO	Q5hnp7 staphylococ	642	3	12.5	20	2	Q5J4W2_ORYSA	Q5j4w2 oryza sattiv
570	3	12.5	19	2	P70242_MOUSE	P70242 mus musculu	643	3	12.5	20	2	P82940_HORVU	P82940 hordeum vul
571	3	12.5	19	2	P97555_RAT	P97555 rattus norv	644	3	12.5	20	2	P83423_9ROSA	P83423 morus nigra
572	3	12.5	19	2	Q78DW0_RAT	Q78dw0 rattus norv	645	3	12.5	20	2	Q9S8B8_LUPAL	Q9s8b8 lupinus alb
573	3	12.5	19	2	Q80263_MOUSE	Q80263 mus musculu	646	3	12.5	20	2	Q9S8H1_HORVU	Q9s8h1 hordeum vul
574	3	12.5	19	2	Q8K520_MOUSE	Q8k520 mus musculu	647	3	12.5	20	2	Q9S8J5_PSGTE	Q9s8j5 psophocarpu
575	3	12.5	19	2	Q921B7_MOUSE	Q921b7 mus musculu	648	3	12.5	20	2	Q9S8K0_SOLITU	Q9s8k0 solanum tub
576	3	12.5	19	2	Q9QVN1_9MURI	Q9qvn1 rattus sp.	649	3	12.5	20	2	Q9S8T0_ARTIN	Q9s8t0 artocarpus
577	3	12.5	19	2	Q652S2_MOUSE	Q652s2 mus musculu	650	3	12.5	20	2	Q9S930_SOYBN	Q9s930 glycine max
578	3	12.5	19	2	Q6L8G3_9ZZZZ	Q6l8g3 plaemid prj	651	3	12.5	20	2	Q9SAN5_ARATH	Q9san5 arabidopsis
579	3	12.5	19	2	Q79DT6_9ZZZZ	Q79dt6 plaemid prj	652	3	12.5	20	2	Q9T2K2_PEA	Q9t2k2 pieum sattiv
580	3	12.5	19	2	Q65747_9REOV	Q65747 bluetongue	653	3	12.5	20	2	Q9S8B2_PPAVU	Q9s8b2 phaseolus v
581	3	12.5	19	2	Q9YQW7_9GEMI	Q9yqw7 tomato yell	654	3	12.5	20	2	Q51950_CHLTR	Q51950 chlamydia t
582	3	12.5	19	2	Q7LZW5_HV1	Q7lzw5 human herpe	655	3	12.5	20	2	Q51952_CHLTR	Q51952 chlamydia t
583	3	12.5	19	2	Q85728_9GAMR	Q85728 spleen necr	656	3	12.5	20	2	Q7BVQ6_MYCHY	Q7bvq6 mycoplasma
584	3	12.5	20	1	CER1_CICAR	C83987 ciccer ariet	657	3	12.5	20	2	Q7M0N9_NEIME	Q7m0n9 neisseria m
585	3	12.5	20	1	COXM_THUOB	P80981 thunnus obe	658	3	12.5	20	2	Q7X4Q6_NODSP	Q7x4q6 nodularia s
586	3	12.5	20	1	LEC1_ARTIN	P18571 artocarpus	659	3	12.5	20	2	Q8KTB3_RICHE	Q8ktb3 rickettsia
587	3	12.5	20	1	LEC3_ARTIN	P18573 artocarpus	660	3	12.5	20	2	Q9R4A6_HVDTH	Q9r4a6 hydrogenoba
588	3	12.5	20	1	PGK_BACE	P83075 bacillus ce	661	3	12.5	20	2	Q9R551_BACME	Q9r551 bacillus me
589	3	12.5	20	1	PLS_LUFLU	P83367 lupinus lut	662	3	12.5	20	2	Q9R5Q4_BURCE	Q9r5q4 burkholderi
590	3	12.5	20	1	RIPX_CUCPE	P80750 cucurbita p	663	3	12.5	20	2	P96173_9VIBR	P96173 vibrio sp.
591	3	12.5	20	2	P82263_ASPPU	P82263 aspergillus	664	3	12.5	20	2	Q56130_SALTY	Q56130 salmonella
592	3	12.5	20	2	Q9URC7_YEAST	Q9urc7 saccharomyc	665	3	12.5	20	2	Q64619_RAT	Q64619 rattus norv
593	3	12.5	20	2	Q33623_MAGGR	Q33623 magnaporthe	666	3	12.5	20	2	Q6V0Z2_MUSSP	Q6v0z2 mus spretus
594	3	12.5	20	2	Q7MAQ3_HUMAN	Q7maq3 homo sapien	667	3	12.5	20	2	Q7M023_9MURI	Q7m023 rattus sp.
595	3	12.5	20	2	Q9NZC6_HUMAN	Q9nzc6 homo sapien	668	3	12.5	20	2	Q80Z28_MOUSE	Q80z28 mus musculu
596	3	12.5	20	2	Q9UC20_HUMAN	Q9uc20 homo sapien	669	3	12.5	20	2	Q9ET00_MOUSE	Q9et00 mus musculu
597	3	12.5	20	2	Q9UC86_HUMAN	Q9uc86 homo sapien	670	3	12.5	20	2	Q9QVH2_9MURI	Q9qvhi2 rattus sp.
598	3	12.5	20	2	Q96B47_HUMAN	Q96b47 homo sapien	671	3	12.5	20	2	Q7M0E1_MBSAU	Q7m0e1 mesocricetu
599	3	12.5	20	2	Q9UMU3_HUMAN	Q9umu3 homo sapien	672	3	12.5	20	2	Q84860_9ENTO	Q84860 unidentified
600	3	12.5	20	2	Q37688_9HYME	Q37688 tetraponera	673	3	12.5	20	2	Q86941_9GNMA	Q86941 human herpe
601	3	12.5	20	2	Q5C711_SCHJA	Q5c711 schistosoma	674	3	12.5	20	2	Q86942_9GAMA	Q86942 human herpe
602	3	12.5	20	2	P82215_BOMMO	P82215 bombyx mori	675	3	12.5	20	2	Q912B0_9VIRU	Q912b0 human eryth
603	3	12.5	20	2	Q9GNL7_DROER	Q9gnl7 drosophila	676	3	12.5	20	2	Q912B2_PAVHB	Q912b2 human parvo
604	3	12.5	20	2	Q9TWM1_9TRYP	Q9twm1 trypanosoma	677	3	12.5	20	2	Q912B4_9VIRU	Q912b4 human eryth
605	3	12.5	20	2	Q7RLS2_PLAYO	Q7rls2 plasmodium	678	3	12.5	20	2	Q77859_9RENI	Q77859 oreochromis
606	3	12.5	20	2	Q7BSI9_PLAYO	Q7rsi9 plasmodium	679	3	12.5	20	2	Q7LZ36_RANCA	Q7l236 rana cateeb
607	3	12.5	20	2	Q4XFU6_PLACH	Q4xfu6 plasmodium	680	3	12.5	20	2	Q918U3_FUGRU	Q918u3 fugu rubrip
608	3	12.5	20	2	Q4XKU0_PLACH	Q4xku0 plasmodium	681	3	12.5	20	2	Q9PS63_CHICK	Q9ps63 gallus gall
609	3	12.5	20	2	Q4XU12_PLACH	Q4xu12 plasmodium	682	3	12.5	20	2	Q9PSH5_CHICK	Q9ps5 gallus gall
610	3	12.5	20	2	Q4Y2H3_PLACH	Q4y2h3 plasmodium	683	3	12.5	20	2	Q73917_9HIV1	Q73917 human immun
611	3	12.5	20	2	Q4VB80_PLABE	Q4vb80 plasmodium	684	3	12.5	20	2	Q73918_9HIV1	Q73918 human immun
612	3	12.5	20	2	Q4YCL5_PLABE	Q4ycl5 plasmodium	685	3	12.5	20	2	Q78486_9HIV1	Q78486 human immun
613	3	12.5	20	2	Q4YJK5_PLABE	Q4yjk5 plasmodium	686	3	12.5	21	1	CLH2_CHEAL	P59678 chenopodium
614	3	12.5	20	2	Q42105_PLABE	Q42105 plasmodium	687	3	12.5	21	1	LEC2_ARTIN	P18672 artocarpus
615	3	12.5	20	2	Q42422_PLABE	Q42422 plasmodium	688	3	12.5	21	2	Q9UW10_9EURY	Q9uw10 thermococcu

689	3	12.5	21	2	Q96W03_FUSOX	Q96W03 fusarium ox	762	3	12.5	21	2	Q958Y4_LUPAR	Q958Y4 lupinus arb
690	3	12.5	21	2	Q16366_HUMAN	Q16366 homo sapien	763	3	12.5	21	2	Q56YE9_ARATH	Q56YE9 arabidopsis
691	3	12.5	21	2	Q6LD69_HUMAN	Q6LD69 homo sapien	764	3	12.5	21	2	Q6SKV4_9NARC	Q6SKV4 trichocolea
692	3	12.5	21	2	Q9UC66_HUMAN	Q9UC66 homo sapien	765	3	12.5	21	2	Q7X6U6_CAPBU	Q7X6U6 capsella bu
693	3	12.5	21	2	Q9UCC5_HUMAN	Q9UCC5 homo sapien	766	3	12.5	21	2	Q7X6U5_9BRAS	Q7X6U5 capsella ru
694	3	12.5	21	2	Q9UCH7_HUMAN	Q9UCH7 homo sapien	767	3	12.5	21	2	Q7X6U4_9BRAS	Q7X6U4 capsella ru
695	3	12.5	21	2	Q6LAB3_HUMAN	Q6LAB3 homo sapien	768	3	12.5	21	2	Q7X6U3_9BRAS	Q7X6U3 guillenia f
696	3	12.5	21	2	Q75MT3_HUMAN	Q75MT3 homo sapien	769	3	12.5	21	2	Q7X6U2_THLAR	Q7X6U2 lepidium ph
697	3	12.5	21	2	Q6LEI9_STRPU	Q6LEI9 strongyloce	770	3	12.5	21	2	Q44611_9ENTR	Q44611 thlaspi arv
698	3	12.5	21	2	Q7R9W2_PLAYO	Q7R9W2 plasmodium	771	3	12.5	21	2	Q51540_PSEAE	Q51540 buchnera ap
699	3	12.5	21	2	Q7RG18_PLAYO	Q7RG18 plasmodium	772	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 pseudomonas
700	3	12.5	21	2	Q4X3C0_PLAYO	Q4X3C0 plasmodium	773	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
701	3	12.5	21	2	Q4X3C0_PLAYO	Q4X3C0 plasmodium	774	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
702	3	12.5	21	2	Q4X3C0_PLAYO	Q4X3C0 plasmodium	775	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
703	3	12.5	21	2	Q4X406_PLAYO	Q4X406 plasmodium	776	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
704	3	12.5	21	2	Q4X813_PLAYO	Q4X813 plasmodium	777	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
705	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	778	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
706	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	779	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
707	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	780	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
708	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	781	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
709	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	782	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
710	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	783	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
711	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	784	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
712	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	785	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
713	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	786	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
714	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	787	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
715	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	788	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
716	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	789	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
717	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	790	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
718	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	791	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
719	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	792	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
720	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	793	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
721	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	794	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
722	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	795	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
723	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	796	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
724	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	797	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
725	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	798	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
726	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	799	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
727	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	800	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
728	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	801	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
729	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	802	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
730	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	803	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
731	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	804	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
732	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	805	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
733	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	806	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
734	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	807	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
735	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	808	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
736	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	809	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
737	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	810	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
738	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	811	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
739	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	812	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
740	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	813	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
741	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	814	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
742	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	815	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
743	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	816	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
744	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	817	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
745	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	818	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
746	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	819	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
747	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	820	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
748	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	821	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
749	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	822	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
750	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	823	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
751	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	824	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
752	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	825	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
753	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	826	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
754	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	827	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
755	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	828	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
756	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	829	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
757	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	830	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
758	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	831	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
759	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	832	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
760	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	833	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
761	3	12.5	21	2	Q4XK54_PLAYO	Q4XK54 plasmodium	834	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri



835	3	12.5	22	2	2	0616B1_ECOLI	0616B1_escherichia	908	3	12.5	23	2	2	Q8MFJ5_9FILI	Q8mfj5 hymenophyll
836	3	12.5	22	2	2	0616B8_ECOLI	0616B8_escherichia	909	3	12.5	23	2	2	Q8WBC5_CUCMO	Q8wbc5 cucurbita m
837	3	12.5	22	2	2	079DL8_CHLTR	079dl8 chlamydia t	910	3	12.5	23	2	2	Q9S893_ARAHY	Q9s893 arachis hyp
838	3	12.5	22	2	2	084EW2_LACFE	084ew2 lactobacill	911	3	12.5	23	2	2	Q9SC59_PICAB	Q9sc59 picea abies
839	3	12.5	22	2	2	093R63_YERPE	093r63 yersinia pe	912	3	12.5	23	2	2	Q9SC60_PICAB	Q9sc60 picea abies
840	3	12.5	22	2	2	09FS11_ECOLI	09fs11 escherichia	913	3	12.5	23	2	2	Q9SC61_PICAB	Q9sc61 picea abies
841	3	12.5	22	2	2	09R8J6_CHLTR	09r8j6 chlamydia t	914	3	12.5	23	2	2	Q8SUU4_ANTFO	Q8suu4 anthoceros
842	3	12.5	22	2	2	09R8J8_CHLTR	09r8j8 chlamydia t	915	3	12.5	23	2	2	Q9T3F1_9CHLO	Q9t3f1 bryopsis sp
843	3	12.5	22	2	2	09R8K1_CHLTR	09r8k1 chlamydia t	916	3	12.5	23	2	2	Q9T3F2_9CHLO	Q9t3f2 bryopsis sp
844	3	12.5	22	2	2	09R8K3_CHLTR	09r8k3 chlamydia t	917	3	12.5	23	2	2	Q9T3F3_9CHLO	Q9t3f3 bryopsis sp
845	3	12.5	22	2	2	09R8K5_CHLTR	09r8k5 chlamydia t	918	3	12.5	23	2	2	Q9T4C9_9CHLO	Q9t4c9 bryopsis sp
846	3	12.5	22	2	2	09R8K8_CHLTR	09r8k8 chlamydia t	919	3	12.5	23	2	2	Q9T4Q8_9CHLO	Q9t4q8 bryopsis sp
847	3	12.5	22	2	2	09R8L3_CHLTR	09r8l3 chlamydia t	920	3	12.5	23	2	2	Q9T4R9_9CHLO	Q9t4r9 bryopsis sp
848	3	12.5	22	2	2	09R8L6_CHLTR	09r8l6 chlamydia t	921	3	12.5	23	2	2	Q9THS4_9CHLO	Q9ths4 bryopsis sp
849	3	12.5	22	2	2	09R8L9_CHLTR	09r8l9 chlamydia t	922	3	12.5	23	2	2	Q9THS5_9CHLO	Q9ths5 bryopsis sp
850	3	12.5	22	2	2	09R8M2_CHLTR	09r8m2 chlamydia t	923	3	12.5	23	2	2	Q9TKG7_9CHLO	Q9tkg7 lambda anta
851	3	12.5	22	2	2	09R8M9_CHLTR	09r8m9 chlamydia t	924	3	12.5	23	2	2	Q5G6W7_9ROSA	Q5g6w7 ficus colub
852	3	12.5	22	2	2	09R8N3_CHLTR	09r8n3 chlamydia t	925	3	12.5	23	2	2	Q04274_BORPE	Q04274 bordetella
853	3	12.5	22	2	2	09R8N7_CHLTR	09r8n7 chlamydia t	926	3	12.5	23	2	2	Q59A23_NODSP	Q59a23 nodularia s
854	3	12.5	22	2	2	09R8P3_CHLTR	09r8p3 chlamydia t	927	3	12.5	23	2	2	Q8GL16_BORBU	Q8gl16 borrelia bu
855	3	12.5	22	2	2	09R8P7_CHLTR	09r8p7 chlamydia t	928	3	12.5	23	2	2	Q8KHT3_MYCHO	Q8kht3 mycoplasma
856	3	12.5	22	2	2	09R8P7_CHLTR	09r8p7 chlamydia t	929	3	12.5	23	2	2	Q8AJ07_VIBFI	Q8aj07 vibrio fisc
857	3	12.5	22	2	2	09S551_ACTPL	09s551 actinobacil	930	3	12.5	23	2	2	Q9R3Y4_CLOPE	Q9r3y4 clostridium
858	3	12.5	22	2	2	09KAT7_BACHD	09kat7 bacillus ha	931	3	12.5	23	2	2	Q26030_HELPY	Q26030 helicobacte
859	3	12.5	22	2	2	09QVE0_9MURI	09qve0 rattus sp.	932	3	12.5	23	2	2	Q6GAM3_STAAS	Q6gam3 staphylococ
860	3	12.5	22	2	2	09QWB6_9MURI	09qwb6 mus sp. . s	933	3	12.5	23	2	2	Q6GCP4_STAAR	Q6gcp4 staphylococ
861	3	12.5	22	2	2	Q4H2C4_MESAU	Q4h2c4 mesocricetu	934	3	12.5	23	2	2	Q8VDS5_MOUSE	Q8vds5 mus musculu
862	3	12.5	22	2	2	Q765Z1_CHICK	Q765z1 gallus gall	935	3	12.5	23	2	2	Q61948_MOUSE	Q61948 mus musculu
863	3	12.5	22	2	2	Q7T191_CHICK	Q7t191 gallus gall	936	3	12.5	23	2	2	Q9S553_MOUSE	Q9s553 mus musculu
864	3	12.5	23	1	1	AFP2_BRANA	P30226 brassica na	937	3	12.5	23	2	2	Q8CB74_MOUSE	Q8cb74 mus musculu
865	3	12.5	23	1	1	PA24_BOTAS	Q9prt7 bothrops as	938	3	12.5	23	2	2	Q6H979_VIRU	Q6h979 torque teno
866	3	12.5	23	1	1	UHA4_HUMAN	P49289 homo sapien	939	3	12.5	23	2	2	Q6H983_9VIRU	Q6h983 torque teno
867	3	12.5	23	1	1	XYLC1_ACIGB	P46365 acinetobact	940	3	12.5	23	2	2	Q91KZ6_9MONO	Q91kz6 human metap
868	3	12.5	23	1	1	YFWM_BACSU	Q34890 bacillus su	941	3	12.5	23	2	2	Q91KZ7_9MONO	Q91kz7 human metap
869	3	12.5	23	2	2	O14431_CRYPA	O14431 cryphonectr	942	3	12.5	23	2	2	Q91KZ8_9MONO	Q91kz8 human metap
870	3	12.5	23	2	2	Q96TQ0_FUSOX	Q96tq0 fusarium ox	943	3	12.5	23	2	2	Q91KZ9_9MONO	Q91kz9 human metap
871	3	12.5	23	2	2	Q16209_HUMAN	Q16209 homo sapien	944	3	12.5	23	2	2	Q91L00_9MONO	Q91l00 human metap
872	3	12.5	23	2	2	Q8N674_HUMAN	Q8n674 homo sapien	945	3	12.5	23	2	2	Q91L01_9MONO	Q91l01 human metap
873	3	12.5	23	2	2	Q8N674_HUMAN	Q8n674 homo sapien	946	3	12.5	23	2	2	Q91L02_9MONO	Q91l02 human metap
874	3	12.5	23	2	2	Q8N674_HUMAN	Q8n674 homo sapien	947	3	12.5	23	2	2	Q91L03_9MONO	Q91l03 human metap
875	3	12.5	23	2	2	Q9NS07_HUMAN	Q9ns07 homo sapien	948	3	12.5	23	2	2	Q9PSA8_XENBO	Q9psa8 xenopus bor
876	3	12.5	23	2	2	Q5BR34_SCHJA	Q5br34 schistosoma	949	3	12.5	23	2	2	Q64I71_MELGA	Q64i71 meleagris g
877	3	12.5	23	2	2	Q6QNV8_9CNID	Q6qnv8 anthopleura	950	3	12.5	23	2	2	Q9ESH4_CHICK	Q9esh4 gallus gall
878	3	12.5	23	2	2	Q6QNM5_9CNID	Q6qnm5 anthopleura	951	3	12.5	23	2	2	Q9E8S7_9HIV1	Q9e8s7 human immun
879	3	12.5	23	2	2	Q4X3F1_PLACH	Q4x3f1 plasmodium	952	3	12.5	23	2	2	Q9ENM9_9HIV1	Q9enm9 human immun
880	3	12.5	23	2	2	Q4X443_PLACH	Q4x443 plasmodium	953	3	12.5	23	2	2	Q9QEX5_9HIV1	Q9qex5 human immun
881	3	12.5	23	2	2	Q4X4D7_PLACH	Q4x4d7 plasmodium	954	3	12.5	23	2	2	Q9QEX5_9HIV1	Q9qex5 human immun
882	3	12.5	23	2	2	Q4X514_PLACH	Q4x514 plasmodium	955	3	12.5	23	2	1	COXC_THUOB	P80973 thunus obe
883	3	12.5	23	2	2	Q4XB77_PLACH	Q4xbt7 plasmodium	956	3	12.5	24	1	1	PAN2_PANIM	P23240 pandinus im
884	3	12.5	23	2	2	Q4XCR8_PLACH	Q4xcr8 plasmodium	957	3	12.5	24	1	1	SODC_RANCA	P23217 rana cateeb
885	3	12.5	23	2	2	Q4XEJ3_PLACH	Q4xej3 plasmodium	958	3	12.5	24	2	2	O01228_WILSA	O01228 williopsis
886	3	12.5	23	2	2	Q4XEPI_PLACH	Q4xep1 plasmodium	959	3	12.5	24	2	2	QSMGQ5_PODAN	Qsmgq5 podospira a
887	3	12.5	23	2	2	Q4XF40_PLACH	Q4xf40 plasmodium	960	3	12.5	24	2	2	Q9UR70_ASFPU	Q9ur70 aspergillus
888	3	12.5	23	2	2	Q4XH19_PLACH	Q4xh19 plasmodium	961	3	12.5	24	2	2	Q16333_HUMAN	Q16333 homo sapien
889	3	12.5	23	2	2	Q4XIG4_PLACH	Q4xig4 plasmodium	962	3	12.5	24	2	2	Q86WP5_HUMAN	Q86wp5 homo sapien
890	3	12.5	23	2	2	Q4XKA5_PLACH	Q4xka5 plasmodium	963	3	12.5	24	2	2	Q4VEV5_HUMAN	Q4vev5 homo sapien
891	3	12.5	23	2	2	Q4XMT9_PLACH	Q4xmt9 plasmodium	964	3	12.5	24	2	2	Q5BR43_SCHJA	Q5br43 schistosoma
892	3	12.5	23	2	2	Q4XPS0_PLACH	Q4xps0 plasmodium	965	3	12.5	24	2	2	Q5BVT5_SCHJA	Q5bvt5 schistosoma
893	3	12.5	23	2	2	Q4Y2Q2_PLACH	Q4y2q2 plasmodium	966	3	12.5	24	2	2	Q5BYW2_SCHJA	Q5byw2 schistosoma
894	3	12.5	23	2	2	Q4Y3T7_PLACH	Q4y3t7 plasmodium	967	3	12.5	24	2	2	Q5C2C4_SCHJA	Q5c2c4 schistosoma
895	3	12.5	23	2	2	Q4Y6L9_PLACH	Q4y6l9 plasmodium	968	3	12.5	24	2	2	Q5C644_SCHJA	Q5c644 schistosoma
896	3	12.5	23	2	2	Q4Y811_PLACH	Q4y811 plasmodium	969	3	12.5	24	2	2	Q7M3Q0_LUMRU	Q7m3q0 lumbricus r
897	3	12.5	23	2	2	Q4YAV9_PLABE	Q4yav9 plasmodium	970	3	12.5	24	2	2	Q7YIK2_9PULM	Q7yik2 philonisia
898	3	12.5	23	2	2	Q4YL91_PLABE	Q4yl91 plasmodium	971	3	12.5	24	2	2	Q94XE2_9HEMI	Q94xe2 tectocoris
899	3	12.5	23	2	2	Q4YLG2_PLABE	Q4ylg2 plasmodium	972	3	12.5	24	2	2	Q9GNE5_CABEL	Q9gne5 caenorhabdi
900	3	12.5	23	2	2	Q4YMK2_PLABE	Q4ymk2 plasmodium	973	3	12.5	24	2	2	Q7R8I6_PLAYO	Q7r8i6 plasmodium
901	3	12.5	23	2	2	Q4YMS1_PLABE	Q4yms1 plasmodium	974	3	12.5	24	2	2	Q7RBO0_PLAYO	Q7rbq0 plasmodium
902	3	12.5	23	2	2	Q4YXT6_PLABE	Q4yxt6 plasmodium	975	3	12.5	24	2	2	Q7RL34_PLAYO	Q7rl34 plasmodium
903	3	12.5	23	2	2	Q4YXT8_PLABE	Q4yxt8 plasmodium	976	3	12.5	24	2	2	Q9BM16_DUGTI	Q9bm16 dugesia tig
904	3	12.5	23	2	2	Q4Z0V6_PLABE	Q4z0v6 plasmodium	977	3	12.5	24	2	2	Q4X2M4_PLACH	Q4x2m4 plasmodium
905	3	12.5	23	2	2	Q9TR07_CANFA	Q9tr07 canis famil	978	3	12.5	24	2	2	Q4XA00_PLACH	Q4xa00 plasmodium
906	3	12.5	23	2	2	Q9TRK2_CANFA	Q9trk2 canis famil	979	3	12.5	24	2	2	Q4XA83_PLACH	Q4xa83 plasmodium
907	3	12.5	23	2	2	Q41464_SOLTU	Q41464 solanum tub	980	3	12.5	24	2	2	Q4XFX5_PLACH	Q4xfx5 plasmodium

981 3 12.5 24 2 Q4XB2 PLACH  
 982 3 12.5 24 2 Q4XS8 PLACH  
 983 3 12.5 24 2 Q4XL09 PLACH  
 984 3 12.5 24 2 Q4XTK2 PLACH  
 985 3 12.5 24 2 Q4XUV6 PLACH  
 986 3 12.5 24 2 Q4YIG9 PLACH  
 987 3 12.5 24 2 Q4V667 PLACH  
 988 3 12.5 24 2 Q4V7F5 PLACH  
 989 3 12.5 24 2 Q4Y9Y8 PLACH  
 990 3 12.5 24 2 Q4YAC5 PLACH  
 991 3 12.5 24 2 Q4YD83 PLACH  
 992 3 12.5 24 2 Q4YF84 PLACH  
 993 3 12.5 24 2 Q4YG31 PLACH  
 994 3 12.5 24 2 Q4YGA5 PLACH  
 995 3 12.5 24 2 Q4YGD0 PLACH  
 996 3 12.5 24 2 Q4YGD6 PLACH  
 997 3 12.5 24 2 Q4YGS5 PLACH  
 998 3 12.5 24 2 Q4YJ45 PLACH  
 999 3 12.5 24 2 Q4YLA7 PLACH  
 1000 3 12.5 24 2 Q4YMI4 PLACH

## ALIGNMENTS

RESULT 1  
 Q30135\_HUMAN  
 ID Q30135\_HUMAN PRELIMINARY; PRT; 20 AA.  
 AC Q30135;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE HLA-DRB3 protein (Fragment).  
 GN Name=HLA-DRB3;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=86233452; PubMed=3012569;  
 RA Angelini G., de Preval C., Gorski J., Mach B.;  
 RT "High-resolution analysis of the human HLA-B\* polymorphism by  
 RT hybridization with sequence-specific oligonucleotide probes [published  
 RT erratum appears in Proc Natl Acad Sci U S A 1986 Sep;83(17):6664].";  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:4489-4493(1986).  
 DR EMBL; M13561; AAA59796.1; -; Genomic\_DNA.  
 DR PIR; I59073; I59073.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0045012; F:MHC class II receptor activity; IEA.  
 DR GO; GO:0019884; P:antigen presentation, exogenous antigen; IEA.  
 DR GO; GO:0019886; P:antigen processing, exogenous antigen via M. .; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR000353; MHC\_II\_beta\_N.  
 DR Pfam; PF00969; MHC\_II\_beta; 1.  
 DR ProDom; PD000328; MHC\_II\_beta; 1.  
 DR MHC II; Transmembrane.  
 KW MHC II; Transmembrane.  
 FT NON\_TER 1  
 FT NON\_TER 20  
 FT NON\_TER 20  
 SQ SEQUENCE 20 AA; 2551 MW; 71B5A02E98F4EA97 CRC64;

Query Match 20.8%; Score 5; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDS 5  
 DB 13 LRFDS 17

## RESULT 2

Q4YXD8\_PLABE  
 ID Q4YXD8\_PLABE PRELIMINARY; PRT; 23 AA.  
 AC Q4YXD8;  
 DT 13-SEP-2005 (TREMBLrel. 31, Created)  
 DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 GN ORFNames=PB104671.00.0;  
 OS Plasmodium berghei.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 NCBI\_TaxID=5821;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,  
 RA Herriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,  
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,  
 RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,  
 RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,  
 RA Janse C.J., Barrall B., Turner C.M.R., Waters A.P., Sinden R.S.;  
 RA "A comprehensive survey of the Plasmodium life cycle by genomic,  
 RT transcriptomic, and proteomic analyses.";  
 RL Science 307:82-86(2005).  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; CAAT01001922; CAH97317.1; -; Genomic\_DNA.  
 KW Hypothetical protein.  
 FT NON\_TER 1  
 SQ SEQUENCE 23 AA; 2887 MW; 909377810867FBB0 CRC64;  
 Query Match 20.8%; Score 5; DB 2; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 4e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 16 NNNNS 20  
 DB 16 NNNNS 20  
 RESULT 3  
 Q7REJ5\_PLAYO  
 ID Q7REJ5\_PLAYO PRELIMINARY; PRT; 25 AA.  
 AC Q7REJ5;  
 DT 01-MAR-2004 (TREMBLrel. 26, Created)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 GN Name=PY05069;  
 OS Plasmodium yoelii yoelii  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 NCBI\_TaxID=73239;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=17XNL;  
 RX MEDLINE=2255706; PubMed=12368865; DOI=10.1038/nature01099;  
 RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perte M.,  
 RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,  
 RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,  
 RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,  
 RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,  
 RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,  
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Valdivia A.B.,  
 RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,  
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,  
 RA Carucci D.J.;  
 RA "Genome sequence and comparative analysis of the model rodent malaria  
 RT parasite Plasmodium yoelii yoelii.";  
 RL Nature 419:512-519(2002).  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; AABL01001596; EAA17035.1; -; Genomic\_DNA.  
 KW Hypothetical protein.



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FT NON_TER 1 1
SQ SEQUENCE 25 AA; 2842 MW; 61CA94D3F5398F0F CRC64;

Query Match 20.8%; Score 5; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TNNNN 19
   |||||
Db 8 TNNNN 12

RESULT 4
Q26429 DROPS
ID Q26429 DROPS PRELIMINARY; PRT; 12 AA.
AC Q26429;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE DpseYpb protein (Fragment).
GN Name=pb; Synonyms=DpseYpb;
OS Drosophila pseudoobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7237;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92111389; PubMed=1684932;
RA Randazzo F.M., Cribbs D.L., Kaufman T.C.;
RT "Rescue and regulation of proboscipedia: a homeotic gene of the
RT Antennapedia Complex.";
RL Development 113:257-271(1991).
DR EMBL; S77929; AAB20845.1; -; Genomic_DNA.
DR PIR; A44874; A44874.
DR FlyBase; FBgn0012734; DpseYpb.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1377 MW; 4608DB18E355A5B3 CRC64;

Query Match 16.7%; Score 4; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 NNNN 19
   |||||
Db 8 NNNN 11

RESULT 5
Q36731 HUMAN
ID Q36731 HUMAN PRELIMINARY; PRT; 16 AA.
AC Q36731;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Voltage-dependent anion channel (Fragment).
GN Name=VDAC5P; Synonyms=VDAC3;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94292188; PubMed=7517385;
RA Blachly-Dyson E., Baldini A., Litt M., McCabe E.R., Forte M.;
RT "Human genes encoding the voltage-dependent anion channel (VDAC) of
RT the outer mitochondrial membrane: mapping and identification of two
RT new isoforms.";
RL Genomics 20:62-67(1994).
DR EMBL; S75494; AAD14175.1; -; Genomic_DNA.
DR HGNC; HGNC:12676; VDAC5P.
DR GO; GO:0005739; C:mitochondrion; NAS.
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DR GO; GO:0008308; F:voltage-gated ion-selective channel activity; NAS.
DR GO; GO:0006820; P:anion transport; NAS.
FT NON_TER 1 1
SQ SEQUENCE 16 AA; 1607 MW; 05B3FE870C1F296B CRC64;

Query Match 16.7%; Score 4; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 NNSS 21
   |||||
Db 8 NNSS 11

RESULT 6
Q4YCW9 PLABE
ID Q4YCW9 PLABE PRELIMINARY; PRT; 17 AA.
AC Q4YCW9;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Hypothetical protein (Fragment).
GN ORFNames=P8406143.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAA01006411; CAA01006411.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 1 1
SQ SEQUENCE 17 AA; 2069 MW; 56020C69D44FA945 CRC64;

Query Match 16.7%; Score 4; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 NNNN 19
   |||||
Db 7 NNNN 10

RESULT 7
Q7M2F6 NICPL
ID Q7M2F6 NICPL PRELIMINARY; PRT; 19 AA.
AC Q7M2F6;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Endopeptidase Clp (EC 3.4.21.92) chain P (Fragment).
OS Nicotiana plumbaginifolia (leafwort-leaved tobacco).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4092;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Fejes E., Engler D., Maliga P.;
RT "Extensive homologous chloroplast DNA recombination in the pt14
RT Nicotiana somatic hybrid.";
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RL Theor. Appl. Genet. 79:28-32(1990).
DR PIR; PC1323; PC1323.
DR GO; GO:0008462; F:endorpeptidase Clp activity; IEA.
FT NON_TER 19
SQ SEQUENCE 19 AA; 2155 MW; CF63C012B1EBF689 CRC64;

Query Match
Best Local Similarity 16.7%; Score 4; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 SSFY 23
Db 7 SSFY 10

RESULT 8
Q9RSN8_CLOBO PRELIMINARY; PRT; 19 AA.
AC Q9RSN8
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Neurotoxin type A HN+ 17 kDa subunit (Fragment).
OS Clostridium botulinum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1491;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=92143938; PubMed=1781887;
RA Somers E., DasGupta B.R.
RT "Clostridium botulinum types A, B, C1, and E produce proteins with or
RT without hemagglutinating activity: do they share common amino acid
RT sequences and genes?";
RL J. Protein Chem. 10:415-425(1991).
RL PIR; S67990; S67990.
DR InterPro; IPR008903; Botulinum_HA-17.
DR Pfam; PF05588; Botulinum_HA-17; 1.
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2186 MW; B9FD6ED06D1ACA18 CRC64;

Query Match
Best Local Similarity 16.7%; Score 4; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KSIF 11
Db 15 KSIF 18

RESULT 9
O19726_HUMAN PRELIMINARY; PRT; 20 AA.
AC O19726
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE HLA-DRB3 protein (Fragment).
GN Name=HLA-DRB3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86233452; PubMed=3012569;
RA Angelini G., de Preval C., Gorski J., Mach B.;
RT "High-resolution analysis of the human HLA-DR polymorphism by
RT hybridization with sequence-specific oligonucleotide probes [published
RT erratum appears in Proc Natl Acad Sci U S A 1986 Sep;83(17):6664].";
RL Proc. Natl. Acad. Sci. U.S.A. 83:4489-4493(1986).

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DR EMBL; M13562; AAA59797.1; -; Genomic_DNA.
DR PIR; I79432; I79432.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0045012; P:MHC class II receptor activity; IEA.
DR GO; GO:0019884; P:antigen presentation, exogenous antigen; IEA.
DR GO; GO:0019886; P:antigen processing, exogenous antigen via M. . .; IEA.
DR GO; GO:0000695; P:immune response; IEA.
DR InterPro; IPR00353; MHC II beta_N.
DR Pfam; PF00969; MHC II beta; 1.
DR ProDom; PD000328; MHC II beta; 1.
KW MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 2497 MW; EC677B48F424EA88 CRC64;

Query Match
Best Local Similarity 16.7%; Score 4; DB 2; Length 20;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RFDS 5
Db 14 RFDS 17

RESULT 10
Q4XYLO_PLACH PRELIMINARY; PRT; 20 AA.
AC Q4XYLO
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PC104353.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Jance C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC preliminary data.
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAJ01002246; CAJ78000.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 20 AA; 2169 MW; B919D5390293E578 CRC64;

Query Match
Best Local Similarity 16.7%; Score 4; DB 2; Length 20;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 NNNS 20
Db 1 NNNS 4

RESULT 11
Q8N337_HUMAN PRELIMINARY; PRT; 21 AA.
AC Q8N337
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein (Fragment).

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCB1_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Bladder;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RW EMBL; BC028676; AA28676.1; -; mRNA.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 21 AA; 2244 MW; 4A2E9597DA7B2086 CRC64;

Query Match 16.7%; Score 4; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 4e+03; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 19 NSSF 22
DB 14 NSSF 17

RESULT 12
Q4YK89_PLABE PRELIMINARY; PRT; 21 AA.
AC Q4YK89;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=PB401728.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCB1_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriaman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RA "A comprehensive survey of the Plasmodium life cycle by genomic,
RA transcriptomic, and proteomic analyses.";
RT Science 307:82-86(2005).
RL CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CA01004270; CA101573.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 21 AA; 2498 MW; 5284B6D85E64D037 CRC64;

Query Match 16.7%; Score 4; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 4e+03; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 15 TNNN 18
DB 2 TNNN 5

RESULT 13
Q4Z0T6_PLABE PRELIMINARY; PRT; 21 AA.
AC Q4Z0T6;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PB103144.00.0;
OS Plasmodium berghei.

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OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCB1_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriaman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RA "A comprehensive survey of the Plasmodium life cycle by genomic,
RA transcriptomic, and proteomic analyses.";
RT Science 307:82-86(2005).
RL CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CA01004270; CA101573.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 21 AA; 2457 MW; 0BF3DB8FF930C7P4 CRC64;

Query Match 16.7%; Score 4; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 4e+03; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 16 NNNN 19
DB 9 NNNN 12

RESULT 14
Q7S122_NEUCR PRELIMINARY; PRT; 22 AA.
AC Q7S122;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Predicted protein.
GN Name=NCU04571.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCB1_TaxID=5141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Iankiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothre G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamysisselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmari S.A.,
RA DeSouza C.C., Glas L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RA "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
RL CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABX01000468; EAA29041.1; -; Genomic_DNA.
SQ SEQUENCE 22 AA; 2684 MW; 628E72662E7BBA89 CRC64;

Query Match 16.7%; Score 4; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.1e+03; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 16 NNNN 19

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Db          18 NNNN 21
||||
RESULT 15
Q8WSY1 ANOGA
ID Q8WSY1_ANOGA PRELIMINARY; PRT; 22 AA.
AC Q8WSY1_
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Anopheles gambiae (African malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=7165;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GASUA; TISSUE=Salivary gland;
RX MEDLINE=22057806; PubMed=12062411; DOI=10.1016/S0014-5793(02)02578-4;
RA Lanfrancotti A., Lombardo F., Santolamazza F., Veneri M.,
RA Castrignano T., Coluzzi M., Arca' B.;
RT "Novel cDNAs encoding salivary proteins from the malaria vector
RT Anopheles gambiae."
RL FEBS Lett. 517:67-71(2002).
DR EMBL; AJ419880; CAD12040.1; -; mRNA.
KW Hypothetical protein.
FT NON_TER 22 22
SQ SEQUENCE 22 AA; 2395 MW; 429DAF6FA0D39C2 CRC64;

Query Match 16.7%; Score 4; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SIFE 12
|||
Db 18 SIFE 21

Search completed: January 20, 2006, 17:55:55
Job time : 84 secs
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